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(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



WO 03/042661 A2

METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

5 CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/340,376, filed December 14, 2001; Attorney Docket Number 018501-006400US, filed February 8, 2002; USSN 60/347,211, filed January 8, 2002; USSN 60/334,393, filed November 29, 2001; USSN 60/335,394, filed November 15, 2001; USSN 60/347,349, filed January 10, 2002; USSN 60/368,809, filed March 29, 2002; USSN 60/409,450, filed September 9, 2002; USSN 60/359,077, filed February 20, 2002; USSN 60/386,614, filed June 5, 2002; USSN 60/356,714, filed February 13, 2002; USSN 60/397,775 filed July 22, 2002; USSN 60/332,464, filed November 21, 2001; USSN 60/397,845, filed July 22, 2002; USSN 60/370,110, filed April 4, 2002; USSN 60/396,839, filed July 16, 2002; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002; each of which is incorporated herein by reference for all purposes. The application also incorporates by reference PCT/US02/29560; PCT/US02/02242; and PCT/US02/17594.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer and other diseases; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of these conditions. The invention further relates to methods for identifying and using agents and/or targets that modulate these conditions.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is in Japan.

Cancers share the characteristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over

70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases. Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

5 Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis, prognosis, and treatment of cancer patients.

10 Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be
15 tolerated, e.g., reproductive organs, especially those absent in one sex. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies
20 (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic
25 intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for determining the presence or absence of a
30 pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell.

In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-80; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is suspected of having the pathology or cancer.

Compositions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as described in Tables 2A-80; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targeting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80; and determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression

of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

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DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for

10 treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN:

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20 System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American

25 Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM

30 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini

- (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznick (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwer, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic

Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901; 5 Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the 10 invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., 15 using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also 20 be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

25 Tables 2B-76B provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in diseased samples (see Tables 1-3), particularly sequences involved in angiogenesis, arthritis, prostate cancer, breast cancer, colorectal cancer, cervical cancer, bladder cancer, head and neck cancer, esophageal cancer, lung cancer, ovarian cancer, pancreatic cancer, renal cancer, stomach cancer, skin 30 cancer, testicular cancer, uterine cancer, glioblastoma, Ewing sarcoma, soft tissue sarcoma, and lung fibrosis. Tables 2A-80 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-80; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-80 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a "cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is

typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is about 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from about 20 to 600, usually about 50 to 200, more usually about 100 to 150, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-

scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787.

One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its

native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts,

(et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein;

Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805, Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively

insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including

radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; chemoattracting moieties, immune modulators (micA/B), or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is

achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid

sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to

8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times

5 background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32°-48° C depending on primer length. For
10 high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high
15 stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy
20 permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar
25 stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a cancer protein includes the determination of a parameter that is indirectly
30 or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact

inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for

inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 2A-80.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

5 Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

10 An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these
15 light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild
20 conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant
25 DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies,
30 many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in

Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, effector function, chemoattractant, immune modulator, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis

and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the cancer sequences are from humans; however, cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained using the techniques outlined below.

Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based

upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and
5 non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are
10 applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and
15 disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not
20 necessary (e.g., where organs may be dispensible, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or
25 non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the
30 GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases,

e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have
5 been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher
10 being preferred.

Informatics

The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development,
15 and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1-3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA).

Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).
20

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access
25 to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.
30

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others.

Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is available.

For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with

navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxevanis, et al. (2001) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Wiley; Mount (2001)

Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999)

Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxeavanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999)

- 5 Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the
 10 Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with
 15 data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another
 20 tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

25 The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of
 30 magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention

provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method
5 for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount
10 of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed,
15 Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line,
20 wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes
25 generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a
30 query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute

the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

5 The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can
10 be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal
15 comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

 The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be
20 stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different
25 samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning: Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the
30 smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

Characteristics of cancer-associated proteins

Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus.

5 Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase
10 activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In
15 addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH
20 domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.
25 One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420 ; Bateman, et al. (1999) Nuc.
30 Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may

have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated

molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

5 Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are
10 typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated that a transmembrane protein can be made soluble by
15 removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal
20 sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion
25 into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic
30 markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of cancer nucleic acids

As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally
5 determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment
10 may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the
15 shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g.,
20 moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-80, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of
25 the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent
30 parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or
5 binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and
10 the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid
15 support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

20 The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but
25 are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably
30 fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Natl. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The cancer protein may also be made as a fusion protein, using available techniques. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of cancer proteins

Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will
5 elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are sometimes made by
10 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's
15 properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain,
20 e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same
immune response as the naturally-occurring analog, although variants also are selected to
25 modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of
30 a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminy and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seriny, threony, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57 and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases.

5 See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

10 Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-
15 terminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide
20 with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science
25 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer
5 sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

10 In addition, cancer proteins can be made that are longer than those encoded by the nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

15 Antibodies to cancer proteins

In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell
20 receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

25 Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 2A-80 or
30 fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

5 The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent.

10 Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line
15 using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or
20 more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

25 In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and
30 preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95).

5 Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S.
10 Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

15 By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are
20 raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the cancer proteins against which antibodies are raised are
25 secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may
30 bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, target a drug loaded liposome, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells. See, e.g., USSN 09/544,494.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce

deleterious side effects that may be associated with the untargeted therapeutic moiety. Antibody fragments may be used to target toxin loaded liposomes.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

Detection of cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably
5 labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl
10 phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or
15 corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or
20 diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following
25 separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with
30 from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins.

5 Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

10 In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

15 In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes
20 which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene
25 expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined
30 above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or
5 by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

10 In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of
15 drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be
20 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal
25 versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

30 The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell.

Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of cancer

Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

5 The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

 Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another
10 embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially
15 expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

 In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to
20 modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be
25 identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics, e.g., toxin loaded liposomes, to the treated cancer tissue sample.

 Thus, in one embodiment, a test compound is administered to a population of cancer
30 cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

5 Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

10 Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein
15 need to change.

 In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes
20 are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another
25 embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

 Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a
30 non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

5 In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.

10 Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test
15 compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second
20 sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

25 Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

30 Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

5 A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may
10 be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a
15 cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including
20 chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the
25 compound.

In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising
30 administration of a cancer inhibitor.

In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss; Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) Nature Genet. 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^3H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^3H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, Freshney (1998), *supra*.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al.(1970) J. Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum; Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or
5 immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the
10 endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the
15 chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be
20 used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected
25 into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction
30 (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer
Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

5 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general
10 review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-
15 45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface
20 receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the
25 target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating cancer in cells or organisms are
30 provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene
5 encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386. Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other
10 inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic
15 purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one
25 endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to
30 a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

5 In a preferred embodiment, the cancer genes are used as probes to determine the number of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as
20 the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and
25 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary,
30 vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294.; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in
5 immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p.
10 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al.
15 (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de
20 Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance
25 designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham,
30 Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient.

5 This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S.
10 Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide
15 fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are available for therapeutic
20 administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a
25 cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a
30 cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs affected by disease, referred to in Tables 2A and 3A, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

- 5 blood vessels/angiogenesis: hemangiomas, lymphangiomas, angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma, wound healing, tissue remodeling, psoriasis, ischemic, heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atherosclerosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, lymphadenitis, lymphangitis, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented villonodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (keloid), birth control, uterine fibroids
- 10 bladder: carcinoma in situ, papillary carcinomas, transitional cell carcinoma, squamous cell carcinoma
bone: Ewing sarcoma, sarcomas arising from skeletal and extraskelatal connective tissues, including the peripheral nervous system (e.g. chondrosarcoma, osteosarcoma)
brain: glioblastoma, oligodendroglioma, anaplastic astrocytoma, meningioma, medulloblastoma, neuroblastoma, ependymoma, schwannoma, craniopharyngioma, pineoblastoma, pineocytoma, neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, neuroma, ganglioneuroma
- 15 breast: ductal carcinoma in situ, lobular carcinoma in situ
cervix: cancer of the cervix, vagina, or vulva
colon/rectum: precancerous colorectal disease (e.g., neoplastic polyps (adenomas), familial adenomatous polyposis, ulcerative colitis), colon cancer, e.g., epithelial tumor (e.g., adenocarcinoma, mucinous adenocarcinoma, signet-ring cell adenocarcinoma, squamous cell carcinoma, adenosquamous carcinoma, undifferentiated carcinoma, unclassified carcinoma), carcinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leiomyosarcoma, others), inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease (granulomatous colitis), dysplasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary villous carcinoma, mucinous adenocarcinoma, melanoma)
- 20 esophagus: premalignant or predisposing conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, lung, or cervix), gastroduigestive carcinomas (e.g., cancers of the stomach, colon, or rectum)
fibrosis: lung fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scleroderma, wound healing
- 25 head and neck: tumors of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, lip, larynx, hypopharynx, salivary glands, paragangliomas, esophagus
kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypernephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, angiomyolipoma, oncocytoma
leukocytes: acute lymphoblastic leukemia/lymphoma, chronic lymphocytic leukemia, follicular lymphoma, large B-cell lymphoma, Burkitt lymphoma, plasma cell neoplasms, mantle cell lymphoma, lymphoplasmacytic lymphoma, peripheral T-cell lymphoma, adult T-cell leukemia/lymphoma, Hodgkin disease, acute myelogenous leukemia, chronic myelogenous leukemia, thymic hyperplasia, hairy cell leukemia, malignant transformation, inappropriate activation or abnormalities of leukocytes (e.g., immature, precursor B (pre-B) or precursor T (pre-T) lymphocytes, monocytes, neutrophils, eosinophils, basophils, dendritic cells, lymphoblasts), arthritis, inflammation, leukocytosis, lymphadenitis, lymphangitis, bacteremia, chronic nonspecific lymphadenitis, psoriasis, wound healing
- 30 liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor bile conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder or bile duct
- 35 lung: lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer
- ovary: ovarian carcinoma (e.g., epithelial (serous tumors, mucinous tumors, endometrioid tumors), germ cell (e.g., teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosa stromal cell tumors)), fallopian tube carcinoma, peritoneal carcinoma, leiomyoma
- 40 pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma, pancreatoblastoma, duct-ectatic mucin-hypersecreting tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes mellitus, chronic pancreatitis
prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumors, transitional cell carcinoma, carcinoma in situ, and basal cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia, prostatitis
- 45 skin/melanoma: melanoma, lentigo (common benign localized hyperplasia of melanocytes), nevocellular nevi (congenital or acquired neoplasm of melanocytes), actinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Merkel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histiocytes within the dermis), dermal vascular tumors, seborrheic keratoses (benign tumor), acanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinomas of the skin, lung, cervix, esophagus, uterus, head, neck, or bladder
- 50 soft tissue: soft tissue tumors (e.g., fibrosarcoma, liposarcoma, leiomyosarcoma, histiocytoma, fibrohistiocytic sarcoma) smooth muscle tumors (e.g., rhabdomyoma, rhabdomyosarcoma) tumors of the blood and lymph vessels (e.g., angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma), perivascular tumors (e.g., glomus tumors, hemangiopericytoma), synovial tumors (e.g., mesothelioma), neural tumors (e.g., neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, extraskelatal Ewing's sarcoma, schwannoma, neuroma, ganglioneuroma), paraganglioma, extraskelatal cartilaginous and osseous tumors (e.g., chondrosarcoma, osteosarcoma), pluripotent mesenchymal tumors, epithelioid sarcomas, rhabdoid tumors, desmoplastic small cell tumors, alveolar sarcoma
- 55 stomach: adenocarcinoma, squamous cell carcinoma, adenocanthoma, carcinoid, leiomyosarcoma, gastritis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas
- 60 testicles: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, choriocarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblastomas), adnexal and paratesticular tumors (e.g., mesotheliomas, soft tissue sarcomas, and adnexal of the rete testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)
- uterus: epithelial tumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed mullerian tumors, adenosarcoma)

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70 Tables 2B-2Z, 76B, and 79B list accession numbers for Pkeys lacking UnigeneID's for Tables 2A-2Z, 76A, and 79A, respectively. For each probeset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

75 Tables 2C-2Z, 76C, and 79C list genomic positioning for Pkeys lacking Unigene ID's and accession numbers in Tables 2A-2Z, 76A, and 79A, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Table 2A, Disease Indications and Preferred Utilities for Selected Genes

80 Table 2A provides preferred disease indications and preferred utilities for about 413 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number
UnigeneID: Unigene ID number

Unigene Title: Unigene gene title
 Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), leio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
 Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAccn; UnigenelD; Unigene Title; Disease; Utility

102892; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk; mAb+diag+s.m.
 104865; T79340; Hs.22575; B-cell CLL/lymphoma 6, member ; angio; CTL
 104978; A1199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, lung, pros, blad, stom; CTL
 109424; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb+s.m.
 110765; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag
 110906; AA035211; Hs.17404; SOX7 SRY (sex determining regi; angio, blad; CTL
 115522; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; GTL
 116176; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL
 118695; AK000465; Hs.50081; KIAA1199 protein; colon, lung; diag
 123049; BE047680; Hs.211869; dickkopf (Xenopus laevis) homo; EWS; mAb+diag
 131486; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.
 133370; AF245505; Hs.72157; Adican; breast, lung, panc; diag
 310016; AW449612; Hs.152475; ESTs; colon; CTL
 322303; A1357412; Hs.157601; ESTs; colon, pros, fibro, breast; CTL+diag
 400289; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, cerv, ovar, headnk, esoph; mAb+diag+s.m.
 400297; A1127076; Hs.288381; hypothetical protein DKFZp5640; breast, blad, colon, pros; mAb
 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regula; breast, ovar, pros, stom, uter, blad, lung, headnk; mAb
 400843; ; NM_003105; Homo sapiens sortil; blad; s.m.
 402075; ; ENSP00000251056; Plasma membra; blad, lung, headnk, cerv, mela, esoph; mAb+diag
 402901; ; NM_025206; Homo sapiens hypoth; blad ; CTL
 404287; ; FGENESH predicted novel CUB-do; panc, lung, colon, uter, esoph; mAb+s.m.
 404682; ; ortholog of mouse polydomain p; panc; diag
 404875; ; NM_022819; Homo sapiens phosph; blad; CTL+s.m.
 404977; ; Insulin-like growth factor 2 (; blad, ovar, sarc; mAb+diag
 405033; ; C1002652; gjl544327[sp]Q04799; blad; s.m.
 406400; ; kallikrein 8 (neuropsin/ovasin; ovar, uter; diag
 406964; M21305; ; FGENES predicted novel secrete; angio, blad, fibro, sarc; diag
 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299; glio, blad; CTL
 407792; A1077715; Hs.39384; putative secreted ligand homol; ovar, uter, cerv, panc; mAb+diag
 407811; AW190902; Hs.40098; cysteine knot superfamily 1, B; blad, panc, stom, uter, lung, esoph; diag
 407836; T79340; Hs.22575; B-cell CLL/lymphoma 6, member ; angio; CTL
 407975; X89426; Hs.41716; endothelial cell-specific mole; angio, renal; diag
 408243; Y00787; Hs.624; interleukin 8; blad, stom, headnk, cerv, lung, angio, esoph, panc; diag
 408367; AK001178; Hs.44424; Homo sapiens orphan neurotrans; mela; mAb+s.m.
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family ; pros, lung, fibro, uter, glio, cerv, ovar; mAb
 408380; AF123050; Hs.44532; diubiquitin; lung, blad, headnk, panc, stom, fibro, esoph, mela; CTL
 408482; NM_000676; Hs.45743; adenosine A2b receptor; lung, esoph, headnk, colon; mAb+s.m.
 408562; A1436323; Hs.31141; roundabout (axon guidance rece; uter, fibro, sarc; mAb+s.m.
 408790; AW580227; Hs.47860; neurotrophic tyrosine kinase, ; lung; mAb+s.m.
 408908; BE296227; Hs.250822; serine/threonine kinase 15; blad, lung, headnk, stom, colon; s.m.
 409041; AB033025; Hs.50081; Hypothetical protein, XP_05186; uter, ovar, lung, colon, stom, headnk, breast, panc; CTL+diag
 409079; W87707; Hs.82065; interleukin 6 signal transduce; breast, pros; mAb+s.m.
 409103; AF251237; Hs.112208; XAGE-1 protein; lung; CTL
 409178; BE393948; Hs.50915; kallikrein 5; ovar, breast, mela; diag
 409220; BE243323; Hs.51233; tumor necrosis factor receptor; angio, renal, colon, stom; mAb+s.m.
 409420; Z15008; Hs.54451; laminin, gamma 2 (niceln (100k; lung, headnk, panc, stom, cerv, esoph, blad; diag
 409632; W74001; Hs.55279; serine (or cysteine) proteinase; lung, blad, headnk; diag
 409663; A1743750; Hs.98306; KIAA1862 protein; renal; CTL
 409757; NM_001898; Hs.123114; cystatin SN; panc, stom, lung, blad; diag
 409889; AW630041; Hs.56937; suppression of tumorigenicity ; colon, ovar, pros; mAb+s.m.
 409893; AW247090; Hs.57101; minichromosome maintenance def; lung, cerv, blad, test, esoph; CTL+s.m.
 409956; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, panc, ovar, colon, headnk, lung, blad, esoph; diag
 410001; AB041036; Hs.57771; kallikrein 11; ovar, pros, uter, cerv, lung ; diag
 410055; AJ250839; Hs.58241; gene for serine/threonine prot; renal; s.m.
 410153; BE311926; Hs.15830; hypothetical protein FLJ12691; renal,blad; CTL
 410274; AA381807; Hs.336402; hypoxia-inducible protein 2; lung, renal; CTL
 410309; BE043077; Hs.278153; alpha-2,8-sialyltransferase II; panc; s.m.
 410407; X66839; Hs.63287; carbonic anhydrase IX; renal, lung, colon, stom, ovar, uter, blad, sarc; mAb+s.m.
 410418; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 411274; NM_002776; Hs.69423; kallikrein 10; colon, ovar, uter, cerv, headk, panc; diag
 411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA13; renal; mAb+s.m.
 411773; NM_006799; Hs.72026; protease, serine, 21 (testisin; ovar; diag
 411975; A1916058; Hs.144583; 3'UTR of: dead ringer (Drosoph; test, colon; CTL
 412078; X69699; Hs.73149; paired box gene 8; ovar; CTL
 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, headnk, breast, ovar, panc, angio, test, mela; s.m.
 412314; AA825247; Hs.356084; G protein-coupled receptor 27 ; ovar, uter, test; mAb+s.m.
 412609; Z48804; Hs.74124; ocular albinism 1 (Nettleship; mela; s.m.
 412628; A1972402; Hs.306051; hypothetical protein MGC2648; pros; diag
 412709; AL022327; Hs.74518; KIAA0027 protein; glio, sarc; mAb+s.m.
 412719; AW016610; Hs.816; ESTs; lung, headnk, blad, glio, cerv, sarc; s.m.
 412959; D87458; Hs.75090; KIAA0282 protein; glio; CTL+s.m.
 413048; M93221; Hs.75182; mannose receptor, C type 1; fibro, panc; mAb

- 413063; AL035737; Hs.75184; chitinase 3-like 1 (cartilage ; glio, ovar, blad, lung ; diag
 413278; BE563085; Hs.833; interferon-stimulated protein.; panc, lung, blad, breast, cerv, ovar, headnk, esoph, mela; CTL+s.m.
 413324; V00571; Hs.75294; corticotropin releasing hormon; blad; diag
 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxyg; blad, lung, mela, fibro, uter, sarc; s.m.
 413554; AA319146; Hs.75426; secretogranin II (chromogranin; panc, glio; diag
 413719; BE439580; Hs.75498; small inducible cytokine subfa; leuk, panc, lung, headnk, cerv, colon, uter, stom, esoph; diag
 414555; N98569; Hs.76422; phospholipase A2, group IIA (p; pros; s.m.
 414577; AI056548; Hs.378938; hypothetical protein FLJ20992 ; angio; CTL+diag
 414774; X02419; Hs.77274; plasminogen activator, urokina; lung, blad, headnk, panc, stom, ovar, esoph; diag
 414812; X72755; Hs.77367; monokine induced by gamma inte; breast, blad, lung, fibro, panc, colon, headnk, cerv, stom, renal, ovar, test, mela, esoph; diag
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; lung, ovar, stom, colon, cerv, headnk, test; s.m.
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; blad, lung, ovar, test; s.m.
 414991; C17898; ; Homo sapiens up-regulated by B; fibro, lung; mAb+diag
 415138; C18356; Hs.295944; tissue factor pathway inhibito; angio, panc, stom, lung, uter; CTL+diag
 415539; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb+s.m.
 415668; AW957684; Hs.306814; Homo sapiens lysyl oxidase-lik; mela; diag
 415669; NM_005025; Hs.78589; serine (or cysteine) proteinas; lung; mAb+diag+s.m.
 415817; U88967; Hs.78867; protein tyrosine phosphatase, ; lung, glio, headnk, cerv, mela, esoph, fibro; mAb+s.m.
 415929; AA724373; Hs.304950; Homo sapiens mucollipin-3 (MCOL; mela; mAb
 416091; AF295370; Hs.283082; defensin, beta 3; headnk, esoph, mela; CTL+diag
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient; lung, headnk, colon, uter, stom; CTL+s.m.
 416250; AA581386; Hs.73452; Kremen 2; esoph, lung, cerv, ovar; mAb+s.m.
 416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyme); ovar, uter; diag
 416636; N32536; Hs.42645; solute carrier family 16 (mono; breast, panc, uter, mela; mAb+s.m.
 416658; U03272; Hs.79432; fibrillin 2 (congenital contra; lung, ovar, uter, blad, angio, test, sarc; diag
 416836; D54745; Hs.80247; cholecystokinin; pros, EWS, glio ; diag
 416857; AA188775; Hs.292453; FGENSESH predicted TM containin; glio; mAb+s.m.
 416965; N26223; Hs.160436; MDAC1; fibro, ovar, uter; mAb
 417034; NM_006183; Hs.80962; neurotensin; lung, headnk, cerv; diag
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; blad, lung, headnk, cerv, esoph; diag
 417166; AA431323; Hs.42146; Paired box protein Pax-3; mela, sarc; CTL
 417389; BE260964; Hs.82045; midkine (neurite growth-promot; ovar, lung, blad, uter, cerv, panc, stom, mela, test, colon, sarc; mAb+diag
 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glyco; panc, breast, blad, lung, headnk, cerv, uter, ovar, stom, renal; mAb
 417771; AA804698; Hs.82547; retinoic acid receptor respond; blad, cerv, panc, pros, ovar; mAb
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; lung, panc, breast, ovar, headnk, stom, sarc; CTL
 417931; W95642; Hs.82961; trefoil factor 3 (intestinal); ovar, panc, stom, colon, uter, pros; diag
 417933; X02308; Hs.82962; thymidylate synthetase; blad, lung, angio, colon, panc, esoph; s.m.
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (in; lung, blad, fibro, headnk, panc, stom, colon, ovar, esoph, mela; mAb+diag+s.m.
 418030; BE207573; Hs.83321; neuromedin B; glio, panc; diag
 418064; BE387287; Hs.83384; S100 calcium-binding protein, ; mela; diag
 418281; U09550; Hs.1154; oviductal glycoprotein 1, 120k; uter, ovar; CTL+diag
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk, panc, cerv, mela, sarc; s.m.
 418506; AA084248; Hs.372651; Unknown protein for MGC:29643 ; angio, ovar, glio, uter, lung, blad, panc, mela, sarc; mAb+diag
 418526; BE019020; Hs.85838; solute carrier family 16 (mono; lung, blad, renal, panc, stom, colon, ovar; mAb+s.m.
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via d; esoph, headnk; s.m.
 418678; NM_001327; Hs.87225; cancer/testis antigen (NY-ESO-; lung, blad, stom, ovar, panc, esoph, cerv, sarc; CTL
 418738; AW388633; Hs.6682; solute carrier family 7, (cat; angio, lung, ovar, blad, colon, stom, panc, uter, leuk; mAb+s.m.
 418830; BE513731; Hs.348874; hypothetical protein MGC4816; lung; CTL
 418867; D31771; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad, renal; mAb+s.m.
 419080; AW150835; Hs.18878; hypothetical protein FLJ21620; renal, lower uter, lung; CTL
 419121; AA374372; Hs.89626; parathyroid hormone-like hormo; lung, esoph, headnk, blad; diag
 419171; NM_002846; Hs.89655; protein tyrosine phosphatase, ; lung; mAb+s.m.
 419172; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio, renal; mAb+s.m.
 419183; U60669; Hs.89663; cytochrome P450, subfamily XXI; blad, lung, headnk, panc; CTL+s.m.
 419216; AU076718; Hs.164021; small inducible cytokine subfa; panc, lung, stom, cerv, pros, headnk, esoph; diag
 419235; AW470411; Hs.288433; neurotrophin; panc, fibro, headnk, lung; mAb+diag
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ovar, pros, lung, breast, uter, test, panc, stom, sarc; mAb+s.m.
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-fami; glio, omuc, stom, lung, panc, colon, renal, uter; mAb+s.m.
 419556; U29615; Hs.91093; chitinase 1 (chitotriosidase); lung, fibro, test; mAb+diag
 419704; AA429104; Hs.45057; ESTs; glio; CTL+s.m.
 419723; AL120193; Hs.339810; longevity assurance (LAG1, S. ; glio; mAb+diag
 419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; blad, lung, colon, ovar, test, esoph, mela, sarc; CTL+s.m.
 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA; fibro, stom, blad, esoph, uter; diag
 420159; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 fi; blad, stom; mAb
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; lung, mela, sarc; s.m.
 420370; Y13645; Hs.97234; uroplakin 2; blad; mAb
 420440; NM_002407; Hs.97644; mammaglobin 2; ovar, uter, cerv; diag
 420502; AF060877; Hs.99236; regulator of G-protein signal; headnk, glio, cerv, mela; CTL+s.m.
 420610; AI683183; Hs.99348; distal-less homeo box 5; uter, endo, lung; CTL
 420737; L08096; Hs.99899; CD70 ; tumor necrosis factor ; renal; mAb+s.m.
 420876; AA918425; Hs.177744; FGENSES predicted novel protein; panc, blad; s.m.
 421066; AU076725; Hs.101408; branched chain aminotransferas; blad, lung; CTL+s.m.
 421110; AJ250717; Hs.1355; cathepsin E; blad, panc, stom, lung, fibro, ovar, esoph; sm+diag
 421340; F07783; Hs.1369; decay accelerating factor for ; angio, panc, stom; diag
 421379; Y15221; Hs.103982; small inducible cytokine subfa; breast, panc, headnk, lung, stom, blad, cerv, colon, leuk, fibro, test, mela, esoph; diag
 421471; U90545; Hs.327179; solute carrier family 17 (sodi; renal; mAb+s.m.
 421474; U76362; Hs.104637; solute carrier family 1 (gluta; lung; mAb+s.m.
 421524; AA312082; Hs.105445; GDNF family receptor alpha 1; breast; mAb+s.m.
 421552; AF026692; Hs.105700; secreted frizzled-related prot; breast, ovar, panc, cerv, uter, pros, lung, stom, headnk; diag
 421563; NM_006433; Hs.105806; granulysin; fibro; diag
 421574; AJ000152; Hs.105924; defensin, beta 2; headnk, lung; CTL+diag
 421582; AI910275; Hs.350470; trefoil factor 1 (breast cance; breast, panc, lung, omuc; diag

- 421659; NM_014459; Hs.106511; protocadherin 17; fibro; mAb
 421753; BE314828; Hs.107911; ATP-binding cassette, sub-fam1; lung; mAb+s.m.
 421817; AF146074; Hs.108660; ATP-binding cassette, sub-fam1; lung, cerv, headnk, blad; mAb+s.m.
 421829; AB018330; Hs.108708; calcium/calmodulin-dependent p; pros; s.m.
 5 422048; NM_012445; Hs.288126; spondin 2, extracellular matr; panc, pros, sarc; diag
 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, ; pros; s.m.
 422109; S73265; Hs.1473; gastrin-releasing peptide; panc, lung, colon, fibro; diag
 422158; L10343; Hs.112341; protease inhibitor 3, skin-der; headnk, blad, lung, cerv, stom, esoph; diag
 10 422192; AA305159; Hs.113019; fls485; mela; s.m.
 422260; AA315993; Hs.105484; regenerating gene type IV; colon, omuc, stom, panc; mAb+diag
 422282; AF019225; Hs.114309; apolipoprotein L; blad, lung, headnk, renal; diag
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45; lung, blad, test, cerv, headnk, esoph; s.m.
 422330; D30783; Hs.115263; epiregulin; panc, colon, blad; mAb+diag
 15 422397; AJ223366; Hs.116051; MYEOV Myeloma overexpressed ge; panc, stom, colon, esoph, renal, blad; CTL+s.m.
 422424; AI186431; Hs.296638; prostate differentiation facto; blad, panc, pros, angio, colon, stom, lung, mela; diag
 422578; AF239666; Hs.1545; caudal type homeo box transcrip; colon; CTL
 422627; BE336857; Hs.118787; transforming growth factor, be; colon, renal, sarc; mAb+diag
 20 422765; AW409701; Hs.1578; baculoviral IAP repeat-contain; lung, blad; s.m.
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; blad, cer, lung, uter, angio, stom, test; s.m.
 422867; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar, pros, panc, lung, colon, uter, sarc; diag
 422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell ; ovar, blad, panc, lung, headnk, colon, stom; CTL+s.m.
 423161; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar, blad; mAb+s.m.
 423184; NM_004428; Hs.1624; ephrin-A1; pros, panc, renal, colon; mAb+s.m.
 25 423242; AL039402; Hs.125783; DEME-6 protein; breast, renal, ovar, pros, colon; CTL
 423508; AW604297; Hs.129711; hepatitis A virus cellular rec; renal, colon; mAb
 423593; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
 423634; AW959908; Hs.1690; heparin-binding growth factor ; lung, blad, headnk, panc; diag
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (m; blad, lung, headnk, ovar, panc, colon, stom, uter, cerv, esoph, test; mAb+diag+s.m.
 30 423936; U77629; Hs.135639; achaete-scute complex (Drosoph; colon, stom, ovar; CTL
 423961; D13666; Hs.136348; periostin (OSF-2os); breast, colon, blad, lung, fibro, panc, headnk, ovar, mela, sarc; mAb+diag
 424008; R02740; Hs.137555; putative chemokine receptor; G; blad, headnk, stom, cerv, esoph; mAb+s.m.
 424046; AF027866; Hs.138202; serine (or cysteine) proteinase; headnk, lung, cerv; diag
 424321; W74048; Hs.1765; lymphocyte-specific protein ty; mela, fibro; s.m.
 35 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); lung, colon, test; s.m.
 424411; NM_005209; Hs.146549; crystallin, beta A2; panc, sarc; s.m.
 424502; AF242388; Hs.149585; lengsin; lung; s.m.
 424503; NM_002205; Hs.149609; integrin, alpha 5 (fibronectin; panc, pros, angio, blad, lung; mAb+s.m.
 424620; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (ge; headnk, panc, lung, blad, uter, cerv, colon, stom, test, mela, sarc; diag
 40 424735; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.
 424825; AF207069; Hs.153357; procollagen-lysine, 2-oxogluta; mela; CTL+s.m.
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a); ovar, blad, lung, headnk, panc, stom; s.m.
 424917; AI636208; Hs.96901; hypothetical protein FLJ23049; fibro, uter, ovar; CTL
 424943; AU077260; Hs.153924; death-associated protein kinase; fibro; s.m.
 45 425009; X58288; Hs.154151; protein tyrosine phosphatase, ; renal, fibro; mAb+s.m.
 425071; NM_013989; Hs.154424; deiodinase, lodothyronine, typ; pros, colon, stom, uter, cerv, headnk, esoph, panc; diag
 425115; R44664; Hs.123956; downstream of: G protein-coupl; glio; mAb+s.m.
 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, ovar, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph, sarc; mAb+diag+s.m.
 50 425263; NM_001197; Hs.155419; BCL2-interacting killer (apopt; pros; s.m.
 425322; U63630; Hs.155637; protein kinase, DNA-activated,; lung, headnk; s.m.
 425535; AB007937; Hs.158287; syndecan 3; mela, glio; mAb+s.m.
 425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, headnk, cerv, esoph, blad; mAb
 425721; AC002115; Hs.159309; uroplakin 1A; blad; mAb
 55 425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homo; endo, uter, colon; CTL+diag
 425734; AF056209; Hs.159396; peptidylglycine alpha-amidatin; lung; s.m.
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; ovar, uter, lung; mAb+diag
 425842; AI587490; Hs.159623; NK-2 (Drosophila) homolog B; panc, glio; s.m.
 425852; AK001504; Hs.159651; death receptor 6, TNF superfam; blad, lung, headnk; mAb+s.m.
 60 425883; AL137708; Hs.161031; Homo sapiens mRNA; cDNA DKFZp4; blad, panc; mAb
 425998; AU076629; Hs.165950; fibroblast growth factor recep; renal; mAb+s.m.
 426028; NM_001110; Hs.172028; a disintegrin and metalloprote; blad; mAb+diag
 426215; AW963419; Hs.155223; stanniocalcin 2; breast, lung, renal, colon, ovar, uter; mAb+diag
 426227; U67058; Hs.154299; Human proteinase activated rec; panc, lung, colon, esoph, stom; mAb+s.m.
 65 426322; J05068; Hs.2012; transcobalamin I (vitamin B12 ; panc, blad, stom; diag
 426344; H41821; Hs.322469; transcriptional activator of t; glio; CTL+s.m.
 426427; M86699; Hs.169840; TTK protein kinase; ovar, lung, headnk, cerv, colon, uter, stom, test; CTL+s.m.
 426451; AI908165; Hs.169946; GATA-binding protein 3 (T-cell; blad, breast; s.m.
 426514; BE616633; Hs.170195; bone morphogenetic protein 7 (; ovar, colon, blad, lung, cerv; mAb+diag
 70 426600; NM_003378; Hs.171014; VGF nerve growth factor induci; mela, sarc; diag
 426761; AI015709; Hs.172089; PORIMIN Pro-oncogene receptor f; lung, esoph, pros, uter, panc, colon, ovar, headnk; mAb+s.m.
 426812; AF105365; Hs.172613; solute carrier family 12 (pota; renal; mAb+s.m.
 426890; AA393167; Hs.41294; ESTs; renal, colon, ovar, uter, stom; CTL
 427239; BE270447; Hs.355512; ubiquitin carrier protein; lung, blad, test, mela, sarc; CTL+s.m.
 427335; AA448542; Hs.278444; G antigen 7B; lung, headnk, blad, mela, esoph, sarc; CTL
 75 427343; AI880044; Hs.176977; protein kinase C binding prote; glio; CTL+s.m.
 427722; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, stom, panc; CTL
 427747; AW411425; Hs.180655; serine/threonine kinase 12; blad, lung, ovar, stom, test, esoph, sarc; s.m.
 427923; AW274357; Hs.301406; FGENSEH predicted 11 TM protei; mela; mAb
 427969; NM_001963; Hs.2230; epidermal growth factor (beta-; panc; mAb+diag
 80 428093; AW594506; Hs.104830; ESTs; ovar, panc; CTL
 428179; AI127772; Hs.380877; serum/glucocorticoid regulated; breast; s.m.
 428187; AI687303; Hs.285529; G protein-coupled receptor 49; ovar, uter, colon, stom; mAb+s.m.
 428242; H55709; Hs.2250; leukemia inhibitory factor (ch; ovar, panc, leuk, lung; diag

- 428296; NM_003058; Hs.183572; solute carrier family 22 (orga; renal; mAb+s.m.
 428330; L22524; Hs.2256; matrix metalloproteinase 7 (ma; uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela; mAb+diag+s.m.
 428368; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk, stom, esoph, colon; diag
 428392; H10233; Hs.2265; secretory granule, neuroendocr; panc; diag
 5 428450; NM_014791; Hs.184339; KIAA0175 gene product; ovar, cerv, panc, lung, blad, mela; s.m.
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S; lung, blad, colon, uter, ovar; s.m.
 428484; AF104032; Hs.184601; solute carrier family 7 (catio; lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela; mAb+s.m.
 428486; AW583497; Hs.184604; pancreatic polypeptide; panc; diag
 10 428505; AL035461; Hs.2281; chromogranin B (secretogranin ; panc, lung; diag
 428513; BE220806; Hs.184697; plexin C1; mela, panc, breast stom, headnk; mAb
 428579; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.
 428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosoph; blad, ovar, pros, lung, stom, test; CTL+s.m.
 428698; AA852773; Hs.334838; KIAA1866 protein; breast, colon, lung, panc, stom, headnk, ovar, EWS; mAb
 15 428748; AW593206; Hs.98785; Ksp37 protein; lung, sarc; diag
 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; ovar, cerv, lung, panc, stom, renal; diag
 428778; AK000530; Hs.193326; fibroblast growth factor recep; ovar; mAb+s.m.
 428953; AA306610; Hs.348183; tumor necrosis factor receptor; cerv, panc, colon, stom, headnk, renal; mAb+diag
 428969; AF120274; Hs.194689; artemin; lung, cerv; diag
 20 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG; stom, panc, colon, ovar, fibro; mAb+s.m.
 429149; AW193360; Hs.197962; Homolog of mouse ADP-ribosylat; glio; mAb+s.m.
 429211; AF052693; Hs.198249; gap junction protein, beta 5 (; lung, blad, headnk, cerv, esoph, stom, mela; mAb+s.m.
 429263; AA019004; Hs.198396; ATP-binding cassette, sub-fami; lung; mAb+s.m.
 429276; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad, glio; mAb+s.m.
 25 429353; AL117406; Hs.335891; ATP-binding cassette transport; breast, pros ; mAb+s.m.
 429547; AW009166; Hs.99376; FGENESH predicted novel secret; panc, headnk, lung, ovar; diag
 429610; AB024937; Hs.211092; LUNC protein; PLUNC (palate lu; lung, fibro; mAb+diag
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, reg; lung, mela; s.m.
 429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin; leio; mAb+s.m.
 30 430147; R60704; Hs.234434; hairy/enhancer-of-split relate; glio; s.m.
 430178; AW449612; Hs.152475; 3'UTR of: achaete-scute comple; colon, stom, ovar; CTL
 430377; NM_001922; Hs.301865; dopachrome tautomerase (dopach; mela; CTL
 430413; AW842182; Hs.241392; small inducible cytokine A5 (R; fibro, esoph, mela; diag
 430486; BE062109; Hs.241551; chloride channel, calcium acti; lung, blad, headnk, cerv, esoph; mAb+s.m.
 35 430822; AJ005371; Hs.248017; glyceraldehyde-3-phosphate deh; mela, sarc; s.m.
 431130; NM_006103; Hs.2719; HE4; epididymis-specific, whey; ovar, uter; diag
 431462; AW583672; Hs.256311; granin-like neuroendocrine pep; panc, lung, glio, test; diag
 431515; NM_012152; Hs.258593; EDG-7 (endothelial differenti; ovar, pros, lung, blad; mAb+s.m.
 431620; AA126109; Hs.264981; 2'-5'-oligoadenylate synthetas; esoph, cerv; CTL+s.m.
 431629; AU077025; Hs.265827; interferon, alpha-inducible pr; panc, uter, cerv, stom, esoph, mela; mAb+diag
 40 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD4; ovar, panc, blad, headnk, mela, renal; mAb+s.m.
 431745; AW972448; Hs.163425; Novel FGENESH predicted cadher; fibro, ovar, uter; mAb
 431840; AA534908; Hs.2860; POU domain, class 5, transcrip; test, renal, blad; CTL
 431846; BE019924; Hs.271580; uroplakin 1B; lung, blad, headnk, uter, cerv, stom, ovar; mAb+diag
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, cerv, headnk, ovar, colon, pros, panc, breast, esoph, test, mela; mAb+diag
 45 432101; AI918950; Hs.123642; EphA3; pros, panc, EWS sarc; s.m.
 432179; X75208; Hs.2913; EphB3; ovar, colon; mAb+s.m.
 432196; AW300888; Hs.273230; hypothetical protein FLJ10830; renal; CTL
 432201; AI538613; Hs.298241; Transmembrane protease, serine; breast, colon, ovar, stom, panc, uter, cerv, lung ; mAb+diag+s.m.
 50 432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis; renal; CTL
 432596; AJ227471; Hs.278461; matrilin 3; panc, breast, sarc; diag
 432606; NM_002104; Hs.3066; granzyme K (serine protease, g; renal, breast, lung, stom, hepC, fibro, leuk; CTL
 432829; W60377; Hs.57772; ESTs; blad; CTL+s.m.
 432874; W94322; Hs.279651; melanoma inhibitory activity; panc, stom, mela, sarc; diag
 55 432990; AL036071; Hs.279899; tumor necrosis factor receptor; pros, renal; mAb+s.m.
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; colon, breast, lung, blad, cerv, uter, test, mela; s.m.
 433447; U29195; Hs.3281; neuronal pentraxin II; mela, esoph, colon, renal; diag
 433848; AF095719; Hs.93764; carboxypeptidase A4; headnk, esoph, lung; s.m.
 433867; AK000596; Hs.3618; hippocalcin-like 1; renal; CTL
 434206; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung, stom; CTL+s.m.
 60 434276; AF123659; Hs.93605; leucine zipper, putative tumor; mela; s.m.
 434293; NM_004445; Hs.3796; EphB6; blad, pros; s.m.
 435013; H91923; Hs.110024; NM_020142: Homo sapiens NADH:ub; renal, lung, sarc; CTL
 435472; AW972330; Hs.283022; triggering receptor expressed ; glio; mAb
 435505; AF200492; Hs.211238; interleukin-1 homolog 1; lung, headnk; diag
 65 436456; AW292677; Hs.248122; melanin-concentrating hormone ; mela, glio; mAb+s.m.
 436480; AJ271643; Hs.87469; putative acid-sensing ion chan; glio; mAb+s.m.
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubi; lung, blad, colon, ovar, uter, headnk, test; s.m.
 436576; AI458213; Hs.77542; ESTs; renal, panc, headnk, lung; mAb+s.m.
 436608; AA628980; Hs.192371; down syndrome critical region ; blad, lung, sarc; CTL+s.m.
 70 436895; AF037335; Hs.5338; carbonic anhydrase XII; breast, renal, ovar, glio; mAb+s.m.
 436961; AW375974; Hs.156704; ESTs; lung, panc, renal, uter, colon ; CTL
 436982; AB018305; Hs.5378; spondin 1, (f-spondin) extrace; ovar, fibro; diag
 437016; AU076916; Hs.5398; guanine monophosphate synthetas; lung, blad, cerv, esoph, colon, headnk; s.m.
 437044; AL035864; Hs.69517; differentially expressed in Fa; headnk, cerv, lung, blad, breast, pros, ovar, stom, esoph; CTL
 75 437789; AI581344; Hs.127812; ESTs, Weakly similar to T17330; lung; CTL
 437852; BE001836; Hs.256897; putative GPCR; blad, lung; mAb+s.m.
 438380; T06430; Hs.6194; chondroitin sulfate proteoglyc; glio, mela; diag
 438549; BE386801; Hs.21858; trinucleotide repeat containin; mela, sarc; CTL+diag
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, s; uter, stom, pros, fibro; mAb
 439223; AW238299; Hs.250618; UL16 binding protein 2; lung, headnk, cerv, esoph, leuk, blad, colon; mAb
 439477; W69813; Hs.58042; ESTs, Moderately similar to GF; lung; mAb+s.m.
 439569; AW602166; Hs.222399; CEGP1 protein; breast, pros, blad; diag
 80 439606; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv, esoph; mAb+s.m.

- 439738; BE246502; Hs.9598; sema domain, immunoglobulin do; blad, lung, cerv, renal; mAb+s.m.
 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; renal, cerv, pros, headnk, colon, test, sarc; mAb
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containin; blad, ovar, lung, headnk, test; s.m.
 440065; W03476; Hs.266331; Homo sapiens Fc receptor homol; mela; diag
 440304; BE159984; Hs.125395; hepatitis A virus cellular rec; renal, colon, blad; mAb+s.m.
 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin; glio, ovar, uter, renal, hepC; mAb+diag
 440672; AF083811; Hs.7345; MAD1 (mitotic arrest deficient; mela; s.m.
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog; lung, blad, headnk, test, mela, esoph; s.m.
 442117; AW664964; Hs.128899; ESTs; hypothetical protein for; breast, lung, blad, panc, headnk, stom, ovar, pros, sarc; mAb+s.m.
 442133; AW874138; Hs.129017; ESTs; type Ia transmembrane p; ovar, uter; mAb
 442275; AW449467; Hs.54795; Homo sapiens secretoglobulin, fa; fibro; diag
 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; fibro, ovar, uter; CTL
 443105; X96753; Hs.9004; chondroitin sulfate proteoglyc; mela; mAb+diag
 443247; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL
 443324; R44013; Hs.164225; ESTs; fibro; mAb+diag
 443426; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad, stom, test, mela, sarc; CTL
 443595; AF169312; Hs.9613; PPAR(gamma) angiotensin relat; renal; diag
 443646; AI085198; Hs.164226; Thrombospondin 1; angio, panc, uter; diag
 443859; NM_013409; Hs.9914; follistatin; lung, cerv, headnk, blad, esoph; diag
 443987; AW163123; Hs.10071; seven transmembrane protein TM; renal; mAb+s.m.
 444006; BE395085; Hs.334762; type I transmembrane protein F; panc, colon, lung, ovar, renal, esoph, mela, blad, stom, cerv; mAb
 444090; S69115; Hs.10306; natural killer cell group 7 se; fibro, renal, mela; diag
 444371; BE540274; Hs.239; forkhead box M1; lung, headnk, blad, glio, test, mela; s.m.
 444381; BE387335; Hs.283713; hypothetical protein BC014245; breast, colon, blad, lung, panc, headnk, ovar, stom, uter, renal, angio, test, mela, esoph, sarc; CTL+diag
 444488; AW192879; Hs.355660; ancient conserved domain prote; renal; mAb+s.m.
 444527; NM_005408; Hs.11383; small inducible cytokine subfa; fibro, esoph; diag
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk, cerv; mAb+diag
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon, esoph; CTL+s.m.
 445417; AK001058; Hs.12680; a disintegrin-like and metallo; panc, headnk, stom, lung, esoph, sarc, colon; diag
 445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; ovar, blad, uter, breast, lung, headnk, renal, fibro, panc, cerv, sarc; mAb+diag
 445891; AW391342; Hs.199460; DPCR1 protein; stom, panc, esoph, omuc, esoph; mAb
 445895; D29954; Hs.13421; KIAA0056 protein; pros; CTL
 446051; BE048061; Hs.37054; ephrin-A3; colon, breast; mAb+diag
 446163; AA026880; Hs.25252; prolactin receptor; breast, cerv, uter; mAb+s.m.
 446341; AL040763; Hs.310735; FGENESH prediction similar to; mela; mAb+s.m.
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (ost; ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter, sarc; diag
 446650; AB016625; Hs.15813; solute carrier family 22 (orga; renal; mAb+s.m.
 446921; AB012113; Hs.16530; small inducible cytokine subfa; breast, panc, headnk, lung, fibro, mela; diag
 447033; AI357412; Hs.157601; Predicted gene: Eos cloned; se; colon, pros, fibro, breast, ovar, lung, panc, sarc; CTL+diag
 447072; D61594; Hs.17279; tyrosylprotein sulfotransferas; glio, panc; CTL+s.m.
 447131; NM_004585; Hs.17466; retinoic acid receptor respond; renal, breast, stom, lung, mela, ovar; mAb+s.m.
 447208; BE315291; Hs.237971; hypothetical protein MGC5627; esoph, stom, colon; CTL+diag
 447269; NM_004861; Hs.17958; cerebroside (3'-phosphoadenyly; renal; CTL
 447342; AI199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, blad, pros, lung, stom, ovar; CTL
 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; mela; s.m.
 448243; AW369771; Hs.367688; integrin, beta 8; ovar, uter, lung, stom, headnk, glio, panc; mAb+s.m.
 448610; NM_006157; Hs.21602; nel (chicken)-like 1; mela, sarc; diag
 448733; NM_005629; Hs.187958; solute carrier family 6 (neuro; lung, renal; mAb+s.m.
 448844; AI581519; Hs.177164; FGENESH predicted novel cell s; panc, lung, stom, omuc; mAb+s.m.
 449032; AA045573; Hs.22900; nuclear factor (erythroid-deri; colon, test, stom; CTL+s.m.
 449048; Z45051; Hs.22920; similar to S68401 (cattle) glu; panc, ovar, uter, glio, headnk, lung, sarc; mAb
 449444; AW818436; Hs.351306; solute carrier family 16 (mono; renal, panc; mAb+s.m.
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor; lung, panc, renal, stom, hepC, fibro, leuk, mela; mAb+s.m.
 449720; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL
 449722; BE280074; Hs.23960; cyclin B1; headnk, blad, lung, panc, angio, test, mela, esoph; s.m.
 450001; NM_001044; Hs.406; solute carrier family 6 (neuro; renal; mAb+s.m.
 450375; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc, lung, esoph, colon, sarc; mAb+diag+s.m.
 450531; AW301032; Hs.203800; (BC017500) Similar to hypothet; colon; CTL
 450701; H39960; Hs.288467; hypothetical protein XP_098151; lung, headnk, panc, breast, stom, ovar, esoph, colon, sarc; mAb+diag
 450726; AW204600; Hs.355462; HUMPSBA Human pulmonary surfa; fibro, lung; s.m.
 450931; N25156; Hs.25648; tumor necrosis factor receptor; lung, renal; mAb+s.m.
 450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; blad, lung, ovar, panc; diag
 451310; AW250651; Hs.26213; Human DNA sequence from clone; colon, panc; CTL
 451527; AF022813; Hs.26518; transmembrane 4 superfamily me; renal; mAb
 451537; R56631; Hs.26550; retinoid X receptor, gamma; mela; CTL+s.m.
 451668; Z43948; Hs.326444; cartilage acidic protein 1; blad, ovar, lung; mAb+diag
 451939; U80456; Hs.27311; single-minded (Drosophila) hom; pros; CTL
 451979; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.
 451988; AF263928; Hs.27410; papillomavirus regulatory fact; renal; CTL
 452017; AF109302; Hs.27495; prostate cancer associated pro; pros; s.m.
 452097; AB002364; Hs.27916; a disintegrin-like and metallo; ovar; mAb+s.m.+diag
 452190; H26735; Hs.91668; Homo sapiens clone PP1498 unkn; breast, stom, panc; mAb
 452194; AI694413; Hs.373599; olfactory receptor, family 2, ; stom, panc, renal, colon, mela, fibro; mAb+s.m.
 452203; X57522; Hs.352018; transporter 1, ATP-binding cas; cerv, esoph, blad, stom, mela, renal; mAb+s.m.
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast, headnk, panc, stom, lung, esoph, fibro; diag
 452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-i; blad, breast, panc, headnk, stom, lung, leuk, renal, esoph; diag
 452431; U88879; Hs.29499; toll-like receptor 3; renal, hepC; mAb
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung, headnk, ovar, stom, uter, panc; mAb
 452838; U65011; Hs.30743; preferentially expressed antig; lung, ovar, breast, mela, test, esoph, renal, sarc; CTL
 452862; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like a; headnk, breast, colon, leuk, lung, blad, esoph, stom, sarc; mAb+diag
 453195; BE241876; Hs.32352; hypothetical protein DKFZp434K; renal; CTL
 453496; AA442103; Hs.33084; solute carrier family 2 (facil; renal, pros; mAb+s.m.

453837; AL138387; Hs.256126; baculoviral IAP repeat-contain; renal, mela, sarc; s.m.
 453968; AA847843; Hs.62711; High mobility group (nonhiston; lung, uter, blad, test; CTL+s.m.
 456546; A1690321; Hs.203845; KCNK15 potassium channel, subf; ovar; mAb+s.m.
 456662; NM_002448; Hs.1494; msh (Drosophila) homeo box hom; uter, ovar; CTL
 457133; M54968; Hs.351221; v-Ki-ras2 Kirsten rat sarcoma; panc; s.m.
 457489; A1693815; Hs.127179; cryptic gene; panc, pros, lung; diag
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein; lung, cerv, headnk; mAb+diag
 458079; A1796870; Hs.381220; Homo sapiens similar to RIKEN; mela, fibro, sarc; mAb
 458627; AW088642; Hs.97984; SRY (sex determining region Y); ovar, uter, test; CTL

TABLE 2B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414991	1785136_1	D78831 C17898 D78863

TABLE 2C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
402901	8894222	Minus	175426-175667
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 3A. Disease Indications and Preferred Utilities for Selected Genes

Table 3A provides preferred disease indications and preferred utilities for about 2709 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number
 UnigenelD: Unigene ID number
 Unigene Title: Unigene gene title
 Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), lei (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
 Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAccn; UnigenelD; Unigene Title; Disease; Utility

100125; R02740; Hs.137555; putative chemokine receptor; G; blad; mAb+s.m.
 100131; D12485; Hs.11951; ectonucleotide pyrophosphatase; breast; mAb
 100147; D13666; Hs.136348; periostin (OSF-2os); breast, colon, blad, lung, fibro, panc; mAb+diag
 100241; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; blad; mAb
 100299; D49493; Hs.2171; growth differentiation factor; EWS; diag
 100335; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.
 100365; A1878927; Hs.79284; mesoderm specific transcript; colon, pros; diag
 100372; NM_014791; Hs.184339; KIAA0175 gene product; ovar, lung, cerv, panc; s.m.
 100405; AW291587; Hs.82733; nidogen 2; angio; diag
 100420; D86983; Hs.118893; Melanoma associated gene; breast, pros, lung, colon, angio, leuk; diag
 100448; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G; breast; mAb+s.m.
 100452; D87742; Hs.241552; KIAA0268 protein; pros; diag
 100559; NM_000094; Hs.1640; collagen, type VII, alpha 1 (e; lung; CTL+s.m.
 100654; A03758; Hs.184411; NM_000477; Homo sapiens albumi; pros; diag
 100655; A03758; Hs.184411; Empirically selected from AFFX; pros; diag
 100668; L05424; Hs.169610; CD44 antigen (homing function; lung, breast; mAb
 100824; A1393237; Hs.193989; runt-related transcription fac; ovar; CTL+s.m.
 100930; J04129; Hs.82269; progesterone-associated endomet; lung; diag
 101063; D54745; Hs.80247; cholecystokinin; pros, EWS; diag
 101097; BE245301; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad; mAb+s.m.
 101104; AW862258; Hs.169266; neuropeptide Y receptor Y1; breast, EWS; mAb
 101192; BE247295; Hs.78452; solute carrier family 20 (phos; angio; mAb+s.m.
 101193; L20861; Hs.152213; wingless-type MMTV integration; blad, lung; diag
 101249; L18964; Hs.1904; protein kinase C, iota; ovar; s.m.

- 101261; D30857; Hs.82353; protein C receptor, endothelia; angio; mAb+s.m.
 101389; AW951430; Hs.78888; diazepam binding inhibitor (GA; pros; mAb+s.m.
 101431; BE185289; Hs.1076; small proline-rich protein 1B; lung, blad; diag
 101447; M21305; ; gb:Human alpha satellite and s; angio, blad; diag
 101461; N98569; Hs.76422; phospholipase A2, group IIA (p; pros; diag
 101485; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, ovar; mAb
 101506; J02931; Hs.62192; coagulation factor III (thromb; pros; mAb
 101526; NM_002197; Hs.220529; aconitase 1, soluble; lung, colon, headnk, panc; mAb
 101543; M31166; Hs.2050; pentaxin-related gene, rapidly; angio, ovar; diag
 101545; BE246154; Hs.154210; endothelial differentiation, s; angio; mAb+s.m.
 101560; AW958272; Hs.347326; intercellular adhesion molecul; angio; mAb
 101626; M57399; Hs.44; pleiotrophin (heparin binding ; lung; diag
 101649; AW959908; Hs.1690; heparin-binding growth factor ; lung, blad; diag
 101714; M68874; Hs.211587; phospholipase A2, group IVA (c; angio; s.m.
 101724; L11690; Hs.198689; bullous pemphigoid antigen 1 (; breast, pros, blad, lung; mAb+CTL
 101741; NM_003199; Hs.326198; transcription factor 4; angio; CTL+s.m.
 101748; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, blad, headnk, cerv; mAb
 101759; M80244; Hs.184601; solute carrier family 7 (catio; lung, glio, blad, headnk; mAb+s.m.
 101791; M83822; Hs.62354; cell division cycle 4-like; pros; s.m.
 101804; M86699; Hs.169840; TTK protein kinase; ovar, lung, blad, cerv; CTL+s.m.
 101806; AA586894; Hs.112408; S100 calcium-binding protein A; lung, breast, blad; diag
 101809; M86849; Hs.323733; gap junction protein, beta 2, ; colon, blad, lung, panc, headnk; mAb
 101839; AA446644; Hs.692; GA733-2 antigen; epithelial gt; ovar, pros; mAb
 101845; U88967; Hs.78867; protein tyrosine phosphatase, ; lung, glio, headnk, cerv; mAb+s.m.
 101851; BE260964; Hs.82045; midkine (neurite growth-promot; lung, blad, ovar, breast, panc; mAb+diag
 102009; BE245149; Hs.82643; protein tyrosine kinase 9; ovar; s.m.
 102012; BE259035; Hs.118400; singed (Drosophila)-like (sea ; angio; diag
 102024; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
 102048; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
 102076; BE299197; Hs.179665; cyclin-dependent kinase inhibi; pros; CTL+s.m.
 102125; NM_006456; Hs.288215; sialyltransferase; breast, lung, ovar; s.m.
 102136; AA300576; Hs.85769; acidic 82 kDa protein mRNA; ovar; diag
 102151; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
 102154; U17760; Hs.75517; laminin, beta 3 (nicein (125kD; lung, blad, headnk; diag
 102178; AW178761; Hs.227948; serine (or cysteine) proteinas; blad; mAb+diag
 102187; U20325; Hs.1707; cocaine- and amphetamine-regul; breast; diag
 102193; AL036335; Hs.313; secreted phosphoprotein 1 (ost; ovar, lung, fibro; diag
 102200; AA232362; Hs.317432; branched chain aminotransferas; ovar; s.m.
 102208; U22961; Hs.184411; gb:Human mRNA clone with simil; pros; diag
 102211; BE314524; Hs.78776; putative transmembrane protein; breast, blad; mAb
 102283; AW161552; Hs.83381; guanine nucleotide binding pro; angio; CTL+s.m.
 102297; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
 102304; AF015224; Hs.46452; mammaglobin 1; breast; diag
 102305; AL043202; Hs.90073; chromosome segregation 1 (yeas; ovar, lung, blad ; diag
 102348; U37519; Hs.87539; aldehyde dehydrogenase 3 famil; lung, blad; s.m.
 102380; U40434; Hs.155981; mesothelin; ovar; diag
 102394; NM_003816; Hs.2442; a disintegrin and metalloprote; panc; s.m.
 102455; U48705; Hs.75562; discoidin domain receptor fami; breast; mAb
 102457; NM_001394; Hs.2359; dual specificity phosphatase 4; breast; s.m.
 102522; BE250944; Hs.183556; solute carrier family 1 (neutr; pros; mAb
 102581; AU077228; Hs.77256; enhancer of zeste (Drosophila); blad, EWS, leuk; CTL+s.m.
 102610; U65011; Hs.30743; preferentially expressed antig; lung, ovar; CTL
 102623; AW249285; Hs.37110; melanoma antigen, family A, 9; lung, blad; mAb+CTL
 102669; U71207; Hs.29279; eyes absent (Drosophila) homol; lung, pros; CTL+s.m.
 102696; BE540274; Hs.239; forkhead box M1; lung, blad; s.m.
 102725; AB026187; Hs.374280; protocadherin 11; EWS; mAb
 102742; U79293; Hs.159264; Human clone 23948 mRNA sequenc; breast, ovar ; diag
 102745; AW753865; Hs.74376; olfactomedin related ER locali; EWS; diag
 102803; H48299; Hs.26126; claudin 10; ovar; mAb
 102829; NM_006183; Hs.80962; neurensin; lung, ovar, headnk; diag
 102836; U94320; Hs.158330; neuropeptide Y receptor Y5; EWS; mAb
 102852; V00571; Hs.75294; corticotropin releasing hormon; blad; diag
 102898; NM_002205; Hs.149609; integrin, alpha 5 (fibronectin; angio, blad, lung, pros; mAb+s.m.
 102915; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, ovar; mAb+diag+s.m.
 102917; AL016712; Hs.287797; integrin, beta 1 (fibronectin ; angio; mAb
 102927; BE512730; Hs.65114; keralin 18; ovar; diag
 102968; AU076611; Hs.154672; methylene tetrahydrofolate deh; ovar; s.m.
 102994; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 103003; A1910275; Hs.350470; trefoil factor 1 (breast cance; breast, panc; diag
 103021; BE001596; Hs.85266; integrin, beta 4; lung blad; mAb
 103036; M13509; Hs.83169; matrix metalloproteinase 1 (in; angio, colon, blad, lung, leuk, ovar, headnk, fibro, panc, stom; mAb+diag+s.m.
 103037; BE018302; Hs.2894; placental growth factor, vascu; angio; diag
 103060; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, lung, ovar, panc; mAb+diag+s.m.
 103080; AU077231; Hs.82932; cyclin D1 (PRAD1: parathyroid ; breast, EWS; diag
 103095; NM_005424; Hs.78824; tyrosine kinase with immunoglo; angio; mAb
 103111; NM_006103; Hs.2719; epididymis-specific, whey-acid; ovar, uter; diag
 103119; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, ovar, colon, pros, panc, breast; mAb+diag
 103206; X72755; Hs.77367; monokine induced by gamma inte; breast, lung; diag
 103210; X72925; Hs.69752; desmocollin 1; pros; mAb
 103280; U84722; Hs.76206; cadherin 5, type 2, VE-cadheri; angio, fibro; mAb+s.m.
 103299; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar; mAb+s.m.
 103312; Y12642; Hs.3185; lysosomal; lung, blad; mAb
 103365; X90908; Hs.74126; fatty acid binding protein 6, ; blad; diag

- 103408; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
 103478; BE514982; Hs.38991; S100 calcium-binding protein A; lung, blad, headnk; diag
 103587; BE270266; Hs.82128; 5T4 oncofetal trophoblast glyc; breast, blad, lung; mAb
 103594; AI368680; Hs.816; SRY (sex determining region Y); lung, glio; s.m.
 103692; AW137912; Hs.227583; Homo sapiens chromosome X map; angio; mAb+s.m.
 103739; AA115173; ; gb:zn30d02.s1 Stratagene neuro; pros; s.m.
 103767; BE244667; Hs.348996; CGI-100 protein; angio; diag
 103989; AA315993; Hs.105484; regenerating gene type IV; colon, omuc; mAb+diag
 104052; NM_002407; Hs.97644; mammaglobin 2; ovar; diag
 104115; AF183810; Hs.26102; opposite strand of: trichorhi; breast; mAb
 104252; AF002246; Hs.210863; cell adhesion molecule with ho; ovar; diag
 104301; AA768491; Hs.6783; hypothetical protein FLJ22724; ovar; diag
 104308; N25117; Hs.355957; ribosomal protein S26; pros; diag
 104394; AA129551; Hs.172129; Homo sapiens cDNA: FLJ21409 fi; colon; diag
 104542; R29657; ; gb:F1-1179D 22 week old human; pros; diag
 104608; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb
 104659; AW969769; Hs.100343; ESTs; EWS; diag
 104660; BE298665; Hs.14846; Homo sapiens mRNA; cDNA DKFZp5; uter, colon, pros; mAb
 104667; AI239923; Hs.63931; dachshund (Drosophila) homolog; breast, pros, colon; diag
 104689; AA420450; Hs.380088; Plakophilin; lung; diag
 104691; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
 104755; T49951; Hs.9029; DKFZP434G032 protein; breast, colon; diag
 104764; AI039243; Hs.278585; ESTs; angio; diag
 104786; AA027167; Hs.380438; KIAA0955 protein; angio; CTL+s.m.
 104877; AI138635; Hs.22968; intron of VEGFR; renal; diag
 104888; AW939591; Hs.5940; mucin 13, epithelial transmembr; colon, stom, uter; mAb+s.m.
 104919; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 fis; breast, cerv, uter; mAb+s.m.
 104943; AF072873; Hs.114218; frizzled (Drosophila) homolog; ovar; mAb+s.m.
 104954; AW250651; Hs.26213; Human DNA sequence from clone; colon; diag
 104971; BE311926; Hs.15830; hypothetical protein FLJ12691; blad; CTL
 105012; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad; CTL
 105038; AW503733; Hs.9414; KIAA1488 protein; breast, angio; CTL+s.m.
 105039; AA907305; Hs.36475; ESTs; breast; diag
 105093; AL137566; Hs.32405; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 105149; BE089288; Hs.8958; Homo sapiens cDNA FLJ12024 fis; pros; diag
 105175; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; colon, lung; mAb
 105263; AW388633; Hs.6682; solute carrier family 7, (cat); angio, lung, ovar, blad, panc; mAb+s.m.
 105298; BE387790; Hs.26369; hypothetical protein FLJ20287; ovar, lung; diag
 105301; AW352357; Hs.7457; MAGE1 protein; EWS; diag
 105316; AI671245; Hs.24835; hypothetical protein FLJ14594; EWS; mAb
 105329; AA234561; Hs.22862; ESTs; breast, pros; CTL+s.m.
 105330; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 105370; AF179274; Hs.22791; transmembrane protein with EGF; pros; mAb+s.m.
 105500; AW602166; Hs.222399; CEGP1 protein; breast, pros; diag
 105503; AW963624; Hs.31707; ESTs, Weakly similar to YEW4_Y; pros, breast, colon; CTL+s.m.
 105507; BE268348; Hs.380963; CCR4-NOT transcription complex; colon; diag
 105516; AK001269; Hs.30738; hypothetical protein FLJ10407; ovar; diag
 105564; BE616694; Hs.288042; hypothetical protein FLJ14299; breast; diag
 105645; AW294631; Hs.351270; ESTs; pros; diag
 105715; BE621800; Hs.29444; putative small membrane protei; colon; diag
 105743; BE246502; Hs.9598; sema domain, immunoglobulin do; breast, lung; mAb+s.m.
 105746; AW151952; Hs.46679; hypothetical protein FLJ20739; breast; CTL+s.m.
 105777; R42755; Hs.23096; ESTs; breast; diag
 105782; H09748; Hs.57987; B-cell CLL/lymphoma 11B (zinc); EWS; CTL+s.m.
 105826; AA478756; Hs.194477; E3 ubiquitin ligase SMURF2; angio; s.m.
 105990; AI690586; Hs.29403; hypothetical protein FLJ22060; breast; diag
 106000; AW194426; Hs.20726; ESTs; breast; diag
 106012; AI240665; Hs.352537; ESTs; breast, lung; diag
 106014; AF123094; Hs.180566; mucosa associated lymphoid tis; leuk; diag
 106063; BE260415; Hs.348198; hypothetical protein FLJ20262; pros; diag
 106066; AW274357; Hs.301406; hypothetical protein PP3501; mela; CTL+s.m.
 106111; AW875398; Hs.6451; PRO0659 protein; EWS; CTL+s.m.
 106124; H93366; Hs.7567; branched chain aminotransferas; angio; s.m.
 106155; AA425414; Hs.33287; nuclear factor I/B; breast, pros, angio; diag
 106373; AW503807; Hs.21907; histone acetyltransferase; breast; s.m.
 106400; BE397649; Hs.279607; Homo sapiens cDNA FLJ13634 fis; colon; diag
 106414; BE568205; Hs.28827; mitogen-activated protein kina; breast; s.m.
 106448; Z42061; Hs.27004; ESTs; pros; diag
 106533; AL134708; Hs.145998; ESTs; EWS; diag
 106574; BE044325; Hs.227280; U6 snRNA-associated Sm-like pr; colon; diag
 106579; AA456135; Hs.23023; ESTs; pros; diag
 106632; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk; mAb+diag
 106738; AW149266; Hs.25130; Homo sapiens cDNA FLJ14923 fis; ovar; diag
 106793; H94997; Hs.16450; ESTs; angio; diag
 106844; AA485055; Hs.158213; sperm associated antigen 6; breast; mAb+CTL
 106906; AA861271; Hs.222024; transcription factor BMAL2; lung, blad; diag
 106990; AA280722; Hs.24758; ESTs, Weakly similar to I38022; breast; diag
 107036; AI973016; Hs.15725; hypothetical protein SBB148; pros; diag
 107102; AB037765; Hs.30652; KIAA1344 protein; pros, breast; diag
 107105; AW963419; Hs.155223; stanniocalcin 2; breast; diag
 107136; AV661958; Hs.8207; GK001 protein; breast, colon; diag
 107151; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like a; breast, colon, leuk, lung, blad; mAb+diag
 107216; D51069; Hs.211579; melanoma cell adhesion molecul; angio; diag

- 107248; AW263124; Hs.350547; nuclear receptor co-repressor; breast, colon, pros; mAb+s.m.
 107284; NM_005629; Hs.187958; solute carrier family 6 (neuro; lung; mAb+s.m.
 107385; NM_005397; Hs.16426; podocalyxin-like; angio; diag
 107901; L42612; Hs.335952; keratin 6B; breast, blad, lung; diag
 5 107922; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung; mAb
 107932; AW392555; Hs.18878; hypothetical protein FLJ21620; lung; CTL
 108055; AJ404672; Hs.334483; hypothetical protein FLJ23571; breast, ovar; diag
 108059; S69002; Hs.234773; Homo sapiens cDNA: FLJ22281 fi; ovar; CTL+s.m.
 108153; AW519204; Hs.40808; ESTs; pros; diag
 10 108186; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 108242; AA062746; Hs.355244; gb:zm03g12.s1 Stratagene corne; pros; diag
 108282; AA065142; ; gb:zm50h11.r1 Stratagene fibro; pros; diag
 108505; AA083376; ; gb:zn09g08.s1 Stratagene hNT n; pros; diag
 108679; AA115963; Hs.323423; ESTs, Moderately similar to B ; pros; diag
 15 108695; AB029000; Hs.70823; KIAA1077 protein; breast, colon, lung; diag
 108732; AA258888; Hs.107476; ATP synthase, H+ transporting.; pros; s.m.
 108778; AF133123; Hs.90847; general transcription factor I; ovar; diag
 108828; AK001693; Hs.273344; DKFZP564O0463 protein; breast; diag
 108860; AA133334; Hs.816; ESTs; lung; s.m.
 20 109001; AI056548; Hs.72116; hypothetical protein FLJ20992 ; angio; CTL+diag
 109032; AI219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
 109077; AI732617; Hs.182362; ESTs; blad; diag
 109112; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
 25 109141; AF174600; Hs.5978; ESTs, Highly similar to AF1746; colon; CTL+s.m.
 109166; AA219691; Hs.73625; RAB6 Interacting, kinesin-like; lung, blad, breast, colon, ovar, headnk, EWS; s.m.
 109220; AW958181; Hs.189998; ESTs; pros; diag
 109273; AA375752; Hs.348140; Homo sapiens mRNA; cDNA DKFZp5; breast; diag
 109292; AW975746; Hs.188662; KIAA1702 protein; breast; diag
 30 109454; AA232255; Hs.295232; ESTs, Moderately similar to A4; ovar; diag
 109456; AW956580; Hs.42699; ESTs; angio, panc; diag
 109514; AA234087; Hs.262346; ESTs, Weakly similar to S72482; breast ; diag
 109530; AA908645; Hs.19597; KIAA1694 protein; pros; CTL+s.m.
 109648; H17800; Hs.7154; ESTs; ovar; diag
 35 109680; AB037734; Hs.4993; KIAA1313 protein; ovar; diag
 110009; BE075297; Hs.6614; ESTs, Weakly similar to A43932; breast, colon; diag
 110151; H18835; Hs.31608; hypothetical protein FLJ20041; pros, EWS; diag
 110156; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 110240; AI668594; Hs.176588; ESTs, Weakly similar to CP4Y_H; breast; diag
 40 110278; AF061573; Hs.19492; protocadherin 8; EWS; mAb+s.m.
 110675; H89355; Hs.249159; adrenergic, alpha-2A-, receptor; pros; mAb+s.m.
 110728; AA737108; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.
 110844; AI740792; Hs.167531; methylcrotonyl-Coenzyme A car; pros, pros; s.m.
 110915; BE092285; Hs.29724; hypothetical protein FLJ13187; breast, pros; diag
 45 110971; AI760098; Hs.21411; ESTs; pros; diag
 111157; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
 111179; AK000136; Hs.10760; asporin (LRR class 1); breast, colon; CTL+s.m.
 111185; AJ245671; Hs.12844; EGF-like-domain, multiple 6; ovar, blad; mAb+diag
 111223; AA852773; Hs.334838; KIAA1866 protein; breast, colon, lung, EWS; mAb
 50 111299; AB033091; Hs.355925; KIAA1265 protein; ovar; diag
 111357; BE314949; Hs.87128; hypothetical protein FLJ23309; breast; diag
 111384; N94606; Hs.288969; HSCARG protein; breast; diag
 111900; AF131784; Hs.25318; Homo sapiens clone 25194 mRNA ; breast; diag
 111929; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
 55 112134; R41823; Hs.7413; ESTs; calyntenin-2; breast, EWS; diag
 112244; AB029000; Hs.70823; KIAA1077 protein; breast, colon, blad, lung; diag
 112280; AA863360; Hs.26040; ESTs, Weakly similar to fatty ; breast; s.m.
 112283; L14561; Hs.20952; ATPase, Ca++ transporting, pla; ovar; mAb
 112287; AB033064; Hs.236463; KIAA1238 protein; breast ; diag
 60 112971; Z42387; Hs.83883; transmembrane, prostate androg; colon, pros, pros; mAb+s.m.
 113003; AW292315; Hs.7215; ESTs; EWS; diag
 113021; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
 113047; AI571940; Hs.7549; ESTs; breast, colon; diag
 113073; N39342; Hs.103042; microtubule-associated protein; pros; CTL+s.m.
 65 113168; AW002393; Hs.337629; gb:wu61d05.x1 NCL_CGAP_GC6 Hom; ovar; diag
 113195; H83265; Hs.8881; ESTs, Weakly similar to S41044; angio, lung; diag
 113230; T61430; ; gb:yc06a03.s1 Stratagene lung ; blad; diag
 113361; T79589; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 113374; T79925; Hs.269165; ESTs, Weakly similar to ALU1_H; leuk; diag
 70 113443; AW083920; Hs.16098; claudin 2; colon, panc; mAb
 113471; AI765890; Hs.16341; MAWD binding protein; pros; diag
 113490; BE178110; Hs.173374; Homo sapiens cDNA FLJ10500 fis; colon; diag
 113950; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; breast, pros ; diag
 113970; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
 114124; W57554; Hs.125019; lymphoid nuclear protein (LAF-; breast; diag
 75 114251; H15261; Hs.21948; ESTs; breast; diag
 114292; AI815395; Hs.184641; fatty acid desaturase 2; breast; s.m.
 114334; AB037784; Hs.22941; KIAA1363 protein; ovar; diag
 114407; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, colon, lung; diag
 114452; AI369275; Hs.243010; Homo sapiens cDNA FLJ14445 fis; angio; diag
 80 114480; BE066778; Hs.151678; UDP-N-acetyl-alpha-D-galactosa; breast; s.m.
 114531; AA053033; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 114540; AI904232; Hs.75323; prohibitin; breast; diag
 114542; AW970128; Hs.91011; anterior gradient 2 (Xenopus l; breast, pros; diag

- 114587; AF086009; Hs.296398; gb:Homo sapiens full length in; colon; diag
 114724; R64730.comp; Hs.155986; DEAD/H (Asp-Glu-Ala-Asp/His) b; ovar; CTL+s.m.
 114768; AF212848; Hs.182339; ets homologous factor; pros; breast; colon; CTL+s.m.
 114798; AA159181; Hs.54900; serologically defined colon ca; pros; CTL+s.m.
 114908; AA454985; Hs.54973; cadherin-like protein VR20; pros; diag
 114918; BE165762; Hs.23518; hypothetical protein from BCRA; pros; diag
 114965; A1733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb
 115060; AF052693; Hs.198249; gap junction protein, beta 5 (; lung, blad, headnk; mAb+s.m.
 115221; AW365434; Hs.79741; hypothetical protein FLJ10116; ovar; diag
 115239; BE251328; Hs.73291; hypothetical protein FLJ10881; colon; diag
 115291; BE545072; Hs.122579; hypothetical protein FLJ10461; ovar; lung; CTL+s.m.
 115412; AW131168; Hs.372382; ESTs, Weakly similar to I38022; pros; diag
 115536; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon; CTL+s.m.
 115674; AW992356; Hs.380760; Homo sapiens pyruvate dehydrog; ovar; s.m.
 115675; W87707; Hs.82065; interleukin 6 signal transduce; breast; pros; mAb+s.m.
 115683; AF255910; Hs.54650; junctional adhesion molecule 2; angio, glio; mAb
 115697; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 115719; AW992405; Hs.352406; Homo sapiens, clone IMAGE:3507; pros; breast; colon; CTL+s.m.
 115819; AA486620; Hs.41135; endomucin-2; angio; diag
 115827; AA428000; Hs.283072; actin related protein 2/3 comp; angio; diag
 115844; A1373062; Hs.332938; hypothetical protein MGC5370; pros; diag
 115881; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.
 115892; AA291377; Hs.50831; ESTs; ovar, blad, lung; diag
 115909; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar, lung; diag
 115947; R47479; Hs.94761; KIAA1691 protein; colon; diag
 115978; AL035864; Hs.69517; cDNA for differentially expres; lung, blad, breast, pros, ovar, headnk; CTL
 116003; BE275469; Hs.66493; Down syndrome critical region ; colon; mAb
 116011; AL359053; Hs.57664; Homo sapiens mRNA full length ; breast; diag
 116028; H59799; Hs.42644; thioredoxin-like; ovar, lung; diag
 116107; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag
 116202; BE159395; Hs.294092; ESTs; pros; diag
 116238; AV660717; Hs.47144; DKFZP586N0819 protein; ovar; diag
 116301; AW969706; Hs.293332; ESTs; EWS; diag
 116334; AL038450; Hs.48948; ESTs; pros; diag
 116335; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk; diag
 116393; A1972402; Hs.306051; hypothetical protein MGC2648; pros; diag
 116399; AA889120; Hs.110637; homeo box A10; pros; CTL+s.m.
 116401; AW893940; Hs.59698; ESTs; ovar; diag
 116416; AW753676; Hs.39982; ESTs; ovar; diag
 116470; A1272141; Hs.351928; SRY (sex determining region Y); colon, breast, angio, blad; diag
 116483; A1346201; Hs.76118; ubiquitin carboxyl-terminal es; angio, lung; s.m.
 116610; D80449; Hs.184841; ESTs; pros; diag
 116732; AW152225; Hs.165909; ESTs, Weakly similar to I38022; colon; diag
 116787; AW362955; Hs.356547; Homo sapiens cDNA FLJ14415 fis; pros, breast, colon, pros; mAb
 116962; H79677; ; gb:yu76g10.s1 Soares fetal liv; pros; diag
 117027; AW085208; Hs.130093; ESTs; breast; diag
 117280; M18217; Hs.172129; Homo sapiens cDNA: FLJ21409 fi; breast, colon, pros; diag
 117284; AK001701; Hs.183779; Homo sapiens cDNA FLJ10590 fis; pros; diag
 117320; AB024937; Hs.211092; LUNX protein; PLUNC (palate lu; lung; mAb+diag
 117367; A1041793; Hs.42502; ESTs; breast; diag
 117412; N32536; Hs.42645; solute carrier family 16 (mono; breast, ovar ; mAb+s.m.
 117425; AK000028; Hs.356100; ribosomal protein S24; pros; diag
 117563; AF055634; Hs.44553; unc5 (C.elegans homolog) c; leuk ; diag
 117602; N35020; Hs.44685; C3HC4-like zinc finger protein; EWS; CTL+s.m.
 117921; AA021459; Hs.306480; Homo sapiens mRNA; cDNA DKFZp7; pros ; diag
 117984; AF189723; Hs.106778; ATPase, Ca++ transporting, typ; pros, breast, colon; mAb
 118049; N53145; ; gb:yv55f09.s1 Soares fetal liv; pros; diag
 118314; N48580; Hs.46692; ESTs; blad, lung; diag
 118336; BE327311; Hs.47166; HT021; breast, ovar, blad, pros; CTL+s.m.
 118368; N64339; Hs.48956; gap junction protein, beta 6 (; lung, blad; mAb
 118417; AF080229; ; gb:Human endogenous retrovirus; pros; s.m.
 118472; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag
 118511; N75620; Hs.43157; ESTs; angio; diag
 118901; AW292577; Hs.94445; ESTs; breast; diag
 118905; AW973708; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
 119018; AA631143; Hs.278695; Homo sapiens prostein mRNA, co; pros, pros; diag
 119036; R95872; Hs.117572; chemokine binding protein 2; breast, ovar; mAb
 119073; BE245360; Hs.45514; v-ets erythroblastosis virus E; angio, pros; CTL+s.m.
 119082; AF252297; Hs.91546; cytochrome P450 retinoid metab; EWS; diag
 119126; R45175; Hs.117183; ESTs; pros, breast, colon; diag
 119279; N57568; Hs.48028; EST; breast; diag
 119307; BE048061; Hs.37054; ephrin-A3; colon, breast; mAb+diag
 119478; A1624342; Hs.179082; ESTs; breast; diag
 119617; AA516531; Hs.55999; NK homeobox (Drosophila), fami; pros; diag
 119743; AA947552; Hs.58086; branched chain aminotransferas; ovar; s.m.
 119771; A1905687; Hs.348419; A1905687:IL-BT095-190199-019 B; breast; diag
 119780; NM_016625; Hs.191381; hypothetical protein; ovar, lung; CTL+s.m.
 119789; BE393948; Hs.50915; kallikrein 5; ovar; diag
 119845; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv; mAb+s.m.
 119940; AL050097; Hs.272531; DKFZP586B0319 protein; pros; diag
 120104; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, lung; diag
 120132; W57554; Hs.126019; lymphoid nuclear protein (LAF-; pros, breast; diag
 120147; A1917116; Hs.348941; hemoglobin, beta; EWS; diag

- 120206; H26735; Hs.91668; Homo sapiens clone PP1498 unkn; breast; mAb
 120242; AW969587; Hs.86366; ESTs; blad; diag
 120326; AA923278; Hs.290905; ESTs, Weakly similar to protea; pros; s.m.
 120438; AW015242; Hs.99488; ESTs, Weakly similar to YK54_Y; ovar; diag
 5 120471; AA251944; Hs.104058; CGI-29 protein; colon; diag
 120486; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk; diag
 120588; AA703226; Hs.16193; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 120624; AW407987; Hs.173518; M-phase phosphoprotein homolog; breast; s.m.
 120830; AI568170; Hs.96886; ESTs; EWS; diag
 10 120977; AA398155; Hs.97600; ESTs; breast, ovar; diag
 121027; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 fi; blad; mAb
 121231; AA814948; Hs.96343; ESTs, Weakly similar to ALUC_H; EWS; diag
 121335; AA404418; ; gb:zw37e02.s1 Soares_total_fet; angio; diag
 121362; AF050147; Hs.97932; chondromodulin I precursor; EWS; mAb
 15 121457; W07404; Hs.102558; hypothetical protein FLJ22055; colon; diag
 121619; AA528339; Hs.178062; ESTs, Weakly similar to phosph; EWS; s.m.
 121710; AF163474; Hs.96744; prostate androgen-regulated tr; pros; diag
 121721; AL047051; Hs.199961; ESTs, Weakly similar to ALU7_H; pros; diag
 20 121723; AA243499; Hs.104800; hypothetical protein FLJ10134; breast; diag
 121748; BE536911; Hs.234545; hypothetical protein NUF2R; breast; diag
 121779; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
 121791; AA815378; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar; mAb+CTL
 121792; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
 25 121913; AI249368; Hs.98558; ESTs; protease inhibitor 15 (i; breast, pros; s.m.
 121920; AA428300; ; gb:zw18b02.s1 Soares ovary tum; ovar, uter, cerv; diag
 122041; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 122520; AW951324; Hs.173609; pregnancy specific beta-1-glyc; colon; diag
 122797; AJ251027; Hs.99526; odorant-binding protein 2B (OB; breast; diag
 30 122802; AI687303; Hs.285529; G protein-coupled receptor 49; ovar, uter; mAb+s.m.
 122969; AW821252; Hs.104336; hypothetical protein; ovar; diag
 123005; AW369771; Hs.367688; integrin, beta 8; ovar, lung, headnk, glio; mAb+s.m.
 123044; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc ; lung; diag
 123137; AI073913; Hs.100686; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom; diag
 35 123158; AF161426; Hs.218329; hypothetical protein; breast; diag
 123160; AA488687; Hs.284235; ESTs, Weakly similar to I38022; lung; diag
 123169; AI950087; Hs.369628; gb:wq05c02.x1 NCL_CGAP_Kid12 H; ovar; diag
 123209; AW968543; Hs.203270; ESTs, Weakly similar to ALU1_H; pros; diag
 123308; C14187; Hs.157208; ESTs; EWS; diag
 40 123339; AW188464; Hs.101515; ESTs; ovar; diag
 123475; BE439553; Hs.12329; Homo sapiens, clone IMAGE:4098; pros; diag
 123494; AW179019; Hs.112110; mitochondrial ribosomal protei; ovar; diag
 123520; AA608550; ; gb:ae53d12.s1 Stratagene lung ; pros; s.m.
 123533; AA608751; ; gb:ae56h07.s1 Stratagene lung ; colon; diag
 45 123619; AA602964; Hs.366318; gb:no97c02.s1 NCL_CGAP_Pr2 Hom; breast; CTL+s.m.
 123689; AA399323; Hs.285130; Homo sapiens pinch-2 protein m; ovar; diag
 123709; AA706910; Hs.112742; ESTs; breast; diag
 123829; AF251237; Hs.112208; XAGE-1 protein; lung, blad, test; CTL
 123972; T46848; Hs.70337; immunoglobulin superfamily, me; ovar; diag
 50 124006; AI147155; Hs.279727; ESTs; homologue of PEM-3 [Cion; breast, angio, lung, ovar, EWS; diag
 124059; BE387335; Hs.283713; ESTs, Weakly similar to S64054; breast, colon, blad, lung; CTL+diag
 124153; AU077333; Hs.160483; erythrocyte membrane protein b; pros; mAb
 124352; AA640891; Hs.102406; ESTs; breast, pros, ovar, lung; diag
 124526; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros; mAb+s.m.
 55 124579; AI693815; Hs.127179; cryptic gene; panc; diag
 124777; R41933; Hs.140237; ESTs, Weakly similar to ALU1_H; pros, breast; diag
 125103; AA570058; Hs.122730; ESTs, Moderately similar to KI; colon; mAb
 125154; W38419; ; gb:zc78a07.s1 Pancreatic Islet; ovar; diag
 125250; W26524; Hs.356686; protein phosphatase 4 regulato; ovar; CTL+s.m.
 60 125266; W90022; Hs.186809; ESTs, Highly similar to LCT2_H; angio; diag
 125453; BE385523; Hs.18048; melanoma antigen, family A, 10; blad; mAb+CTL
 125666; AL390172; Hs.317432; Homo sapiens cDNA: FLJ21270 fi; ovar; diag
 125770; AA143045; Hs.81665; v-kit Hardy-Zuckerman 4 feline; EWS; diag
 125976; AA436760; Hs.35552; gb:zv67d11.r1 Soares_total_fet; pros; diag
 65 126399; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
 126645; AA316181; Hs.61635; six transmembrane epithelial a; pros, breast, lung, panc, headnk, EWS; mAb+CTL
 126758; AI559444; Hs.104679; ESTs; pros, breast; mAb
 126799; AW753865; Hs.74376; olfactomedin related ER local; EWS; diag
 126872; AW450979; ; gb:UL-H-BI3-ala-a-12-0-UL.s1 N; blad; diag
 70 126892; AF121856; Hs.284291; sorting nexin 6; ovar; diag
 126960; AL390172; Hs.317432; branched chain aminotransferas; ovar; s.m.
 126966; R38438; Hs.118747; solute carrier family 15 (H+/-p; pros; mAb
 127003; AW816515; Hs.173540; ATPase, Class V, type 10D; pros; mAb
 127221; BE062109; Hs.241551; chloride channel, calcium acti; lung, blad, headnk, cerv; mAb+s.m.
 75 127240; AJ005683; Hs.86998; nuclear factor of activated T-; pros; CTL+s.m.
 127425; AF183810; Hs.26102; trichorhinophalangeal syndrome; breast; mAb
 127479; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc; diag
 127537; AI926047; Hs.162859; ESTs; pros; diag
 127664; AA806164; Hs.116502; ESTs; EWS; diag
 80 128046; AA873285; Hs.357313; gb:oh68h05.s1 NCL_CGAP_Kid5 Ho; pros, breast, colon; diag
 128305; AI954968; Hs.365706; matrix Gla protein; breast; diag
 128478; AA708205; Hs.100343; ESTs; EWS; CTL+s.m.
 128515; BE395085; Hs.334762; type I transmembrane protein F; panc; mAb
 128595; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.

- 128610; N48373; Hs.10247; activated leucocyte cell adhes; breast, pros, lung, ovar; diag
 128734; AB008390; Hs.104570; kallikrein 8 (neuropsin/ovasin; ovar; diag
 128790; AF026692; Hs.105700; secreted frizzled-related prot; breast, colon, pros, ovar, uter, panc; diag
 128797; NM_002975; Hs.105927; stem cell growth factor; lymph; EWS, leuk; diag
 128854; BE159181; Hs.168232; hypothetical protein FLJ13855; breast; diag
 128925; R67419; Hs.21851; Homo sapiens cDNA FLJ12900 fis; breast; diag
 128949; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc; mAb+diag+s.m.
 128969; Z42047; Hs.107479; Homo sapiens PRO2751 mRNA, com; pros; diag
 129041; BE382756; Hs.169902; solute carrier family 2 (faci); lung, blad; mAb+s.m.
 129097; BE243933; Hs.108642; zinc finger protein 22 (KOX 15; ovar; CTL+s.m.
 129099; AF146074; Hs.108660; ATP-binding cassette, sub-fam1; lung, blad, headnk ; mAb+s.m.
 129184; AW161450; Hs.109201; CGI-86 protein; pros; mAb
 129260; AF077200; Hs.279813; hypothetical protein; colon; diag
 129284; AA318224; Hs.296141; ESTs; colon; diag
 129362; U30246; Hs.110736; solute carrier family 12 (sodi; colon, breast, pros; mAb
 129366; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA ; breast; diag
 129389; NM_012445; Hs.288126; spondin 2, extracellular matri; colon, pros; diag
 129404; AI267700; Hs.351201; ESTs; pros, ovar, lung, blad, headnk, panc; diag
 129466; L42583; Hs.334309; keratin 6A; lung, blad; diag
 129482; AA188185; Hs.289043; spindlin; breast; diag
 129534; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag
 129571; X51630; Hs.1145; Wilms tumor 1; ovar; CTL+s.m.
 129605; AF061812; Hs.115947; keratin 16 (focal non-epidermo; lung, blad, headnk; diag
 129620; D79338; Hs.239720; CCR4-NOT transcription complex; breast, angio; diag
 129628; U38945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk; s.m.
 129650; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
 129689; AW748482; Hs.77873; B7 homolog 3; breast; diag
 129703; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457; EWS, leuk; diag
 129720; AA156214; Hs.12152; APMCF1 protein; breast; diag
 129750; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad; mAb+s.m.
 129869; AI222069; Hs.13015; hypothetical protein similar t; breast; diag
 129912; AF155096; Hs.107213; hypothetical protein FLJ20585; ovar; CTL+s.m.
 129936; AJ250717; Hs.1355; cathepsin E; blad; sm+diag
 129953; AA412195; Hs.13740; ESTs; breast; diag
 129977; NM_000399; Hs.1395; early growth response 2 (Krox-; EWS; CTL+s.m.
 130010; AA301116; Hs.142838; nucleolar phosphoprotein Nopp3; ovar; diag
 130057; AF027153; Hs.324787; solute carrier family 5 (inosi; breast; mAb
 130095; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag
 130155; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
 130181; AF052119; Hs.151608; Homo sapiens clone 23622 mRNA ; pros; diag
 130184; H58306; Hs.15165; retinoic acid induced 14; angio; diag
 130262; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renal; diag
 130343; AB040914; Hs.278628; KIAA1481 protein; breast; diag
 130376; R40873; Hs.155174; CDC5 (cell division cycle 5, S; ovar; CTL+s.m.
 130385; AW067800; Hs.155223; stanniocalcin 2; breast, lung; mAb+diag
 130455; D90041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.
 130511; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar; diag
 130558; BE564937; Hs.15984; pp21 homolog; pros; CTL+s.m.
 130577; M69241; Hs.162; insulin-like growth factor bin; ovar; diag
 130604; AA383256; Hs.1657; estrogen receptor 1; breast; mAb+s.m.
 130627; BE003054; Hs.1695; matrix metalloproteinase 12 (m; lung, colon, blad, headnk, ovar, panc; mAb+diag+s.m.
 130637; AA356764; Hs.17109; integral membrane protein 2A; EWS; mAb+s.m.
 130648; AI458165; Hs.17296; hypothetical protein MGC2376; colon; diag
 130667; BE246961; Hs.17639; Homo sapiens ubiquitin protein; breast; s.m.
 130690; AB006625; Hs.139033; paternally expressed 3; ovar; diag
 130714; AI348274; Hs.18212; DNA segment on chromosome X (u; breast; diag
 130760; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
 130800; AI187292; Hs.19574; hypothetical protein MGC5469; colon, lung; diag
 130839; AB011169; Hs.380875; similar to S. cerevisiae SSM4; angio; diag
 130844; U76248; Hs.20191; seven in absentia (Drosophila); breast; diag
 130892; AL120837; Hs.20993; high-glucose-regulated protein; breast; CTL+s.m.
 130941; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb
 130967; AA393071; Hs.182579; leucine aminopeptidase; ovar; s.m.
 130972; D81866; Hs.374468; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 130987; BE613269; Hs.21893; hypothetical protein DKFZp761N; colon; diag
 131046; AA321649; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, fibro; diag
 131080; NM_001955; Hs.2271; endothelin 1; angio; diag
 131083; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros; mAb
 131148; AW953575; Hs.303125; p53-induced protein PIGPC1; breast, colon, angio; diag
 131216; AI815486; Hs.243901; Homo sapiens cDNA FLJ20738 fis; colon, breast; diag
 131228; AW207469; Hs.24485; chondroitin sulfate proteoglyc; ovar; diag
 131244; AI638429; Hs.24763; RAN binding protein 1; lung, blad, headnk; CTL+s.m.
 131288; AA278482; Hs.25328; ESTs, Moderately similar to AL; pros; diag
 131289; AA296696; Hs.333418; FXFD domain-containing ion tra; colon; diag
 131307; NM_000025; Hs.2549; adrenergic, beta-3-, receptor; EWS; mAb
 131313; R96290; Hs.75874; ribosomal protein L44; EWS; diag
 131492; AI452601; Hs.288869; nuclear receptor subfamily 2, ; pros; mAb+s.m.
 131544; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
 131559; AL078599; Hs.10784; hypothetical protein FLJ20037; breast; diag
 131564; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast; diag
 131603; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad; s.m.
 131643; AW410601; Hs.30026; HSPC182 protein; breast; diag
 131739; AF017986; Hs.31386; secreted frizzled-related prot; breast; mAb+s.m.

- 131817; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, glio; s.m.
 131885; BE502341; Hs.3402; ESTs; breast; diag
 131919; T15803; Hs.272458; protein phosphatase 3 (former); pros, breast; s.m.
 131925; AF151048; Hs.183180; anaphase promoting complex sub; breast; diag
 131965; W79283; Hs.35962; ESTs; lung, ovar; diag
 131985; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
 132050; AI267615; Hs.38022; ESTs; angio; diag
 132173; X89426; Hs.41716; endothelial cell-specific mole; angio; diag
 132180; NM_004460; Hs.418; fibroblast activation protein; colon, panc, esoph; mAb
 132191; AA507576; Hs.288361; Homo sapiens cDNA: FLJ22696 fi; ovar; diag
 132349; AW975654; Hs.181286; serine protease inhibitor, Kaz; pros, blad; s.m.
 132354; BE185289; Hs.1076; small proline-rich protein 1B; lung; diag
 132358; NM_003542; Hs.46423; H4 histone family, member G; pros; CTL+s.m.
 132371; AA235448; Hs.222088; PRO2000 protein; breast; diag
 132454; BE296227; Hs.250822; serine/threonine kinase 15; blad, breast; s.m.
 132490; NM_001290; Hs.4980; LIM domain binding 2; angio; diag
 132520; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.
 132528; T78736; Hs.50758; SMC4 (structural maintenance o; ovar; CTL+s.m.
 132543; BE568452; Hs.344037; protein regulator of cytokines; colon, lung; diag
 132572; AI929659; Hs.237825; signal recognition particle 72; ovar; diag
 132592; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22528 fi; colon; diag
 132624; AA326108; Hs.33829; bHLH protein DEC2; ovar; diag
 132632; AU076916; Hs.5398; guanine monphosphate synthetas; ovar, lung; s.m.
 132669; W38586; Hs.380933; guanine nucleotide binding pro; colon; diag
 132710; W74001; Hs.55279; serine (or cysteine) proteinas; lung, blad, colon, headnk; diag
 132725; NM_006276; Hs.184167; splicing factor, arginine/seri; ovar; CTL+s.m.
 132767; BE182592; Hs.11261; small proline-rich protein 2A; lung; diag
 132791; AB029551; Hs.7910; RING1 and YY1 binding protein; pros; CTL+s.m.
 132837; AA307362; Hs.57958; EGF-TM7-latrophilin-related pr; angio; diag
 132856; NM_001448; Hs.58367; glypican 4; breast, colon, pros; mAb
 132888; NM_005476; Hs.5920; UDP-N-acetylglucosamine-2-epim; pros; s.m.
 132902; AI936442; Hs.59838; hypothetical protein FLJ10808; colon; diag
 132939; AB009284; Hs.61152; exostoses (multiple)-like 2; ovar; diag
 132964; AI362575; Hs.303171; ESTs; pros; diag
 132967; AA316181; Hs.61635; six transmembrane epithelial a; pros, pros; mAb+CTL
 132990; X77343; Hs.334334; transcription factor AP-2 alpha; breast, lung; CTL+s.m.
 132994; AA112748; Hs.279905; clone HQ0310 PRO0310p1; colon, breast; s.m.
 133006; AW978436; Hs.62515; KIAA0494 gene product; colon; diag
 133015; AJ002744; Hs.246315; UDP-N-acetyl-alpha-D-galactosa; breast, colon, pros; s.m.
 133016; AI436688; Hs.6289; hypothetical protein FLJ20886; breast; diag
 133061; AI186431; Hs.296638; prostate differentiation facto; angio, pros, blad; diag
 133063; AI654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.
 133070; U92649; Hs.380136; a disintegrin and metalloprote; leuk; diag
 133179; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
 133199; AF231981; Hs.250175; homolog of yeast long chain po; breast, angio; CTL+s.m.
 133260; AA403045; Hs.6906; Homo sapiens cDNA: FLJ23197 fi; angio; diag
 133272; NM_002776; Hs.69423; kallikrein 10; colon, ovar; diag
 133314; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); breast, panc; mAb
 133321; T79526; Hs.179516; integral type I protein; breast; diag
 133391; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, blad, lung; diag
 133415; X69699; Hs.73149; paired box gene 8; ovar; CTL
 133477; AW502935; Hs.740; PTK2 protein tyrosine kinase 2; breast; s.m.
 133579; X75346; Hs.75074; mitogen-activated protein kina; pros; diag
 133626; AW836130; Hs.75277; hypothetical protein FLJ13910; pros; diag
 133736; D49958; Hs.75819; glycoprotein M6A; pros; mAb
 133829; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; ovar; diag
 133860; S78296; Hs.76888; hypothetical protein MGC12702; blad; diag
 133944; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 133975; C18356; Hs.295944; tissue factor pathway inhibitor; angio, panc; CTL+diag
 133976; AI908165; Hs.169946; GATA-binding protein 3 (T-cell; breast, blad; mAb+s.m.
 134100; AA460085; Hs.171075; replication factor C (activato; pros; diag
 134110; U41060; Hs.79136; LIV-1 protein, estrogen regula; breast, blad, ovar, pros; mAb
 134169; AI690916; Hs.178137; transducer of ERBB2, 1; breast; CTL+s.m.
 134219; NM_000402; Hs.80206; glucose-6-phosphate dehydrogen; breast; s.m.
 134319; BE304999; Hs.285754; fumarate hydratase; colon; s.m.
 134326; AW903838; Hs.81800; chondroitin sulfate proteoglyc; ovar, breast, panc, lung; diag
 134348; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.
 134374; N22687; Hs.8236; ESTs; pros; diag
 134390; R35528; Hs.8258; DKFZP434D1335 protein; pros; CTL+s.m.
 134401; AI916662; Hs.211577; kinesin 1 (kinesin receptor); pros, breast; mAb+s.m.
 134405; AW067903; Hs.82772; collagen, type XI, alpha 1; breast, lung, ovar, headnk; CTL
 134470; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, headnk; s.m.
 134520; BE091005; Hs.349506; activated RNA polymerase II tr; ovar; s.m.
 134529; AW411479; Hs.848; FK506-binding protein 4 (59kD); breast; diag
 134570; U66615; Hs.172280; SWI/SNF related, matrix associ; EWS; CTL+s.m.
 134654; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
 134666; BE391929; Hs.8752; transmembrane protein 4; breast; mAb+s.m.
 134691; AW382987; Hs.88474; prostaglandin-endoperoxide syn; ovar; s.m.
 134727; X80507; Hs.84520; yes-associated protein 65 kDa; blad; diag
 134731; D89377; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
 134786; T29618; Hs.89640; TEK tyrosine kinase, endotheli; angio; s.m.
 134824; S78723; Hs.298623; 5-hydroxytryptamine (serotonin); blad; mAb
 134856; BE281128; Hs.9030; TONDU; blad; CTL+s.m.

- 134868; AB020689; Hs.90419; KIAA0882 protein; breast; diag
 134924; BE294029; Hs.279903; Ras homolog enriched in brain ; breast; mAb
 134972; AL033527; Hs.169252; v-myc avian myelocytomatosis v; ovar; CTL+s.m.
 134975; R50333; Hs.92186; Leman coiled-coil protein; breast; diag
 134989; AW968058; Hs.92381; nudix (nucleoside diphosphate ; colon; diag
 135073; W55956; Hs.94030; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 135117; W52493; Hs.94694; Homo sapiens cDNA FLJ10561 fis; breast; diag
 135166; AA135867; Hs.280858; ESTs, Highly similar to A35661; pros; diag
 135235; AW298244; Hs.266195; ESTs; angio; diag
 135242; AI583187; Hs.9700; cyclin E1; ovar; CTL+s.m.
 135243; BE463721; Hs.97101; putative G protein-coupled rec; colon; mAb+s.m.
 135255; Y13645; Hs.97234; uroplakin 2; blad; mAb
 135309; AI564123; Hs.355689; ADP-ribosylation factor-like 5; pros; diag
 135315; H81136; Hs.334604; Homo sapiens mRNA for KIAA1870; pros; diag
 135389; U05237; Hs.99872; fetal Alzheimer antigen; pros, breast, colon; CTL+s.m.
 135400; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.
 300254; AW183618; Hs.55610; solute carrier family 30 (zinc; pros, breast; mAb+s.m.
 300256; AW591433; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
 300318; AW444502; Hs.256982; ESTs, Weakly similar to NEL1_H; angio; CTL+diag
 300605; AI218847; Hs.152670; ESTs; pros; diag
 300921; AF146747; Hs.232165; polycythemia rubra vera 1; cel; pros; mAb+s.m.
 300923; AW136372; Hs.1852; acid phosphatase, prostate; pros; s.m.
 301042; AI659131; Hs.366053; hypothetical protein MGC2849; pros; mAb
 301043; AI160316; Hs.149155; voltage-dependent anion channe; pros; mAb+s.m.
 301050; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung; CTL+s.m.
 301341; AA887801; Hs.208229; G protein-coupled receptor; breast, lung; mAb+s.m.
 302001; AB020711; Hs.374965; KIAA0904 protein; breast ; CTL+s.m.
 302005; BE252922; Hs.123119; MAD (mothers against decapenta; pros; diag
 302067; BE542706; Hs.222399; CEGP1 protein; breast; diag
 302167; NM_006227; Hs.283007; phospholipid transfer protein; pros; mAb
 302225; NM_007231; Hs.162211; solute carrier family 6 (neuro; panc; mAb+s.m.
 302276; AW057736; Hs.323910; HER2 receptor tyrosine kinase ; breast; mAb+s.m.
 302290; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp5; pros, breast; diag
 302372; AL117406; Hs.335891; ATP-binding cassette transport; breast, pros ; mAb+s.m.
 302384; AI678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag
 302410; NM_004917; Hs.218366; kallikrein 4 (prostase, enamel; pros; diag
 302468; AL133561; Hs.380155; DKFZP434B061 protein; pros; diag
 302562; BE149762; Hs.48956; gap junction protein, beta 6 (; lung, blad; mAb
 302881; AA508353; Hs.105314; relaxin 1 (H1); pros; diag
 303295; AA205625; Hs.208067; ESTs; blad; diag
 303380; AW962764; Hs.303171; olfactory receptor, family 51.; pros; mAb
 303506; AA340605; Hs.105887; ESTs, Weakly similar to Homolo; pros, breast, colon ; diag
 303699; BE143707; Hs.19525; hypothetical protein FLJ22794; pros; diag
 303753; AW503733; Hs.9414; KIAA1488 protein; pros, breast, colon; CTL+s.m.
 305503; AA759177; Hs.298148; ESTs, Weakly similar to KIAA05; pros; diag
 306273; AA936290; ; gb:on70a01.s1 Soares_NFL_T_GBC; pros; diag
 306676; AI005603; ; gb:ov15c10.s1 NCL_CGAP_GC3 Hom; lung; diag
 306840; AI077477; Hs.307912; ESTs; angio; diag
 309177; AI951118; Hs.326736; Homo sapiens breast cancer ant; breast, pros; mAb+CTL
 309583; AW170035; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
 309931; AW341683; Hs.343663; gb:hd13d01.x1 Soares_NFL_T_GBC; lung; mAb
 310382; AI734009; Hs.127699; KIAA1603 protein; pros; diag
 310431; AI420227; Hs.366053; ESTs, Weakly similar to A46010; pros; diag
 310573; AW292180; Hs.156142; ESTs; pros; diag
 310636; AI814373; Hs.164175; ESTs; lung; diag
 310781; AI380797; Hs.158992; ESTs; breast ; diag
 310955; AI476732; Hs.263912; ESTs; breast, angio; diag
 311034; BE567130; Hs.311389; ESTs, Highly similar to NKGD_H; lung; mAb+s.m.
 311166; AI821005; Hs.118599; intron of. BFF9 (GDNFRa); breast ; diag
 311251; AI655662; Hs.197698; ESTs; pros; diag
 311557; AF200492; Hs.211238; interleukin-1 homolog 1; lung; diag
 311596; AI682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
 311630; AI915444; Hs.372037; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 311877; AA084248; Hs.372651; G protein-coupled receptor 39; ovar, angio, glio; mAb+s.m.
 311911; R19175; Hs.169793; ribosomal protein L32; pros; diag
 311928; T62216; Hs.378028; ESTs; pros; diag
 312182; T94344; Hs.326263; ESTs; pros; diag
 312252; AI128388; Hs.143655; ESTs; blad; diag
 312319; AA906997; Hs.180780; TERA protein; colon; CTL+s.m.
 312521; AI263307; Hs.356901; H2B histone family, member L; pros, breast, lung; diag
 312544; AA516420; Hs.352340; ESTs, Weakly similar to I38022; breast; diag
 312742; AI650363; Hs.116462; ESTs; colon; diag
 312795; AW975014; Hs.26; ferrochelatase (protoporphyrin; pros; s.m.
 312857; BE083868; Hs.126914; KIAA1430 protein; colon, pros; CTL+s.m.
 312922; AA329258; Hs.378739; ESTs, Moderately similar to al; pros; diag
 313328; AW449211; Hs.105445; GDNF family receptor alpha 1; breast ; mAb+s.m.
 313513; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 313556; AA628517; Hs.118502; ESTs; angio; diag
 313665; AW751201; Hs.120932; ESTs; angio; diag
 313774; AI916058; Hs.144583; ESTs; colon; CTL
 313915; C18863; Hs.163443; intron of periostin (OSF-2os); breast; diag
 313978; AI870175; Hs.13957; ESTs; angio; diag
 314078; AW129357; Hs.329700; ESTs; breast; diag

- 314097; AA648744; Hs.269493; ESTs; breast; diag
 314121; AI732083; Hs.187619; ESTs; pros; breast; diag
 314171; AI821895; Hs.193481; ESTs; pros; diag
 314506; AA833655; Hs.206868; Homo sapiens cDNA FLJ14056 fis; breast; diag
 314547; AA399272; Hs.144341; ESTs; breast; diag
 314558; AI873274; Hs.370280; ESTs; breast; pros; diag
 314589; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis; lung, blad; diag
 314691; AW207206; Hs.356962; ESTs; breast; pros; diag
 314785; AI538226; Hs.32976; guanine nucleotide binding pro; colon; pros; diag
 314907; AW971082; Hs.222886; ESTs, Weakly similar to TRHY_H; pros; diag
 315006; AI538613; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
 315033; AI493046; Hs.146133; ESTs; colon; diag
 315051; AW292425; Hs.163484; ESTs; breast, pros, blad; diag
 315052; AA876910; Hs.134427; ESTs; pros; breast; diag
 315196; AI367347; Hs.44898; Homo sapiens clone TCCCTA00151; breast; diag
 315368; AB037745; Hs.104696; KIAA1324 protein; pros; diag
 315408; AW273261; Hs.216292; ESTs; pros; diag
 315634; AA837085; Hs.372254; ESTs; breast; pros; diag
 315720; AA292998; Hs.163900; ESTs; blad; diag
 316177; AI904962; Hs.293102; downstream of breast cancer an; breast; mAb+CTL
 316442; AW760894; Hs.125350; ESTs; pros; diag
 316580; AA938198; Hs.146123; poly(A) polymerase gamma; breast, angio; s.m.
 316886; AA836331; Hs.170261; ESTs; breast; diag
 316943; AW014875; Hs.137007; ESTs; blad; diag
 317079; BE159984; Hs.125395; ESTs; blad; mAb+s.m.
 317140; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
 317224; X73608; Hs.93029; sparc/osteoneclin, cwcv and ka; pros, angio; diag
 317548; BE568568; Hs.159066; ESTs; pros; CTL+s.m.
 317803; AW664964; Hs.128899; ESTs; breast, lung, ovar, pros; mAb+s.m.
 317881; AI827248; Hs.224398; Homo sapiens cDNA FLJ11469 fis; breast, lung; diag
 318240; AI085377; Hs.143610; ESTs; lung; diag
 318524; AK001050; Hs.159066; hypothetical protein FLJ10188; pros, colon; CTL+s.m.
 318532; AW139377; Hs.127179; cryptic gene; panc; diag
 318744; AI793124; Hs.144479; ESTs; breast; diag
 318754; W21423; Hs.44222; CGI-90 protein; pros; diag
 319080; AW967646; Hs.23023; ESTs; pros; diag
 319795; AB037821; Hs.146858; protocadherin 10; pros, glio; mAb+s.m.
 320066; BE305242; Hs.16098; claudin 2; colon, panc; diag
 320167; AA984373; Hs.90790; Homo sapiens cDNA: FLJ22930 fi; breast, pros; diag
 320203; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar, mAb+s.m.
 320211; AL039402; Hs.125783; DEME-6 protein; breast, pros; CTL
 320322; AF077374; Hs.139322; small proline-rich protein 3; lung; diag
 320324; AF071202; Hs.139336; ATP-binding cassette, sub-fam1; pros; mAb
 320561; AF085808; Hs.159330; uroplakin 3; pros, blad; diag
 320590; U67058; Hs.154299; Human proteinase activated rec; pros; mAb+s.m.
 320635; N50617; Hs.80506; small nuclear ribonucleoprotein; angio lung; diag
 320736; AA315361; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 320796; AK001541; Hs.31218; secretory carrier membrane pro; pros, colon; diag
 320896; BE019924; Hs.271580; uroplakin 1B; lung, blad, ovar, headnk; mAb+diag
 321023; AW294316; Hs.125608; ESTs; colon; diag
 321107; AI732643; Hs.144151; downstream of breast cancer an; breast; mAb+CTL
 321412; AI674383; Hs.22891; solute carrier family 7 (catio; pros; mAb+s.m.
 321441; AF107493; Hs.201675; Homo sapiens LUCA-15 protein m; pros, breast; diag
 321644; AW975944; Hs.237396; ESTs; breast, pros; diag
 321717; AW956580; Hs.42699; ESTs; angio; diag
 321906; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 321911; AF026944; Hs.293797; ESTs; angio, lung, blad; diag
 322035; AL137517; Hs.306201; hypothetical protein DKFZp564O; breast, blad; mAb
 322521; AF147347; ; gb:Homo sapiens full length in; breast; diag
 322706; AA018899; Hs.127179; cryptic gene; panc; diag
 322782; AA056060; Hs.202577; Homo sapiens cDNA FLJ12166 fis; pros; diag
 322818; AW043782; Hs.293616; ESTs; pros, breast, angio, glio; diag
 322882; AW248508; Hs.279727; Homo sapiens cDNA FLJ14035 fis; breast, lung, ovar, angio, blad; diag
 322975; C16391; ; intron of breast cancer antigen; breast; mAb+CTL
 323168; AL120862; Hs.124165; programmed cell death 9 (PDCD9; breast; diag
 323226; AF055019; Hs.355279; Homo sapiens clone 24670 mRNA; pros; diag
 323262; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
 323287; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
 323332; AI829520; ; gb:wt19c06.x1 NCL_CGAP_Ut1 Hom; breast; diag
 323335; AI655499; Hs.161712; ESTs; pros, breast; mAb
 323587; AI299709; Hs.131886; Homo sapiens cDNA: FLJ22113 fi; colon; diag
 323817; AA410943; ; NAME OMITTED ... receptor kinase; breast; mAb
 324261; BE069341; ; gb:QV3-BT0381-270100-073-c08 B; breast; diag
 324295; AA434579; Hs.143691; ESTs; pros; diag
 324338; AA927668; Hs.145078; regulator of differentiation (; colon; diag
 324430; AA464018; Hs.335798; Homo sapiens cDNA: FLJ23241 fi; pros, colon; diag
 324432; AA464510; Hs.152812; ESTs; breast, lung, panc; diag
 324603; AW993522; Hs.299867; ESTs; pros, breast; diag
 324617; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros; diag
 324658; AI694767; Hs.129179; Homo sapiens cDNA FLJ13581 fis; pros; diag
 324718; AI557019; Hs.116467; small nuclear protein PRAC; colon, pros; diag
 324866; AI541214; Hs.46320; Small proline-rich protein SPR; lung, blad; diag
 324871; AI890347; Hs.271923; Homo sapiens cDNA: FLJ22785 fi; colon; diag

324987; AI375572; Hs.172634; ESTs; breast; diag
 325372; ; Phase 2 & 3 Exons; breast; CTL+s.m.
 325544; ; Phase 2 & 3 Exons; breast; angio; diag
 327036; ; Phase 2 & 3 Exons; lung; angio; diag
 327075; ; Phase 2 & 3 Exons; breast; lung; diag
 327414; ; Phase 2 & 3 Exons; angio; diag
 328700; ; Phase 2 & 3 Exons; breast; angio; diag
 330211; ; Phase 2 & 3 Exons; pros; CTL+s.m.
 330468; L10343; Hs.112341; protease inhibitor 3; skin-der; lung; colon; blad; diag
 330493; M27826; Hs.334372; endogenous retroviral protease; lung; colon; s.m.
 330630; NM_002902; Hs.79088; reticulocalbin 2; EF-hand calc; pros; diag
 330762; AW407332; Hs.13014; ADP-ribosylation factor GTPase; pros; CTL+s.m.
 330790; AI660243; Hs.318545; Hu01 Chip Redos; pros; blad; diag
 330814; AI955040; Hs.265398; PAR-6 beta (partitioning def; breast; diag
 330827; AI961486; Hs.249196; ESTs; lung; uter; diag
 330892; AF109298; Hs.118258; prostate cancer associated pro; pros; diag
 331014; AW770994; Hs.30340; hypothetical protein KIAA1165; colon; diag
 331151; R82331; Hs.121602; ESTs; pros; breast; diag
 331183; T40769; Hs.8469; ESTs; colon; diag
 331237; W87874; Hs.25277; Homo sapiens cDNA FLJ10717 fis; angio; diag
 331490; AF216751; Hs.26813; CDA14; pros; diag
 331578; AI246482; Hs.243010; ESTs; angio; diag
 331614; N92293; Hs.206832; EST; Moderately similar to ALU; breast; diag
 331811; AW885727; Hs.9914; Hu01 Chip Redos; lung; diag
 331889; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 331969; AA526911; Hs.82772; collagen; type XI; alpha 1; breast; lung; CTL
 332180; AF134160; Hs.7327; claudin 1; lung; mAb
 332247; AA669097; ; ESTs; pros; breast; diag
 332396; AW579842; Hs.380730; hypothetical protein FLJ10697; pros; diag
 332453; L42583; Hs.334309; Hu01 Chip Redos; lung; diag
 332466; AB018259; Hs.118140; KIAA0716 gene product; angio; diag
 332530; M31669; Hs.1735; inhibin; beta B (activin AB be; ovar; pros; diag
 332535; AF167706; Hs.19280; cysteine-rich repeat-containing; angio; diag
 332640; BE568452; Hs.344037; protein regulator of cytokines; blad; headnk; diag
 332645; AA284371; Hs.118064; ESTs; breast; colon; diag
 332686; X69699; Hs.73149; paired box gene 8; ovar; CTL+s.m.
 332697; X51405; Hs.75360; carboxypeptidase E; pros; diag
 332740; BE409869; Hs.286241; Homo sapiens cDNA: FLJ22698 fi; pros; diag
 332798; ; C22000007.gi12314195[emb]CAB9; pros; breast; diag
 333769; ; NM_005940*.Homo sapiens matrix; breast; colon; lung; mAb+diag+s.m.
 333904; ; Chromosome 22; pros; diag
 334223; ; NM_005080*.Homo sapiens X-box ; pros; breast; diag
 334447; ; NM_012429*.Homo sapiens SEC14 ; pros; diag
 335115; ; NM_006498*.Homo sapiens lectin; pros; CTL+s.m.
 335809; ; NM_014509*.Homo sapiens kraken; breast; CTL+s.m.
 335824; ; ENSP00000249072*.DJ222E13.1 (N; breast; pros; CTL+s.m.
 335825; ; ENSP00000249072*.DJ222E13.1 (N; breast; diag
 335936; ; Chromosome 22; lung; diag
 336034; ; NM_007172*.Homo sapiens nucleop; breast; angio; CTL+s.m.
 336152; ; NM_014246*.Homo sapiens cadheri; breast ; mAb
 336636; ; C22000024*.gi10645308[gb]AAG2; lung, breast; CTL+s.m.
 338008; ; NM_005940*.Homo sapiens matrix; lung, breast, colon; mAb+diag+s.m.
 338033; ; Chromosome 22; lung, angio; diag
 338158; ; NM_012399*.Homo sapiens phosph; lung, angio; diag
 338255; ; NM_014323*.Homo sapiens zinc f; pros, breast, colon ; CTL+s.m.
 400195; ; Hs.42650; NM_007057*.Homo sapiens ZW10 i; lung; CTL+s.m.
 400269; ; Hs.253495; Eos Control; fibro; diag
 400285; ; Eos Control; lung; diag
 400287; S39329; Hs.181350; kallikrein 2, prostatic; pros; diag
 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin; panc, pros, angio, blad, lung; mAb+s.m.
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; pros, colon, EWS; mAb
 400294; N95796; Hs.278695; Homo sapiens protein mRNA, co; pros, pros; mAb
 400295; W72838; Hs.348419; AI905687:IL-BT095-190199-019 B; breast; diag
 400298; AA032279; Hs.61635; six transmembrane epithelial a; panc, lung, headnk, stom, EWS, ovar; mAb+CTL
 400328; X87344; ; transporter 2, ATP-binding cas; lung; mAb+s.m.
 400409; AF153341; ; Homo sapiens winged helix/fork; blad; CTL+s.m.
 400419; AF084545; ; Target; lung, sarc; diag
 400440; X83957; Hs.83870; nebulin; sarc; diag
 400494; ; ENSP00000238970*.CIG30 (Fragme; angio; mAb
 400517; ; lengsin; stom, cerv, uter, lung, pros, colon, hepC; diag
 400651; ; ENSP00000228031*.COPPER CHAPER; sarc; s.m.
 400665; ; NM_002425; Homo sapiens matrix; lung; mAb+diag+s.m.
 400773; ; NM_003105*.Homo sapiens sortil; blad; mAb
 400844; ; NM_003105*.Homo sapiens sortil; blad; s.m.
 400846; ; sortilin-related receptor, L(D; blad; mAb+s.m.
 400881; ; NM_025080; Homo sapiens hypothe; ovar; diag
 401093; ; C12000586*.gi16330167[db]BAA8; blad, lung; CTL+s.m.
 401234; ; mitogen-activated protein kina; angio; diag
 401424; ; NM_001172; Homo sapiens arginas; pros; s.m.
 401486; ; C4000647*.gi14758508[ref]NP_00; headnk; mAb
 401704; ; NM_021195*.Homo sapiens claudi; test; mAb
 401732; ; NM_001176*.Homo sapiens Rho GD; panc; diag
 401747; ; Homo sapiens keratin 17 (KRT17; blad, lung, headnk, mela; diag

401760;; Target Exon; blad, lung, headnk, esoph; diag
 401780;; NM_005557*:Homo sapiens kerati; lung, blad, headnk, esoph, mela; diag
 401781;; Target Exon; lung, blad, headnk, esoph, cerv; diag
 401785;; NM_002275*:Homo sapiens kerati; lung; diag
 5 401797;; Target Exon; sarc; diag
 401994;; Target Exon; lung; diag
 402145;; Target Exon; test; CTL+s.m.
 402199;; Target Exon; test; CTL+s.m.
 10 402230;; Fgenesh predicted: CYTOCHROME ; blad; diag
 402239;; Target Exon; blad; diag
 402260;; NM_001436*:Homo sapiens fibril; blad; CTL+s.m.
 402265;; Target Exon; lung; diag
 402305;; C19000735*:gil4508027[ref]NP_0; blad; CTL+s.m.
 402420;; C1000823*:gil10432400[emb]CAC1; lung; diag
 15 402424;; NM_024901:Homo sapiens hypothe; blad; CTL+s.m.
 402447;; C1000201:gil204416[gb]AAA02627; esoph; mAb
 402474;; NM_004079:Homo sapiens catheps; lung, colon, stom, fibro; diag
 402550;; Target Exon; fibro; diag
 402604;; Target Exon; glio; diag
 20 402605;; Target Exon; glio; diag
 402606;; NM_024626:Homo sapiens hypothe; ovar, breast; mAb
 402680;; Target Exon; test; mAb
 402777;; C1002652*:gil544327[sp]Q04799; blad; diag
 25 402860;; ENSP00000239210:DJ50O24.4 (nov; mela; CTL+s.m.
 402888;; Target Exon; sarc; diag
 402992;; Target Exon; sarc; diag
 402994;; NM_002463*:Homo sapiens myxovi; esoph; diag
 403046;; NM_005656*:Homo sapiens transm; pros; mAb
 403047;; NM_005656*:Homo sapiens transm; pros, blad, colon; mAb
 30 403071;; NM_003319*:Homo sapiens titin ; sarc; diag
 403088;; NM_003319*:Homo sapiens titin ; sarc; diag
 403171;; C2001472*:gil5809678[gb]AAB418; test; diag
 403328;; Target Exon; mela; diag
 35 403329;; unnamed protein product [Homo ; lung; diag
 403381;; ENSP00000231844*:Ecotropic vir; blad; CTL+s.m.
 403409;; NM_005929:Homo sapiens antigen; mela; mAb
 403433;; NM_001622:Homo sapiens alpha-2; hepC; diag
 403478;; NM_022342:Homo sapiens kinesin; lung; CTL+s.m.
 403715;; Target Exon; lung; diag
 40 403740;; NM_001076*:Homo sapiens UDP gt; pros, hepC; s.m.
 403776;; ENSP00000226542*:Small inducib; panc; diag
 403903;; C5001632*:gil10645308[gb]AAG21; blad; CTL+s.m.
 404029;; NM_018936*:Homo sapiens protoc; glio; mAb
 45 404049;; NM_018937*:Homo sapiens protoc; glio; mAb
 404210;; NM_005936:Homo sapiens myeloid; panc, uter, cerv, lung, ovar, pros, colon, stom; diag
 404240;; NM_018950:Homo sapiens major h; fibro; mAb
 404253;; NM_021058*:Homo sapiens H2B hi; lung; CTL+s.m.
 404286;; C6001909:gil704441[dbj]BAA1890; panc; diag
 404298;; C6001238*:gil121715[sp]P26697; lung; s.m.
 50 404403;; Target Exon; blad; diag
 404440;; NM_021048:Homo sapiens melanom; lung, blad; mAb+CTL
 404866;; ENSP00000251112*:Sodium/potass; panc; s.m.
 404877;; NM_005365:Homo sapiens melanom; lung, blad; CTL+s.m.
 55 404927;; Target Exon; lung, headnk; diag
 404996;; Target Exon; lung, headnk, esoph; diag
 405001;; interleukin enhancer binding f; sarc; diag
 405025;; Homo sapiens bone morphogeneti; angio; diag
 405121;; mitogen-activated protein kina; angio, renal; s.m.
 60 405238;; Target Exon; glio; diag
 405239;; oxidative 3 alpha hydroxystero; glio; s.m.
 405451;; Homo sapiens glutaminy-peptid; mela; s.m.
 405545;; Target Exon; cerv; mAb
 405546;; NM_018833*:Homo sapiens transp; cerv; mAb
 65 405547;; NM_018833*:Homo sapiens transp; cerv, mela; mAb
 405646;; C12000200:gil4557225[ref]NP_00; lung; diag
 405704;; NM_001844*:Homo sapiens collag; sarc; diag
 405770;; NM_002362:Homo sapiens melanom; lung, esoph; mAb+CTL
 405849;; Target Exon; panc; diag
 70 405932;; C15000305:gil3806122[gb]AAC691; blad, lung, headnk, cerv; CTL+s.m.
 406081;; Target Exon; blad; diag
 406137;; NM_000179*:Homo sapiens mutS (; lung; CTL+s.m.
 406173;; ENSP00000250148*:Growth hormon; panc; CTL+s.m.
 406348;; Target Exon; breast; CTL+s.m.
 75 406360;; Target Exon; lung, headnk; diag
 406399;; NM_003122*:Homo sapiens serine; blad; diag
 406434;; NM_030579*:Homo sapiens cytoch; blad; diag
 406467;; Target Exon; lung, headnk, blad; diag
 406506;; Target Exon; angio; diag
 80 406547;; Target Exon; test; diag
 406627; T64904; Hs.163780; ESTs; angio; CTL+s.m.
 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte; panc; mAb
 406672; M26041; Hs.198253; major histocompatibility compl; fibro; mAb
 406685; M18728; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung; mAb+CTL

- 406687; M31126; Hs.352054; matrix metalloproteinase 11 (s; breast, lung, ovar, cerv, uter, panc, esoph, mela, sarc; mAb+diag+s.m.
 406690; M29540; Hs.220529; carcinoembryonic antigen-relat; lung, headnk, panc, stom, blad, colon, cerv; mAb+CTL
 406706; X03740; Hs.231581; myosin, heavy polypeptide 1, s; sarc; diag
 406850; A1624300; Hs.172928; collagen, type I, alpha 1; sarc; CTL+s.m.
 5 406906; Z25424; ; gb:H.sapiens protein-serine/th; blad, lung; s.m.
 406937; U14622; ; gb:Human transketolase-like pr; test; s.m.
 406967; M24349; ; gb:Human parathyroid hormone-l; lung; CTL+s.m.
 406974; M57293; ; gb:Human parathyroid hormone-r; lung, blad; diag
 10 407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial; sarc; diag
 407034; U84540; ; gb:Human dystrobrevin isoform ; glio; diag
 407103; AA424881; Hs.256301; hypothetical protein MGC13170; pros; diag
 407118; AA156790; Hs.262036; ESTs, Weakly similar to Z223_H; pros; diag
 407122; H20276; Hs.31742; ESTs; pros; diag
 15 407137; T97307; ; gb:ye53h05.s1 Soares fetal liv; lung, blad, ovar, pros, panc, headnk; diag
 407168; R45175; Hs.117183; ESTs; pros, breast, colon; diag
 407178; AA195651; Hs.352312; AP-2 beta transcription factor; breast ; CTL+s.m.
 407202; N58172; Hs.109370; ESTs; pros; diag
 407216; N91773; Hs.348385; lysyl oxidase; panc; diag
 20 407242; M18728; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung, ovar, cerv; mAb
 407244; M10014; ; fibrinogen, gamma polypeptide; lung; diag
 407245; X90568; Hs.172004; tilin; sarc; diag
 407251; U67611; Mm.29182; transaldolase 1; pros; s.m.
 407252; AA659037; Hs.163780; ESTs; angio; CTL+s.m.
 25 407276; A1951118; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
 407289; AA135159; Hs.203349; Homo sapiens cDNA FLJ12149 fis; lung; diag
 407366; AF026942; Hs.17518; gb:Homo sapiens cig33 mRNA, pa; ovar, hepC, stom, mela, esoph; diag
 407581; R48402; Hs.173508; P3ECSL; blad; CTL+s.m.
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gat; blad; mAb
 30 407619; AL050341; Hs.37165; collagen, type IX, alpha 2; sarc; diag
 407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-; lung, headnk; s.m.
 407710; AW022727; Hs.23616; ESTs; test; diag
 407720; AB037776; Hs.38002; KIAA1355 protein; lung; mAb
 407746; AK001962; Hs.38114; hypothetical protein FLJ11100; lung; diag
 35 407756; AA116021; Hs.38260; ubiquitin specific protease 18; panc, lung, esoph, fibro, mela; CTL+s.m.
 407758; D50915; Hs.38365; KIAA0125 gene product; lung; diag
 407777; AA161071; Hs.71465; squalene epoxidase; panc, esoph; s.m.
 407782; AA608956; Hs.112619; ESTs, Moderately similar to PU; lung; diag
 407786; AA687538; Hs.38972; tetraspan 1; pros, colon, uter, stom, ovar, cerv; mAb
 40 407788; BE514982; Hs.38991; S100 calcium-binding protein A; headnk, panc, blad, lung, fibro; diag
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; test; CTL+s.m.
 407824; AA147884; Hs.9812; Homo sapiens cDNA FLJ14388 fis; sarc; diag
 407839; AA045144; Hs.161566; ESTs; blad, headnk; mAb
 407846; AA426202; Hs.40403; Cbp/p300-interacting transacti; mela; diag
 45 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homo; colon, stom, renal, breast, ovar, uter, cerv; diag
 407856; AA045281; Hs.266175; phosphoprotein associated with; mela; diag
 407872; AB039723; Hs.40735; frizzled (Drosophila) homolog ; ovar; mAb
 407881; AW072003; Hs.40968; heparan sulfate (glucosamine) ; panc; s.m.
 407910; AA650274; Hs.41296; fibronectin leucine rich trans; fibro; mAb
 50 407944; R34008; Hs.239727; desmocollin 2; lung, headnk, esoph; mAb
 407949; W21874; Hs.247057; ESTs, Weakly similar to 210926; fibro, blad; diag
 407962; A1133530; Hs.62930; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (; breast, pros, blad, lung, headnk, cerv, esoph; mAb+CTL
 408015; AW136771; Hs.244349; epidermal differentiation comp; mela, sarc; diag
 55 408045; AW138959; Hs.245123; ESTs; breast ; diag
 408056; AA312329; Hs.42331; ephrin-A4; ovar; diag
 408063; BE086548; Hs.381047; calcineurin-binding protein ca; pros, lung; diag
 408081; AW451597; Hs.167409; intron of basic-helix-loop-hel; ovar, glio; diag
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; breast, lung, stom; s.m.
 408122; A1432652; Hs.42824; hypothetical protein FLJ10718; lung; diag
 60 408209; NM_004454; Hs.43697; ets variant gene 5 (ets-relate; mela; CTL+s.m.
 408296; AL117452; Hs.44155; DKFZP586G1517 protein; angio; diag
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D; panc, renal, colon; mAb
 408353; BE439838; Hs.44298; mitochondrial ribosomal protei; lung; diag
 65 408430; S79876; Hs.44926; dipeptidylpeptidase IV (CD26, ; pros; mAb
 408522; A1541214; Hs.46320; Small proline-rich protein SPR; lung, blad, headnk, eosph, cerv; diag
 408561; A1308037; Hs.84120; hypothetical protein MGC13016; mela; CTL+s.m.
 408570; AL046406; Hs.103483; KIAA1798 protein; angio; CTL+s.m.
 408572; AA055611; Hs.226568; ESTs, Moderately similar to AL; lung; diag
 70 408591; AF015224; Hs.46452; mammaglobin 1; breast, cerv; diag
 408611; NM_004367; Hs.46468; chemokine (C-C motif) receptor; mela; mAb
 408633; AW963372; Hs.222088; PRO2000 protein; blad, lung, headnk, pros; diag
 408660; AA525775; Hs.89040; ESTs, Moderately similar to PC; ovar, panc, pros, esoph, sarc; diag
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; test; diag
 408758; NM_003686; Hs.47504; exonuclease 1; mela; CTL+s.m.
 75 408770; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 408771; AW732573; Hs.47584; potassium voltage-gated channe; lung; mAb
 408780; D31797; Hs.652; tumor necrosis factor (ligand); leuk; diag
 408795; AW749126; Hs.170345; hypothetical protein FLJ13710; ovar; diag
 80 408826; AF216077; Hs.48376; Homo sapiens clone HB-2 mRNA s; panc, pros; diag
 408833; AW612232; Hs.254835; ESTs; pros; diag
 408877; AA479033; Hs.130315; ESTs, Weakly similar to A47582; breast; diag
 408915; NM_016651; Hs.48950; heptacellular carcinoma novel ; panc, sarc; diag
 408930; AA146721; Hs.334686; hypothetical protein FLJ21588; blad; CTL+s.m.

- 408962; BE386436; Hs.44317; SRY (sex determining region Y); mela; diag
 408992; AA059325; Hs.30114; guanine nucleotide binding pro; lung; diag
 408996; AI979168; Hs.82226; glycoprotein (transmembrane) n; mela; mAb+s.m.
 409012; AL117435; Hs.49725; DKFZP434I216 protein; sarc; CTL+s.m.
 409038; T97490; Hs.50002; small inducible cytokine subfa; mela; diag
 409051; AA080912; ; gb:zn04d03.r1 Stratagene hNT n; pros; s.m.
 409077; AA063037; Hs.66803; ESTs; lung; diag
 409093; BE243834; Hs.50441; CGI-04 protein; lung; diag
 409123; AA063403; ; gb:zm04d12.s1 Stratagene corne; pros; s.m.
 409142; AL136877; Hs.50758; SMC4 (structural maintenance o; ovar, lung, mela; diag
 409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibro; diag
 409200; AL042914; Hs.51039; KIAA0076 gene product; sarc; CTL+s.m.
 409203; AA780473; Hs.687; cytochrome P450, subfamily IVB; fibro, blad, ovar; diag
 409228; R16811; Hs.22010; ESTs, Weakly similar to 210926; lung; mAb
 409231; AA446644; Hs.692; GA733-2 antigen; epithelial gl; pros, ovar, breast, uter, panc, colon, stom; mAb
 409243; AB037761; Hs.51743; KIAA1340 protein; test; diag
 409262; AK000631; Hs.52256; hypothetical protein FLJ20624; pros; CTL+s.m.
 409264; NM_014937; Hs.52463; KIAA0966 protein; mela; CTL+s.m.
 409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-li; breast, ovar, lung, panc, uter; mAb
 409327; L41162; Hs.53563; collagen, type IX, alpha 3; colon, panc, sarc; CTL+s.m.
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; mela; CTL+s.m.
 409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; test; CTL+s.m.
 409346; AI401535; Hs.146090; ESTs; renal, glio; diag
 409361; NM_005982; Hs.54416; sine oculis homeobox (Drosophi; blad, lung, pros; CTL+s.m.
 409389; AB007979; Hs.301281; Homo sapiens mRNA, chromosome ; glio; diag
 409395; U46745; Hs.336678; dystrobrevin, alpha; glio; diag
 409402; AF208234; Hs.695; cystatin B (stefin B); blad; diag
 409415; AA579258; Hs.6083; Homo sapiens cDNA: FLJ21028 fi; mela; diag
 409421; AA199883; Hs.67624; ESTs; test; diag
 409430; R21945; Hs.346735; splicing factor, arginine/seri; mela; diag
 409432; D49372; Hs.54460; small inducible cytokine subfa; stom, esoph; diag
 409433; AA074382; Hs.135255; ESTs; glio, sarc; diag
 409509; AL036923; Hs.322710; ESTs; angio; diag
 409512; AW979187; Hs.293591; melanoma differentiation assoc; mela, esoph; CTL+s.m.
 409542; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
 409582; R27430; Hs.271565; ESTs; lung; diag
 409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyper; headnk, mela, sarc; CTL+s.m.
 409633; AW449822; Hs.55200; ESTs; sarc; diag
 409637; AA323948; Hs.55407; Homo sapiens mRNA; cDNA DKFZp4; renal; diag
 409638; AW450420; Hs.21335; ESTs; glio; diag
 409670; AI368109; Hs.381163; KIAA1856 protein; test; CTL+s.m.
 409703; NM_006187; Hs.56009; 2'-5'-oligoadenylate synthetas; panc, esoph, mela; s.m.
 409705; M37762; Hs.56023; brain-derived neurotrophic fac; lung; diag
 409719; AI769160; Hs.108681; Homo sapiens brain tumor assoc; lung; diag
 409731; AA125985; Hs.56145; thymosin, beta, identified in ; pros, sarc; CTL+s.m.
 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal ; ovar, renal; CTL+s.m.
 409935; AW511413; Hs.187393; ESTs; lung; diag
 409958; NM_001523; Hs.57697; hyaluronan synthase 1; panc, ovar; mAb
 409988; N27687; Hs.334334; transcription factor AP-2 alph; mela; diag
 410006; AW732308; Hs.57783; eukaryotic translation initiat; test; diag
 410037; AB020725; Hs.58009; KIAA0918 protein; pros; diag
 410044; BE566742; Hs.58169; highly expressed in cancer, ri; blad; diag
 410048; W76467; Hs.343874; proline oxidase homolog; test; s.m.
 410076; T05387; Hs.7991; ESTs; lung, pros; diag
 410079; U94362; Hs.380757; glycogenin 2; mela; diag
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; pros; diag
 410102; AW248508; Hs.279727; ESTs; homologue of PEM-3 [Cion; ovar, breast, blad, lung, angio, sarc; diag
 410174; AA306007; Hs.59461; DKFZP434C245 protein; mela; diag
 410240; AL157424; Hs.61289; synaptotagmin 2; angio; diag
 410247; AF181721; Hs.61345; RU2S; ovar; CTL+s.m.
 410268; AA316181; Hs.61635; six transmembrane epithelial a; panc, pros, EWS; mAb+CTL
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A; mela; diag
 410310; J02931; Hs.62192; coagulation factor III (thromb; pros, panc; mAb
 410361; BE391804; Hs.62661; guanylate binding protein 1, i; mela, esoph, hepC, fibro, uter; diag
 410438; AW748012; Hs.45207; hypothetical protein KIAA1335; lung; CTL+s.m.
 410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; breast, colon, uter, stom; diag
 410480; R97457; Hs.63984; cadherin 13, H-cadherin (heart; angio; mAb
 410491; AA465131; Hs.64001; Homo sapiens clone 25218 mRNA ; mela, esoph; diag
 410530; M25809; Hs.64173; ATPase, H transporting, lysoso; ovar; mAb
 410553; AW016824; Hs.272068; hypothetical protein MGC14128; blad, lung; diag
 410555; U92649; Hs.380136; a disintegrin and metalloprote; leuk, lung; mAb
 410561; BE540255; Hs.6994; Homo sapiens cDNA: FLJ22044 fi; lung; diag
 410566; AA373210; Hs.43047; Homo sapiens cDNA FLJ13585 fis; panc; diag
 410600; AW575742; Hs.351676; ESTs, Moderately similar to S6; mela; mAb+s.m.
 410621; AA194329; Hs.172004; titin; sarc; diag
 410681; AW246890; Hs.65425; calbindin 1, (28kD); lung; diag
 410687; U24389; Hs.65436; lysyl oxidase-like 1; panc; diag
 410733; D84284; Hs.66052; CD38 antigen (p45); pros; mAb+CTL
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; panc; mAb
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; test; CTL+s.m.
 410867; X63556; Hs.750; fibrillin 1 (Marfan syndrome); panc; diag
 410870; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
 410883; D43767; Hs.66742; CCL17 chemokine (TARC) (SCYA1; leuk; diag

- 410889; X91662; Hs.66744; twist (Drosophila) homolog (ac; sarc; CTL+s.m.
 410929; H47233; Hs.30643; ESTs; ovar, test; diag
 411078; A1222020; Hs.182364; CocoaCrisp; pros, glio, breast; diag
 411089; AA456454; Hs.214291; cell division cycle 2-like 1; lung, fibro; CTL+s.m.
 411243; AB039886; Hs.69319; CA11; esoph; diag
 411248; AA551538; Hs.69321; Homo sapiens cDNA FLJ14408 fis; blad; diag
 411257; AA628967; Hs.115274; Indian hedgehog protein (IHH); ovar; diag
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centro; lung, blad, headnk; CTL+s.m.
 411296; BE207307; Hs.10114; growth suppressor 1; sarc; diag
 411358; R47479; Hs.94761; KIAA1691 protein; mela,renal, sarc; mAb
 411388; X72925; Hs.69752; desmocollin 1; headnk, mela; mAb
 411393; AW797437; Hs.69771; B-factor, properdin (COMPLEMEN; ovar; diag
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); panc, pros, stom, breast, uter, cerv, ovar; mAb
 411573; AB029000; Hs.70823; KIAA1077 protein; panc, headnk, lung, stom; diag
 411579; AC005258; Hs.70830; U6 snRNA-associated Sm-like pr; lung; diag
 411732; U47924; Hs.71642; guanine nucleotide binding pro; lung; diag
 411768; NM_013371; Hs.71979; interleukin 19; ovar, uter, cerv; diag
 411789; AF245505; Hs.72157; Adican; breast, panc, lung, stom, headnk, ovar, uter, esoph, sarc; diag
 411825; AK000334; Hs.352415; solute carrier family 39 (zinc; colon, ovar; mAb
 411828; AW161449; Hs.72290; wingless-type MMTV integration; ovar; diag
 411869; W20027; Hs.23439; ESTs; angio; diag
 411874; AA096106; Hs.20403; ESTs; blad; diag
 411880; AW872477; ; gb:hm30f03.x1 NCI_CGAP_Thy4 Ho; blad; diag
 411945; AL033527; Hs.92137; L-my-2 protein (MYCL2); blad, ovar; CTL+s.m.
 412006; AW451618; Hs.380683; ESTs; sarc; diag
 412026; AA383618; Hs.73073; testis-specific ankyrin motif; test; diag
 412045; AA099802; Hs.83883; transmembrane, prostate androg; pros; mAb+s.m.
 412099; U64198; Hs.73165; interleukin 12 receptor, beta; leuk, mela; mAb
 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN; panc, fibro; diag
 412115; AK001763; Hs.73239; hypothetical protein FLJ10901; lung, blad; CTL+s.m.
 412116; AW402166; Hs.784; Epstein-Barr virus induced gen; panc; mAb
 412133; U83460; Hs.380728; solute carrier family 31 (copp; pros; mAb
 412228; AW503785; Hs.73792; complement component (3d/Epste; mela; mAb
 412247; AF022375; Hs.73793; vascular endothelial growth fa; renal, glio, blad, colon; diag
 412265; AA101325; Hs.86154; hypothetical protein FLJ12457; test; CTL+s.m.
 412326; R07566; Hs.73817; small inducible cytokine A3 (h; pros, leuk; diag
 412351; AL135960; Hs.73828; T-cell acute lymphocytic leuke; angio; CTL+s.m.
 412420; AL035668; Hs.73853; bone morphogenetic protein 2; blad, glio, lung, stom, angio; diag
 412448; L12964; Hs.73895; tumor necrosis factor receptor; leuk; mAb
 412471; M63193; Hs.73946; endothelial cell growth factor; cerv, mela, esoph; diag
 412490; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22528 fi; mela; diag
 412519; AA196241; Hs.73980; troponin T1, skeletal, slow; sarc; diag
 412530; AA766268; Hs.266273; hypothetical protein FLJ13346; blad, lung; diag
 412564; X83703; Hs.355934; cardiac ankyrin repeat protein; angio; diag
 412580; AA113262; Hs.17901; similar to CABLES [Homo sapien; mela; diag
 412610; X90908; Hs.74126; fatty acid binding protein 6; ; blad; diag
 412661; N32860; Hs.24611; ESTs, Weakly similar to I54374; blad; CTL+s.m.
 412715; NM_000947; Hs.74519; primase, polypeptide 2A (58kD); pros; s.m.
 412723; AA648459; Hs.335951; hypothetical protein AF301222; lung, blad, headnk, colon, stom, uter; diag
 412755; BE144306; Hs.179891; ESTs, Weakly similar to P4HA_H; angio; s.m.
 412811; H06382; Hs.349705; ESTs; lung; diag
 412817; AL037159; Hs.74619; proteasome (prosome, macropain; lung; s.m.
 412843; AF007555; Hs.74624; protein tyrosine phosphatase, ; pros; mAb
 412856; BE386745; Hs.74631; basigin (OK blood group); mela; mAb
 412926; A1879076; Hs.75061; macrophage myristoylated alani; mela; CTL+s.m.
 412939; AW411491; Hs.75069; eukaryotic translation elongat; mela, renal; diag
 412970; AB026436; Hs.177534; dual specificity phosphatase 1; breast, mela; s.m.
 412986; X81120; Hs.75110; cannabinoid receptor 1 (brain); glio; mAb
 413004; T35901; Hs.75117; interleukin enhancer binding f; lung; diag
 413011; AW068115; Hs.821; biglycan; lung; CTL+s.m.
 413049; NM_002151; Hs.823; hepsin (transmembrane protease; pros; mAb
 413095; AA494359; Hs.30715; potassium voltage-gated channe; panc, stom, renal, colon; mAb+s.m.
 413125; BE244589; Hs.75207; glyoxalase I; pros; s.m.
 413126; AW419203; Hs.174174; ESTs; angio; diag
 413129; AF292100; Hs.104613; RP42 homolog; lung; diag
 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent; angio; CTL+s.m.
 413142; M81740; Hs.75212; ornithine decarboxylase 1; lung; s.m.
 413163; Y00815; Hs.75216; protein tyrosine phosphatase, ; pros; mAb
 413171; AA318325; Hs.75219; tyrosinase-related protein 1; mela; mAb
 413190; AA151802; Hs.40368; adaptor-related protein comple; mela; diag
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis; esoph, cerv; diag
 413223; A1732182; Hs.191866; ESTs; lung; diag
 413268; AL039079; Hs.75256; regulator of G-protein signal; headnk; CTL+s.m.
 413281; AA861271; Hs.222024; transcription factor BMAL2; lung, blad, headnk, panc, angio; diag
 413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; test; s.m.
 413328; Y15723; Hs.75295; guanylate cyclase 1, soluble, ; pros; s.m.
 413335; A1613318; Hs.48442; ESTs; ovar; diag
 413364; BE536218; Hs.137516; fidgetin-like 1; lung; diag
 413372; H55532; Hs.349695; tubulin, alpha 2; test; diag
 413435; X51405; Hs.75360; carboxypeptidase E; pros, glio, panc, sarc; diag
 413436; AF238083; Hs.68061; sphingosine kinase 1; sarc; s.m.
 413472; BE242870; Hs.75379; solute carrier family 1 (glial; glio; mAb
 413566; AW604451; Hs.381153; sprouty (Drosophila) homolog 4; sarc; CTL+s.m.

- 413573; AI733859; Hs.149089; ESTs; lung; diag
 413582; AW295647; Hs.71331; hypothetical protein MGC5350; lung; diag
 413597; AW302885; Hs.117183; ESTs; pros; diag
 413623; AA825721; Hs.246973; intron of Bicaudal D homolog 1; ovar, pros; diag
 413691; AB023173; Hs.75478; ATPase, Class VI, type 11B; lung; mAb
 413711; AW291765; Hs.75486; heat shock transcription facto; renal; diag
 413753; U17760; Hs.75517; laminin, beta 3 (nicein (125kD); lung, blad, headnk, panc, cerv, esoph, colon; diag
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); test; diag
 413778; AA090235; Hs.75535; myosin, light polypeptide 2, r; sarc; diag
 413794; AF234532; Hs.61638; myosin X; mela; diag
 413804; T64682; ; gb:yc48b02.r1 Stratagene liver; blad; diag
 413808; J00287; Hs.350038; Homo sapiens mRNA for caldesmo; esoph; diag
 413813; M96956; Hs.75561; teratocarcinoma-derived growth; colon; diag
 413833; Z15005; Hs.75573; centromere protein E (312kD); lung; CTL+s.m.
 413842; M29383; Hs.856; interferon, gamma; leuk; diag
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; fibro, renal; mAb
 413880; AI660842; Hs.110915; interleukin 22 receptor; panc, colon; mAb+s.m.
 413924; AL119964; Hs.75616; seladin-1; pros, breast, ovar; diag
 413943; AW294416; Hs.144687; Homo sapiens cDNA FLJ12981 fis; blad, lung; CTL+s.m.
 413985; AI018666; Hs.75667; synaptophysin; glio, sarc; mAb
 414004; AA737033; Hs.7155; ESTs, Moderately similar to 21; panc, mela; diag
 414020; NM_002984; Hs.75703; CCL4 Chemokine (C-C motif) lig; pros; diag
 414034; U89277; Hs.305985; early development regulator 1; test; CTL+s.m.
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase; lung, cerv, headnk, blad; s.m.
 414053; BE391635; Hs.75725; transgelin 2; blad; diag
 414061; NM_000699; Hs.300280; amylase, alpha 2A; pancreatic; ovar; diag
 414065; AW515373; Hs.271249; Homo sapiens cDNA FLJ13580 fis; pros; diag
 414085; AA114016; Hs.75746; aldehyde dehydrogenase 1 famil; pros, panc, sarc; s.m.
 414142; AW368397; Hs.334485; hemicentin (fibulin 6); fibro, panc, sarc; diag
 414161; AA136106; Hs.184852; KIAA1553 protein; test; diag
 414166; AW888941; Hs.75789; N-myc downstream regulated; pros, renal; diag
 414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fi; glio; diag
 414219; W20010; Hs.75823; ALL1-fused gene from chromosom; sarc; diag
 414221; AW450979; ; gb:U1-H-BI3-ala-a-12-0-UI.s1 N; blad; diag
 414251; AL042306; Hs.97689; VASA protein; test; CTL+s.m.
 414259; W44633; Hs.301296; integrin, beta-like 1 (with EG; panc; diag
 414334; AA824298; Hs.21331; hypothetical protein FLJ10036; test; diag
 414359; M62194; Hs.75929; cadherin 11, type 2, OB-cadher; breast, ovar, uter, pros, colon, panc, sarc; mAb
 414368; W70171; Hs.75939; uridine monophosphate kinase; lung; s.m.
 414386; X00442; Hs.75990; haptoglobin; ovar; diag
 414416; AW409985; Hs.76084; hypothetical protein MGC2721; blad, lung; CTL+s.m.
 414420; AA043424; Hs.76095; immediate early response 3; panc, colon; diag
 414430; AI346201; Hs.76118; ubiquitin carboxyl-terminal es; lung; s.m.
 414443; AU077268; Hs.76144; platelet-derived growth factor; sarc, panc, headnk; mAb
 414476; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
 414477; U41635; Hs.76228; amplified in osteosarcoma; sarc; diag
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antig; mela; mAb
 414521; D28124; Hs.76307; neuroblastoma, suppression of; breast, ovar, uter, pros, blad, panc, colon, stom, fibr; diag
 414565; AA502972; Hs.183390; hypothetical protein FLJ13590; pros; diag
 414569; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
 414575; H11257; Hs.375743; Homo sapiens clone IMAGE:45193; renal; diag
 414595; AA641726; Hs.289015; hypothetical protein MGC4171; blad; diag
 414602; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; pros; mAb
 414683; S78296; Hs.76888; hypothetical protein MGC12702; blad, lung, test; diag
 414732; AW410976; Hs.77152; minichromosome maintenance def; test, blad; diag
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila); lung, blad, test; CTL+s.m.
 414776; AA155598; Hs.212839; hypothetical protein FLJ14195; angio; diag
 414786; AI246482; Hs.243010; Homo sapiens cDNA FLJ14372 fis; angio; diag
 414799; AI752416; Hs.77326; insulin-like growth factor bin; renal; diag
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; lung; mAb
 414807; AI738616; Hs.77348; hydroxyprostaglandin dehydroge; blad; s.m.
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD7; lung; mAb+s.m.
 414825; X06370; Hs.77432; epidermal growth factor recept; glio, lung, renal, esoph, panc, headnk, leuk; mAb+s.m.
 414915; NM_002462; Hs.76391; myxovirus (influenza) resistant; esoph; diag
 414918; AI219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
 414921; BE390551; Hs.77628; steroidogenic acute regulatory; breast; diag
 414945; BE076358; Hs.77667; lymphocyte antigen 6 complex, ; mela; mAb
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; blad, panc, esoph; diag
 414998; NM_002543; Hs.77729; oxidised low density lipoprote; fibro, ovar, panc, colon; mAb
 415003; M11437; Hs.77741; kininogen; panc; diag
 415025; AW207091; Hs.72307; ESTs; blad; diag
 415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-Co; lung, headnk; s.m.
 415178; D80503; Hs.46692; ESTs; blad; diag
 415214; AI445236; Hs.125124; EphB2; colon, stom; mAb
 415314; N88802; Hs.5422; glycoprotein M6B; mela; mAb
 415457; AW081710; Hs.7369; Homo sapiens testes specific A; fibro, ovar, uter; CTL+s.m.
 415511; AI732617; Hs.182362; ESTs; blad, ovar, renal; diag
 415542; R13474; Hs.290263; ESTs, Weakly similar to I38022; blad; diag
 415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SM; test; CTL+s.m.
 415752; BE314524; Hs.78776; putative transmembrane protein; endo, uter, breast, stom, blad, mela; mAb
 415786; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
 415787; H01463; Hs.93534; ESTs; pros; diag
 415819; AU077330; Hs.360791; transcription elongation facto; test; CTL+s.m.

- 415829; AW450198; Hs.163742; ESTs; test; diag
 415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fis; lung, test; diag
 415910; U20350; Hs.78913; chemokine (C-X3-C) receptor 1; glio; mAb
 415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colo; test; diag
 415989; AI267700; Hs.351201; ESTs; pros, ovar, blad, lung, headnk, panc, colon, sarc; diag
 415992; C05837; Hs.145807; hypothetical protein FLJ13593; pros, fibro; mAb
 415999; AA172179; Hs.294029; ESTs; pros, uter; diag
 416018; AW138239; Hs.78977; proprotein convertase subtilis; colon, panc, lung; diag
 416030; H15261; Hs.21948; ESTs; breast, fibro; diag
 416065; BE267931; Hs.78996; proliferating cell nuclear ant; blad, lung, headnk, mela; CTL+s.m.
 416111; AA033813; Hs.79018; chromatin assembly factor 1, s; lung, stom; CTL+s.m.
 416188; BE157260; Hs.79070; v-myc avian myelocytomatosis v; pros; diag
 416201; AA467752; Hs.195161; ESTs; test; diag
 416208; AW291168; Hs.41295; ESTs, Weakly similar to MUC2_H; lung; diag
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calc; ovar; diag
 416225; AA577730; Hs.188684; ESTs, Weakly similar to PC4259; pros, blad; diag
 416350; AF188625; Hs.189507; phospholipase A2, group IID; test, mela, fibro; diag
 416370; N90470; Hs.203697; CD38 antigen (p45); pros, glio; mAb+CTL
 416373; AA195845; Hs.73680; ESTs, Weakly similar to S12658; sarc; diag
 416402; NM_000715; Hs.1012; complement component 4-binding; fibro; diag
 416448; L13210; Hs.79339; lectin, galactoside-binding, s; ovar, colon, stom; diag
 416498; U33632; Hs.79351; potassium channel, subfamily K; panc, stom, breast, ovar, colon; mAb
 416539; Y07909; Hs.79368; epithelial membrane protein 1; pros, headnk; diag
 416602; NM_006159; Hs.367895; Protein kinase C-binding prote; breast; diag
 416640; BE262478; Hs.13406; neuron-specific protein; mela; diag
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; blad, lung, headnk, cerv, panc, angio; diag
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; test; CTL+s.m.
 416815; U41514; Hs.80120; UDP-N-acetyl-alpha-D-galactosa; angio; s.m.
 416819; U77735; Hs.80205; pim-2 oncogene; lung, test; diag
 416881; N32520; Hs.141358; ESTs; mela; diag
 416929; N20535; Hs.43265; melastatin 1; mela; diag
 416975; NM_004131; Hs.1051; granzyme B (granzyme 2, cytol; mela; s.m.
 417003; AL038170; Hs.80756; betaine-homocysteine methyltra; blad; s.m.
 417070; Z19077; Hs.172004; titin; sarc; diag
 417105; X60992; Hs.81226; CD6 antigen; fibro; mAb
 417115; AVW952792; Hs.334612; small nuclear ribonucleoprotei; test; CTL+s.m.
 417124; BE122762; Hs.25338; ESTs; angio; diag
 417148; AA359896; Hs.374554; hypothetical protein FLJ14902; panc; diag
 417151; AA194055; Hs.293858; ESTs; blad; diag
 417153; X57010; Hs.81343; collagen, type II, alpha 1 (pr; pros, sarc; diag
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte; lung; mAb+s.m.
 417237; H86385; Hs.81737; palmitoyl-protein thioesterase; mela; s.m.
 417259; AW903838; Hs.81800; chondroitin sulfate proteoglyc; panc, breast; diag
 417275; X63578; Hs.295449; parvalbumin; blad; diag
 417295; AW993524; Hs.43148; epithelial membrane protein 1; pros; diag
 417308; H60720; Hs.81892; KIAA0101 gene product; lung, headnk, blad, cerv, angio, mela, sarc; diag
 417312; AW888411; Hs.250811; leukemia-associated phosphopro; blad; CTL+s.m.
 417333; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag
 417355; D13168; Hs.82002; endothelin receptor type B; glio, mela; mAb
 417365; D50683; Hs.82028; transforming growth factor, be; fibro, angio; mAb
 417366; BE185289; Hs.1076; small proline-rich protein 1B; lung, blad, headnk, panc, esoph, mela; diag
 417370; T28651; Hs.374466; tryptophanyl-tRNA synthetase; fibro, mela; diag
 417391; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.
 417400; AA663486; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag
 417407; AA923278; Hs.290905; ESTs, Weakly similar to protea; test, pros; s.m.
 417409; BE272506; Hs.82109; syndecan 1; blad; diag
 417412; X16896; Hs.82112; interleukin 1 receptor, type I; fibro, pros, panc; mAb
 417426; NM_002291; Hs.82124; laminin, beta 1; angio; diag
 417437; U52682; Hs.82132; interferon regulatory factor 4; mela; CTL+s.m.
 417512; X76534; Hs.82226; glycoprotein (transmembrane) n; lung, mela, headnk, panc, breast; mAb
 417515; L24203; Hs.82237; ataxia-telangiectasia group D; lung, headnk, blad; diag
 417542; J04129; Hs.82269; progesterone-associated endomet; lung, mela; diag
 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383; test; diag
 417599; AA204688; Hs.62954; ESTs; blad, esoph; diag
 417621; AV654694; Hs.82316; interferon-induced, hepatitis; esoph; diag
 417696; BE241624; Hs.82401; CD69 antigen (p60, early T-cell; pros; mAb
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; test; mAb
 417715; AW969587; Hs.86366; ESTs; blad, lung, headnk; diag
 417720; AA205625; Hs.208067; ESTs; blad, lung, esoph, headnk; diag
 417750; AI267720; Hs.260523; synovial sarcoma, translocated; sarc; diag
 417777; AI823763; Hs.7055; ESTs, Weakly similar to I78885; test; s.m.
 417791; AW965339; Hs.44269; ESTs; ovar, blad, lung, headnk; CTL+s.m.
 417801; AA417383; Hs.82582; integrin, beta-like 1 (with EG; panc, fibro; diag
 417805; U38545; Hs.82587; phospholipase D1, phosphatidylc; angio; s.m.
 417831; H16423; Hs.82685; CD47 antigen (Rh-related antig; ovar; mAb
 417843; W07361; Hs.22545; Homo sapiens cDNA FLJ12935 fis; pros; diag
 417847; AI521558; Hs.7331; hypothetical protein FLJ22316; ovar; diag
 417849; AW291587; Hs.82733; nidogen 2; angio, headnk; diag
 417874; BE616160; Hs.82829; protein tyrosine phosphatase; panc; mAb+s.m.
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesio; mela; mAb
 417886; AA214584; ESTs; test, ovar; diag
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20; lung, stom, test, blad, headnk, cerv, esoph; CTL+s.m.
 417911; AA333387; Hs.82916; chaperonin containing TCP1, su; test; diag

- 417944; AU077196; Hs.82985; collagen, type V, alpha 2; sarc; diag
 417975; AA641836; Hs.30085; hypothetical protein FLJ23186; colon, stom, lung; mAb
 417976; BE565892; Hs.83077; interleukin 18 (interferon-gam; colon, stom, fibros; diag
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 famli; lung, headnk, esoph; s.m.
 418036; Z37976; Hs.83337; latent transforming growth fac; angio; diag
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lung, angio, test, sarc; diag
 418067; AI127958; Hs.83393; cystatin E/M; headnk, panc, blad; diag
 418068; AW971155; Hs.293902; ESTs, Weakly similar to 1SHUSS; blad; s.m.
 418113; AI272141; Hs.83484; SRY (sex determining region Y); blad, breast, uter, colon, lung, ovar, glio, test, sarc; CTL+s.m.
 418134; AA397769; Hs.86617; ESTs; test; diag
 418140; BE613836; Hs.83551; microfibrillar-associated prot; lung, headnk, esoph, ovar, sarc; diag
 418156; W17056; Hs.83623; nuclear receptor subfamily 1, ; fibro; mAb+s.m.
 418203; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, test, mela, stom; s.m.
 418216; AA662240; Hs.283099; AF15q14 protein; headnk, lung, blad; diag
 418245; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
 418283; S79895; Hs.83942; cathepsin K (pseudosostosis); breast, cerv, ovar, uter, pros, headnk, lung, panc, colon, stom; diag
 418318; U47732; Hs.84072; transmembrane 4 superfamily me; panc, pros, colon, stom, omuc; mAb
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibi; headnk, lung, blad; s.m.
 418338; NM_002522; Hs.84154; neuronal pentraxin I; sarc; diag
 418339; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
 418345; AJ001696; Hs.241407; serine (or cysteine) proteinases; cerv, lung; s.m.
 418371; M13560; Hs.84298; CD74 antigen (invariant polype; renal; mAb
 418379; AA218940; Hs.137516; fidgetin-like 1; lung; diag
 418394; AF132818; Hs.84728; Kruppel-like factor 5 (intesti; panc; CTL+s.m.
 418396; AI765805; Hs.26691; SLC2A12 Solute carrier family ; pros; mAb
 418397; NM_001269; Hs.84746; chromosome condensation 1; lung; diag
 418399; AF131781; Hs.84753; hypothetical protein FLJ12442; test, blad, sarc; diag
 418406; X73501; Hs.84905; cytokeratin 20; blad, colon; diag
 418432; M14156; Hs.85112; insulin-like growth factor 1 (; pros, fibro; diag
 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide; fibro; mAb
 418462; BE001596; Hs.85266; integrin, beta 4; lung, blad, cerv, headnk, ovar; mAb
 418543; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb
 418576; AW968159; Hs.302740; Epithelial calcium channel 2, ; pros; mAb+s.m.
 418610; AW245993; Hs.32417; hypothetical protein MGC2742; pros; diag
 418641; BE243136; Hs.86947; a disintegrin and metalloprote; cerv, lung, panc, blad, headnk, stom; mAb
 418655; AA226354; Hs.111240; ESTs; pros; diag
 418661; NM_001949; Hs.1189; E2F transcription factor 3; ovar, lung, mela; CTL+s.m.
 418663; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk, cerv, esoph; mAb
 418683; U90908; Hs.87241; hypothetical protein from clon; angio; CTL+s.m.
 418686; Z36830; Hs.87268; annexin A8; blad, lung; diag
 418693; AI750878; Hs.87409; thrombospondin 1; angio, panc; diag
 418696; AW959433; Hs.326290; hypothetical protein FLJ12581; test; diag
 418739; AA310964; Hs.88012; SHP2 interacting transmembrane; mela; diag
 418756; AA252254; Hs.226949; ESTs; test ; diag
 418825; AA228881; Hs.22394; hypothetical protein FLJ10893; angio; diag
 418829; AA516531; Hs.55999; NK homeobox (Drosophila), fami; pros; diag
 418882; NM_004996; Hs.89433; ATP-binding cassette, sub-fami; ovar, pros, breast, lung; diag
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate r; fibro; s.m.
 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (five; colon, stom, ovar, uter, panc; mAb+s.m.
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red b; mela, fibro; mAb
 418932; L34059; Hs.89484; cadherin 4, type 1, R-cadherin; glio; mAb
 418941; AA452970; Hs.239527; E1B-55kDa-associated protein 5; angio, blad; diag
 418968; NM_000078; Hs.89538; cholesteryl ester transfer pro; mela; diag
 418994; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, angio; mAb
 419038; AW134924; Hs.58290; ESTs; pros; diag
 419073; AW372170; Hs.183918; transmembrane receptor Unc5H2 ; ovar, renal, blad, lung; mAb
 419078; M93119; Hs.89584; insulinoma-associated 1; blad, lung, panc, sarc; diag
 419079; AW014836; Hs.18844; ESTs; esoph, lung, stom, colon; diag
 419086; NM_000216; Hs.89591; Kallmann syndrome 1 sequence; fibro; diag
 419092; J05581; Hs.89603; mucin 1, transmembrane; breast, panc, lung, blad, fibro; mAb
 419222; AD001528; Hs.89718; spermine synthase; pros; s.m.
 419223; X60111; Hs.1244; CD9 antigen (p24); breast, pros, ovar; mAb
 419231; AL046294; Hs.136245; ESTs, Weakly similar to T17227; fibro; diag
 419261; X07876; Hs.89791; wingless-type MMTV integration; panc; diag
 419264; AA877104; Hs.293672; ESTs, Weakly similar to ALUB_H; pros; diag
 419290; AI128114; Hs.112885; spinal cord-derived growth fac; panc; diag
 419356; AI656166; Hs.7331; hypothetical protein FLJ22316; uter, ovar; diag
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeas; lung, blad, test; diag
 419440; AB020689; Hs.90419; KIAA0882 protein; breast; diag
 419485; AA489023; Hs.99807; ESTs, Weakly similar to unname; mela; diag
 419490; NM_006144; Hs.90708; granzyme A (granzyme 1, cytoto; fibro; s.m.
 419519; AI198719; Hs.176376; ESTs; mela; diag
 419551; AW582256; Hs.91011; anterior gradient 2 (Xenopus I; panc, pros, breast; diag
 419559; Y07828; Hs.91096; ring finger protein; blad, colon, stom; CTL+s.m.
 419568; AB026116; Hs.283078; hOAT4; renal; mAb
 419569; AI971651; Hs.91143; jagged 1 (Alagille syndrome); headnk, lung; diag
 419628; H67546; Hs.49768; ESTs; mela, sarc; diag
 419667; AU077005; Hs.92208; a disintegrin and metalloprote; breast, cerv, angio; mAb
 419693; AA133749; Hs.301350; FXYD domain-containing ion tra; pros, breast, ovar, panc, lung; mAb
 419721; NM_001650; Hs.315369; aquaporin 4; glio, lung, fibro; mAb
 419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA ; blad, headnk; diag
 419749; X73608; Hs.93029; sparc/osteoneclin, cwcx and ka; pros, panc, lung; diag
 419752; AA249573; Hs.152618; ESTs, Moderately similar to ZN; lung; diag

- 5 419839; U24577; Hs.93304; phospholipase A2, group VII (p; pros; lung; diag
419870; AW403911; Hs.266175; phosphoprotein associated with; mela; diag
419875; AA853410; Hs.93557; proenkephalin; sarc; diag
419948; AB041035; Hs.93847; NM_016931: Homo sapiens NADPH c; angio; mAb
10 419956; AL137939; Hs.40096; cadherin 19, type 2; mela; mAb
419968; X04430; Hs.93913; interleukin 6 (interferon, bet; lung, panc, esoph; diag
419981; AA897581; Hs.128773; ESTs; angio; diag
420005; AW271106; Hs.133294; ESTs; lung, test, blad, colon; diag
420062; AW411096; Hs.94785; TGF(beta)-induced transcriptio; test; CTL+s.m.
420067; T52431; Hs.94795; Homo sapiens mRNA; cDNA DKFZp5; sarc; diag
420137; AA306478; Hs.95327; CD3D antigen, delta polypeptid; fibro; mAb
420154; AI093155; Hs.95420; G antigen family C 1 protein (; pros, leio; CTL+s.m.
420174; AI824144; Hs.199749; ESTs; angio; CTL+s.m.
15 420208; BE276055; Hs.95972; silver (mouse homolog) like; mela, sarc; mAb
420209; AA256444; Hs.126485; hypothetical protein FLJ12604; angio; diag
420218; AW958037; Hs.381105; ribosomal protein L4; mela, pros; diag
420255; NM_007289; Hs.1298; membrane metallo-endopeptidase; pros; mAb
420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadheri; angio, fibro; mAb
20 420267; N37030; Hs.173337; ESTs; mela, sarc; diag
420281; AI623693; Hs.323494; Predicted cation efflux pump; lung, blad, ovar, panc; mAb
420301; AA767526; Hs.22030; paired box gene 5 (B-cell line; mela; diag
420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339; mela; mAb
420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide; fibro; mAb
25 420344; BE463721; Hs.97101; putative G protein-coupled rec; colon, pros, blad, headnk, panc, stom, ovar; mAb
420347; AL033539; Hs.97124; Human DNA sequence from clone ; test; diag
420360; U83171; Hs.97203; small inducible cytokine subfa; leuk; diag
420367; AA259090; Hs.257028; ESTs; test; diag
420376; AL137471; Hs.97266; protocadherin 18; sarc; mAb+s.m.
30 420378; NM_014143; Hs.97269; B7-H1 protein; leuk; mAb
420380; AA640891; Hs.102406; ESTs; lung; diag
420424; AB033036; Hs.97594; KIAA1210 protein; pros; diag
420462; AF050147; Hs.97932; chondromodulin I precursor; lung, EWS, sarc; mAb
420474; L09753; Hs.1313; tumor necrosis factor (ligand); leuk; mAb
35 420544; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
420576; AA297634; Hs.54925; KIAA1858 protein; sarc; diag
420596; NM_002692; Hs.99185; polymerase (DNA directed), eps; test; CTL+s.m.
420633; NM_014581; Hs.274480; odorant-binding protein 2B (OB; breast, endo; diag
420656; AA279098; Hs.187636; ESTs; fibro; diag
40 420710; NM_007009; Hs.99875; zona pellucida binding protein; test; diag
420729; AW964897; Hs.290825; ESTs; pros; diag
420757; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.
420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 fis; test; diag
420783; AI659838; Hs.99923; lectin, galactoside-binding, s; lung, blad, headnk; diag
45 420789; AI670057; Hs.199882; ESTs; renal; diag
420859; AW468397; Hs.100000; S100 calcium-binding protein A; sarc; diag
420908; AL049974; Hs.100261; Homo sapiens mRNA; cDNA DKFZp5; panc; diag
420923; AF097021; Hs.273321; differentially expressed in he; blad, colon; diag
420931; AF044197; Hs.100431; small inducible cytokine B sub; breast, lung, mela; diag
50 420981; L40904; Hs.100724; peroxisome proliferative activ; colon; mAb+s.m.
421016; AA504583; Hs.101047; transcription factor 3 (E2A im; test; CTL+s.m.
421044; AF061871; Hs.101302; Human DNA sequence from clone ; panc; diag
421059; AI654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.
421064; AI245432; Hs.101382; tumor necrosis factor, alpha-i; blad, uter; diag
55 421070; AA283185; Hs.19327; ESTs; blad; diag
421100; AW351839; Hs.124660; Homo sapiens cDNA: FLJ21763 fi; blad; diag
421133; AA814971; Hs.26410; ESTs; lung; diag
421154; AA284333; Hs.287631; Homo sapiens cDNA FLJ14269 fis; BPH; diag
421155; H87879; Hs.102267; lysyl oxidase; headnk, panc, renal, sarc; diag
60 421218; NM_000499; Hs.72912; cytochrome P450, subfamily I (; blad, angio; diag
421233; AA209534; Hs.284243; tetraspan NET-6 protein; pros, breast, ovar; mAb
421241; X91817; Hs.102866; transketolase-like 1; test; s.m.
421302; T34462; Hs.103291; neuritin; uter, endo ; diag
421305; BE397354; Hs.324830; diphtheria toxin resistance pro; ovar; diag
65 421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, lung, angio, test, sarc; diag
421341; AJ243212; Hs.279611; deleted in malignant brain tum; panc, lung; diag
421350; AW301608; Hs.278188; ESTs, Moderately similar to I5; test; diag
421373; AA808229; Hs.222088; ESTs; blad; diag
421433; AI829192; Hs.22380; ESTs; pros; diag
70 421451; AA291377; Hs.50831; ESTs; ovar, blad, lung; diag
421458; NM_003654; Hs.104576; carbohydrate (keratan sulfate ; sarc; s.m.
421478; AI683243; Hs.97258; ESTs, Moderately similar to S2; ovar, blad, renal, uter; diag
421481; AW391972; Hs.104696; KIAA1324 protein; pros; diag
421502; AF111856; Hs.105039; solute carrier family 34 (sodi; ovar, fibro; mAb
75 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; lung, headnk, esoph; s.m.
421508; NM_004833; Hs.105115; absent in melanoma 2; blad, esoph, lung, mela; CTL+s.m.
421535; AB002359; Hs.105478; phosphoribosylformylglycinamid; test; s.m.
421537; BE383488; Hs.105547; neural proliferation, differen; pros; diag
421566; NM_000399; Hs.1395; early growth response 2 (Krox-; pros; CTL+s.m.
80 421579; NM_002975; Hs.105927; stem cell growth factor; lymph; sarc; mAb
421633; AF121860; Hs.106260; sorting nexin 10; mela; diag
421650; AA781795; Hs.343800; ESTs; mela; diag
421666; AL035250; Hs.1408; endothelin 3; mela; diag
421727; Y13153; Hs.107318; kynurenine 3-monooxygenase (ky; breast; s.m.

- 421773; W69233; Hs.112457; ESTs; mela, esoph, sarc; diag
 421777; BE562088; Hs.108196; HSPC037 protein; esoph, cerv, lung; diag
 421779; AI879159; Hs.108219; wingless-type MMTV integration; colon, ovar; diag
 421798; N74880; Hs.355462; N-acylsphingosine amidohydrolase; fibro; s.m.
 5 421814; L12350; Hs.108623; thrombospondin 2; panc; diag
 421831; AA298836; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 421887; AW161450; Hs.109201; CGI-86 protein; pros; mAb
 421896; N62293; Hs.45107; ESTs; pros; diag
 10 421917; AB028943; Hs.109445; KIAA1020 protein; test; diag
 421920; BE551245; Hs.1438; gamma-aminobutyric acid (GABA); sarc; mAb
 421924; BE514514; Hs.109606; coronin, actin-binding protein; fibro; diag
 421948; L42583; Hs.334309; keratin 6A; lung, headnk, blad, esoph, cerv, mela; diag
 421952; AA300900; Hs.98849; dynein light chain 2B (DNLC2B); fibro; diag
 15 421991; NM_014918; Hs.110488; KIAA0990 protein; panc; diag
 421996; AW583807; Hs.1460; glucagon; panc; diag
 422002; X70070; Hs.110642; neurotensin receptor 1 (high a; colon; mAb
 422027; AL043100; Hs.288828; fatty acid amide hydrolase; pros; s.m.
 422033; AW245805; Hs.110903; claudin 5 (transmembrane prote; glio; mAb
 20 422087; X58968; Hs.111301; matrix metalloproteinase 2 (ge; sarc; diag
 422089; AA523172; Hs.103135; ESTs, Weakly similar to SFR4_H; pros; diag
 422094; AF129535; Hs.272027; F-box only protein 5; blad, lung; CTL+s.m.
 422095; AI868872; Hs.282804; hypothetical protein FLJ22704; lung, panc, ovar, breast; CTL+s.m.
 422099; AA156022; Hs.111518; hypothetical protein; angio; CTL+s.m.
 25 422100; AI096988; Hs.111554; ADP-ribosylation factor-like 7; lung, esoph; CTL+s.m.
 422110; AI376736; Hs.121555; secreted protein, acidic, cyst; panc; diag
 422119; AI277829; Hs.111862; KIAA0590 gene product; blad; diag
 422134; AW179019; Hs.112110; mitochondrial ribosomal protei; lung; diag
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc; blad; mAb+s.m.
 30 422163; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
 422164; NM_014312; Hs.112377; cortic al thymocyte receptor (; blad; mAb+s.m.
 422168; AA586894; Hs.112408; S100 calcium-binding protein A; lung, blad, headnk, breast, mela, esoph, sarc, cerv; CTL+s.m.
 422170; AI791949; Hs.112432; anti-Mullerian hormone; uter, blad; diag
 422173; BE385828; Hs.250619; phorbol-like protein MDS019 ; mela; diag
 35 422247; U18244; Hs.113602; solute carrier family 1 (high ; blad; mAb
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog ; ovar, headnk, blad, cerv, lung, panc, stom; mAb
 422309; U79745; Hs.114924; solute carrier family 16 (mono; mela; mAb+s.m.
 422311; AF073515; Hs.114948; cytokine receptor-like factor ; lung, fibro; diag
 422355; AW403724; Hs.300697; coagulation factor VII (serum ; fibro; diag
 40 422363; T55979; Hs.115474; replication factor C (activato; mela, colon; diag
 422398; AI476149; Hs.334489; hypothetical protein FLJ21992; fibro; CTL+s.m.
 422406; AF025441; Hs.116206; Opa-interacting protein 5; blad, lung; diag
 422420; U03398; Hs.1524; tumor necrosis factor (ligand); colon, panc, stom, leuk; mAb
 422423; AF283777; Hs.116481; CD72 antigen; spleen, leuk; mAb
 45 422440; NM_004812; Hs.116724; aldo-keto reductase family 1, ; lung, headnk; s.m.
 422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; lung, headnk, panc, sarc; diag
 422532; AL008726; Hs.118126; protective protein for beta-ga; renal, mela; s.m.
 422565; BE259035; Hs.118400; singed (Drosophila)-like (sea ; panc, test, mela; diag
 422573; AW297985; Hs.295726; integrin, alpha V (vitronecti; panc; mAb+s.m.
 50 422596; AF063611; Hs.118633; 2'-5'-oligoadenylate synthetas; esoph, mela; s.m.
 422603; BE242587; Hs.118651; hematopoietically expressed ho; angio; CTL+s.m.
 422633; X56832; Hs.118804; enolase 3, (beta, muscle); sarc; s.m.
 422658; AF231981; Hs.250175; homolog of yeast long chain po; pros; diag
 422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 C; test; diag
 55 422726; U11690; Hs.1572; faciogenital dysplasia (Aarsko; test; diag
 422728; AW937826; Hs.103262; MAD (mothers against decapenta; pros; diag
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; test; CTL+s.m.
 422835; BE218705; Hs.121378; metallothionein-like 5, testis; breast; diag
 422871; AL031228; Hs.121509; collagen, type XI, alpha 2; sarc; diag
 422887; AI751848; Hs.49215; ESTs; sarc; CTL+s.m.
 60 422938; NM_001809; Hs.1594; centromere protein A (17kD); lung, test; CTL+s.m.
 422963; M79141; Hs.13234; ESTs; lung, panc; diag
 422997; BE018212; Hs.122908; DNA replication factor; test; CTL+s.m.
 423017; AW178761; Hs.227948; serine (or cysteine) proteinase; blad, headnk, mela; mAb+diag
 65 423052; M28214; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag
 423189; M59371; Hs.171596; EphA2; colon, ovar; mAb
 423196; AK001866; Hs.125139; hypothetical protein FLJ11004; fibro; CTL+s.m.
 423198; M81933; Hs.1634; cell division cycle 25A; test; CTL+s.m.
 423201; NM_000163; Hs.125180; growth hormone receptor; pros; mAb
 70 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (e; lung, esoph; diag
 423271; W47225; Hs.126256; interleukin 1, beta; blad, stom, esoph; diag
 423309; BE006775; Hs.126782; sushi-repeat protein; lung, colon; diag
 423354; AB011130; Hs.127436; calcium channel, voltage-depen; test, fibro; mAb
 423387; AJ012074; Hs.348500; vasoactive intestinal peptide ; pros; mAb
 75 423397; NM_001838; Hs.1652; chemokine (C-C motif) receptor; blad, mela; mAb
 423412; AF109300; Hs.351615; prostate cancer associated pro; pros; diag
 423422; AC005175; Hs.128425; NY-REN-24 antigen; glio; mAb+CTL
 423445; NM_014324; Hs.128749; alpha-methylacyl-CoA racemase; pros; s.m.
 423453; AW450737; Hs.128791; CGI-09 protein; lung; CTL+s.m.
 80 423458; AI204212; Hs.351113; ESTs; test; CTL+s.m.
 423511; AF036329; Hs.129715; gonadotropin-releasing hormone; lung; diag
 423515; AA327017; Hs.176594; ESTs; ovar; diag
 423541; AA296922; Hs.129778; serine protease inhibitor, Kaz; colon, panc; diag
 423575; C18863; Hs.163443; intron of periostin (OSF-2os); headnk, breast, panc, lung, fibro, esoph; diag

- 423605; AF047826; Hs.129887; cadherin 19, type 2; mela; mAb
 423642; AW452650; Hs.157148; hypothetical protein MGC13204; lung; diag
 423662; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc); lung; diag
 423685; BE350494; Hs.49753; uveal autoantigen with coiled; panc, uter, colon; CTL+s.m.
 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; lung, headnk, blad; diag
 423739; AA398155; Hs.97600; ESTs; breast, ovar, panc; diag
 423761; NM_006194; Hs.132576; paired box gene 9; headnk; CTL+s.m.
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840; test; diag
 423778; Y09267; Hs.132821; flavin containing monooxygenase; fibro; s.m.
 423779; AW071837; Hs.57971; TRANSCRIPTION FACTOR HES-5; glio; diag
 423787; AJ295745; Hs.236204; nuclear pore complex protein; test, esoph; diag
 423798; AF047033; Hs.132904; solute carrier family 4, sodium; angio; mAb
 423799; AW026300; Hs.132906; 19A24 protein; mela; mAb
 423849; AL157425; Hs.133315; Homo sapiens mRNA; cDNA DKFZp7; lung; diag
 423887; AL080207; Hs.134585; DKFZP434G232 protein; headnk, lung; diag
 423899; NM_001427; Hs.134989; engrailed homolog 2; mela; CTL+s.m.
 423905; AW579960; Hs.135150; lung type-I cell membrane-asso; test; mAb
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, me; test; diag
 423934; U89995; Hs.159234; forkhead box E1 (thyroid trans; lung; CTL+s.m.
 424001; W67883; Hs.137476; paternally expressed 10; breast, ovar; diag
 424012; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk, esoph; diag
 424036; AA770688; Hs.348495; H2A histone family, member L; panc, ovar; CTL+s.m.
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, s; pros, fibro; mAb
 424078; AB006625; Hs.139033; paternally expressed 3; ovar, uter; CTL+s.m.
 424081; NM_006413; Hs.139120; ribonuclease P (30kD); test; s.m.
 424098; AF077374; Hs.139322; small proline-rich protein 3; lung, blad, headnk, esoph, cerv; diag
 424125; M31669; Hs.1735; inhibin, beta B (activin AB be; ovar, pros; diag
 424144; AA454033; Hs.41644; AKAP-associated sperm protein; fibro; diag
 424153; AA451737; Hs.141496; MAGE-like 2; mela; CTL+s.m.
 424165; AW582904; Hs.142255; islet amyloid polypeptide; panc; mAb
 424212; NM_005814; Hs.143131; glycoprotein A33 (transmembran; colon, stom, ovar; mAb
 424218; AF031824; Hs.143212; cystatin F (leukocystatin); mela, fibro; diag
 424244; AV647184; Hs.143601; hypothetical protein hCLA-iso; blad; diag
 424252; AK000520; Hs.143811; hypothetical protein FLJ20513; colon, stom; diag
 424264; D80400; Hs.239388; Human DNA sequence from clone; blad; mAb
 424308; AW975531; Hs.154443; minichromosome maintenance def; blad, lung, test; diag
 424310; AA338648; Hs.50334; testes development-related NYD; fibro; diag
 424332; AA338919; Hs.101615; ESTs; pros; diag
 424339; BE257148; Hs.145416; endoglycan; pros, lung; diag
 424343; AW956360; Hs.4748; adenylate cyclase activating p; glio, ovar, uter; mAb
 424364; AW363226; Hs.163834; ESTs, Weakly similar to G01763; lung, blad, headnk, cerv; diag
 424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 B; breast, uter, headnk; diag
 424420; BE614743; Hs.146688; prostaglandin E synthase; lung, blad; s.m.
 424440; AA340743; Hs.133208; ESTs; sarc; diag
 424441; X14850; Hs.147097; H2A histone family, member X; lung; diag
 424450; AL137526; Hs.147472; dynein intermediate chain 2; fibro; diag
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 9; breast, cerv, ovar, uter, blad, colon, stom; s.m.
 424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374; fibro; diag
 424578; AK001973; Hs.150890; hypothetical protein; test; CTL+s.m.
 424581; M62062; Hs.150917; catenin (cadherin-associated p; glio, ovar, uter; mAb+s.m.
 424586; NM_003401; Hs.150930; X-ray repair complementing def; panc; CTL+s.m.
 424629; M90656; Hs.151393; glutamate-cysteine ligase, cat; lung; CTL+s.m.
 424635; AA420687; Hs.115455; Homo sapiens cDNA FLJ14259 fis; glio; diag
 424676; Y08565; Hs.151678; UDP-N-acetyl-alpha-D-galactose; breast; s.m.
 424704; AI263293; Hs.152096; cytochrome P450, subfamily IIJ; renal; s.m.
 424711; NM_005795; Hs.152175; calcitonin receptor-like; angio; mAb
 424717; H03754; Hs.152213; wingless-type MMTV integration; blad, lung, headnk; diag
 424800; AL035588; Hs.153203; MyoD family inhibitor; test, pros; diag
 424806; AA382523; Hs.105689; MSTP031 protein; angio; mAb
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis; lung, blad, ovar, headnk, esoph, cerv, uter; diag
 424846; AU077324; Hs.1832; neuropeptide Y; pros; diag
 424897; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renal; diag
 424902; NM_003866; Hs.153687; inositol polyphosphate-4-phosp; panc, leuk, mela; CTL+s.m.
 424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni); mela, colon; CTL+s.m.
 424971; AA479005; Hs.154036; tumor suppressing subtransfera; panc, mela; CTL+s.m.
 424998; U58515; Hs.154138; chitinase 3-like 2; glio; diag
 425023; AW956889; Hs.154210; EDG-1 (endothelial different); angio; mAb
 425048; H05468; Hs.164502; ESTs; lung, blad; diag
 425057; AA826434; Hs.1619; achaete-scute complex (Drosoph; glio, lung; CTL+s.m.
 425088; AA663372; Hs.169395; hypothetical protein FLJ12015; glio, mela; diag
 425154; NM_001851; Hs.154850; collagen, type IX, alpha 1; sarc; diag
 425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase; lung, test; s.m.
 425200; BE255203.comp; Hs.155101; ATP synthase, H transporting, ; panc; s.m.
 425206; NM_002153; Hs.155109; hydroxysteroid (17-beta) dehyd; blad; mAb
 425211; M18667; Hs.1867; progastricin (pepsinogen C); fibro, esoph, pros; diag
 425234; AW152225; Hs.165909; ESTs, Weakly similar to I38022; lung, angio, blad, mela; diag
 425235; AA353113; Hs.105468; Homo sapiens cDNA: FLJ22743 fi; angio; diag
 425237; U07695; Hs.155227; EphB4; test; mAb
 425245; AI751768; Hs.155314; KIAA0095 gene product; lung; diag
 425259; AL049280; Hs.145010; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 425262; D87119; Hs.155418; GS3955 protein; mela, renal; CTL+s.m.
 425266; J00077; Hs.155421; alpha-fetoprotein; lung; diag
 425274; BE281191; Hs.155462; minichromosome maintenance def; test; diag

- 425289; AW139342; Hs.155530; interferon, gamma-inducible pr; mela; CTL+s.m.
 425308; M97639; Hs.155585; receptor tyrosine kinase-like ; pros; sarc; mAb
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, ; fibro; diag
 425371; D49441; Hs.155981; mesothelin; ovar, lung, fibro; mAb
 5 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (; lung, blad, panc, angio, test, mela, esoph; CTL+s.m.
 425427; A1652662; Hs.317432; branched chain aminotransferas; test; s.m.
 425428; AL110261; Hs.157211; DKFZP586B0621 protein; panc; diag
 425465; L18964; Hs.1904; protein kinase C, iota; ovar, pros, colon; s.m.
 10 425525; AA358883; Hs.23871; ESTs; sarc; diag
 425545; N98529; Hs.158295; Homo sapiens, clone MGC:12401,; sarc; diag
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 fi; fibro; CTL+s.m.
 425572; AB011076; Hs.158307; undifferentiated embryonic cel; test; CTL+s.m.
 425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; test; CTL+s.m.
 15 425606; U52112; Hs.158331; renin-binding protein; mela; diag
 425628; NM_004476; Hs.1915; folate hydrolase (prostate-spe; pros; s.m.
 425638; NM_012337; Hs.158450; nasopharyngeal epithelium spec; fibro; CTL+s.m.
 425679; X05997; Hs.159177; lipase, gastric; esoph; s.m.
 425692; D90041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.
 20 425695; NM_005401; Hs.159238; protein tyrosine phosphatase, ; lung; mAb+s.m.
 425709; AA383076; Hs.159274; outer dense fibre of sperm tai; test; diag
 425710; AF030880; Hs.159275; solute carrier family, member ; pros; mAb
 425722; A1659076; Hs.97031; hypothetical protein MGC13047; mela; diag
 425726; AF085808; Hs.159330; uroplakin 3; pros, blad; diag
 25 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA,; test; diag
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort; test; diag
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated; lung, headnk; s.m.
 425921; NM_007231; Hs.162211; solute carrier family 6 (neuro; stom, panc; mAb
 425976; C75094; Hs.334514; NG22 protein; pros, ovar; mAb
 30 426027; NM_002608; Hs.1976; platelet-derived growth factor; sarc; diag
 426050; AF017307; Hs.166096; E74-like factor 3 (ets domain ; ovar, blad, stom; CTL+s.m.
 426059; BE292842; Hs.166120; interferon regulatory factor 7; esoph, cerv; CTL+s.m.
 426067; AW664691; Hs.97053; ESTs; lung; diag
 426088; AF038007; Hs.166196; ATPase, Class I, type 8B, memb; blad, lung; mAb
 35 426094; AF034611; Hs.166206; cubilin (intrinsic factor-coba; renal; diag
 426116; AA868729; Hs.144694; ESTs; fibro; diag
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophi; colon, stom, panc, pros, renal, fibro, cerv; mAb
 426156; BE244537; Hs.167382; natriuretic peptide receptor A; ovar; mAb
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic ; breast, ovar, uter, pros, blad, panc, colon, fibro, mela; diag
 40 426172; AA371307; Hs.125056; ESTs; pros; diag
 426174; AA547959; Hs.115838; Homo sapiens similar to Echino; breast, pros, fibro; diag
 426212; S71824; Hs.167988; neural cell adhesion molecule ; glio; mAb
 426271; AF026547; Hs.169047; chondroitin sulfate proteoglyc; glio; diag
 426274; D38122; Hs.2007; tumor necrosis factor (ligand); fibro, mela; mAb
 45 426300; U15979; Hs.169228; delta-like homolog (Drosophila; ovar, sarc; mAb
 426310; NM_000909; Hs.169266; neuropeptide Y receptor Y1; breast; mAb
 426312; AF026939; Hs.181874; interferon-induced protein wit; esoph, mela; diag
 426320; W47595; Hs.169300; transforming growth factor, be; ovar, pros, blad, panc; diag
 426350; NM_003245; Hs.2022; transglutaminase 3 (E polypept; cerv; s.m.
 50 426363; M58524; Hs.2025; transforming growth factor, be; pros; diag
 426370; R98288; Hs.281706; sortilin 1; sarc; diag
 426416; AW612744; Hs.169824; killer cell lectin-like recept; fibro; mAb
 426440; BE382756; Hs.169902; solute carrier family 2 (facil; lung, panc, ovar, blad, headnk, esoph; mAb
 426462; U59111; Hs.169993; dermatan sulphate proteoglycan; sarc; diag
 55 426470; AA528794; Hs.128644; ESTs; mela; diag
 426471; M22440; Hs.170009; transforming growth factor, al; headnk, renal, panc; diag
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; panc; mAb+s.m.
 426501; AW043782; Hs.293616; ESTs; pros, breast, glio, lung, mela; mAb
 426502; Y07759; Hs.170157; myosin VA (heavy polypeptide 1; mela; diag
 60 426534; U58096; Hs.2051; testis specific protein, Y-lin; test; CTL+s.m.
 426535; AU077012; Hs.170279; ESTs, Weakly similar to ubiqui; angio; diag
 426555; NM_000372; Hs.2053; tyrosinase (oculocutaneous alb; mela, sarc; mAb
 426559; AB001914; Hs.170414; paired basic amino acid cleavi; hepC, breast, ovar, renal; diag
 426575; M74826; Hs.170808; glutamate decarboxylase 2 (pan; panc; s.m.
 65 426627; AF012359; Hs.195685; ESTs; test; diag
 426635; BE395109; Hs.129327; hypothetical protein MGC13057; ovar; CTL+s.m.
 426682; AV660038; Hs.2056; UDP glycosyltransferase 1 fami; blad, lung; s.m.
 426691; NM_006201; Hs.171834; PCTAIRE protein kinase 1; ovar; CTL+s.m.
 426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 fi; angio; mAb
 70 426721; AA383588; Hs.288545; ESTs, Weakly similar to T29012; fibro; diag
 426726; AA488915; Hs.171955; trophinin associated protein (; test; diag
 426747; AA535210; Hs.171995; kallikrein 3, (prostate specif; pros; diag
 426752; X69490; Hs.172004; titin; sarc; diag
 426759; A1590401; Hs.21213; ESTs; mela; diag
 75 426793; X89887; Hs.172350; HIR (histone cell cycle regula; pros; CTL+s.m.
 426828; NM_000020; Hs.172670; activin A receptor type II-like; angio; mAb
 426866; U02330; Hs.172816; neuregulin 1; esoph; CTL+s.m.
 426897; AW976570; Hs.97387; ESTs; lung; diag
 426900; AW163564; Hs.142375; ESTs; blad, pros; mAb
 80 426935; NM_000088; Hs.172928; collagen, type I, alpha 1; test, sarc; CTL+s.m.
 426966; A1493134; Hs.349204; sclerostin; lung; diag
 426968; U07616; Hs.173034; amphiphysin (Stiff-Mann syndro; blad; mAb+CTL
 426991; AK001536; Hs.214410; Homo sapiens cDNA FLJ10674 fis; ovar, sarc; diag
 427080; AW068287; Hs.301175; ras-related C3 botulinum toxin; mela; diag

- 427099; AB032953; Hs.173560; odd Oz/ten-m homolog 2 (Drosop; headnk, esoph; diag
 427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase; breast; mAb
 427244; AA402400; Hs.178045; ESTs; esoph; diag
 427260; AA663848; ; gb:ae70b06.s1 Stratagene schiz; lung; diag
 427274; NM_005211; Hs.174142; colony stimulating factor 1 re; pros, sarc; mAb
 427298; AA400495; ; ESTs; test; diag
 427318; AF186081; Hs.175783; zinc transporter; pros; mAb
 427333; AF067797; Hs.176658; aquaporin 8; panc, colon; mAb
 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb
 427356; AW023482; Hs.97849; ESTs; ovar, breast, pros, blad, lung; diag
 427398; AW390020; Hs.20415; chromosome 21 open reading fra; pros; diag
 427427; AF077345; Hs.177936; lectin, superfamily member 1 (; breast; diag
 427441; AA412605; Hs.293266; SPANX family, member C; lung, esoph; CTL+s.m.
 427461; AA531527; Hs.332040; hypothetical protein MGC13010; pros; mAb
 427474; U13192; Hs.2159; aggrecan 1 (chondroitin sulfat; sarc; diag
 427486; AA974433; Hs.362432; fibroblast growth factor 4 (he; test; diag
 427510; Z47542; Hs.179312; small nuclear RNA activating c; lung; CTL+s.m.
 427515; T79526; Hs.179516; integral type I protein; pros; diag
 427521; AW973352; ; ESTs; test; diag
 427528; AU077143; Hs.179565; minichromosome maintenance def; mela; CTL+s.m.
 427535; R29543; Hs.2164; pro-platelet basic protein (in; fibro; diag
 427546; AA405280; Hs.36793; hypothetical protein FLJ23188; lung; diag
 427550; BE242818; Hs.311609; nuclear RNA helicase, DECD var; mela; CTL+s.m.
 427557; NM_002659; Hs.179657; plasminogen activator, urokina; panc, colon, stom, ovar, cerv, blad, lung, headnk, esoph; mAb
 427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3_H; test; diag
 427583; M82962; Hs.179704; meprin A, alpha (PABA peptide; colon; mAb
 427584; BE410293; Hs.179718; v-myb avian myeloblastosis vir; test; CTL+s.m.
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc, stom, colon, ovar, cerv, sarc; diag
 427615; BE410107; Hs.179817; CGI-82 protein, PSDR1; pros; diag
 427634; AI399745; Hs.18449; hypothetical protein MGC10820; mela, sarc; diag
 427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20653 fis; sarc; diag
 427666; AI791495; Hs.180142; calmodulin-like skin protein (; breast, cerv, blad, lung, headnk, esoph; diag
 427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis; test; diag
 427668; AA298760; Hs.180191; hypothetical protein FLJ14904; lung, test; diag
 427681; AB018263; Hs.284232; tumor necrosis factor receptor; ovar; mAb+s.m.
 427698; AW972594; Hs.335499; ESTs; fibro; CTL+s.m.
 427701; AA411101; Hs.243886; nuclear autoantigenic sperm pr; lung; mAb+CTL
 427715; BE245274; Hs.180428; KIAA1181 protein; pros; diag
 427719; AI393122; Hs.134726; ESTs; test, blad; diag
 427730; AW250549; Hs.180577; granulin; mela; diag
 427786; BE407863; Hs.256871; ESTs; esoph, blad; diag
 427809; M26380; Hs.180878; lipoprotein lipase; ovar; mAb
 427811; M81057; Hs.180884; carboxypeptidase B1 (tissue); breast; s.m.
 427897; NM_017413; Hs.303084; apelin; peptide ligand for APJ; angio, renal, pros; diag
 427912; AL022310; Hs.181097; tumor necrosis factor (ligand); angio; mAb
 427958; AA418000; Hs.376771; potassium intermediate/small c; pros, glio; mAb
 427961; AW293165; Hs.143134; ESTs; lung, sarc; diag
 428001; H97428; Hs.219907; ESTs, Moderately similar to Tr; mela; diag
 428004; AA449563; Hs.151393; glutamate-cysteine ligase, cat; lung; s.m.
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fi; lung; diag
 428046; AW812795; Hs.337534; ESTs, Moderately similar to I3; lung, colon; diag
 428062; AA420683; Hs.98321; hypothetical protein FLJ14103; angio; diag
 428087; AA100573; Hs.182421; troponin C2, fast; sarc; CTL+s.m.
 428141; D50402; Hs.182611; solute carrier family 11 (prot; glio; mAb
 428153; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
 428169; AI928984; Hs.182793; golgi phosphoprotein 2; pros; diag
 428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar, sarc; CTL+s.m.
 428183; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
 428206; AB020643; Hs.183006; KIAA0836 protein; angio; mAb
 428221; U96781; Hs.183075; ATPase, Ca transporting, card; sarc; s.m.
 428227; AA321649; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, headnk, fibro, colon, stom, cerv, leuk, renal, test, mela, esoph, hepC; diag
 428248; AI126772; Hs.40479; ESTs; sarc; diag
 428293; BE250944; Hs.183556; solute carrier family 1 (neutr; pros; mAb
 428305; AA446628; Hs.2799; cartilage linking protein 1; sarc; diag
 428329; AA426091; Hs.98453; ESTs, Moderately similar to R2; test; diag
 428336; AA503115; Hs.183752; microseminoprotein, beta-; pros; diag
 428355; BE256452; Hs.2257; vitronectin (serum spreading f; colon; diag
 428398; AI249368; Hs.98558; ESTs; pros, breast; diag
 428405; Y00762; Hs.2266; cholinergic receptor, nicotini; esoph, sarc; mAb
 428423; AU076517; Hs.184276; solute carrier family 9 (sodi; ovar; CTL+s.m.
 428434; AW363590; Hs.65551; Homo sapiens, Similar to DNA s; lung, fibro; diag
 428467; AK002121; Hs.184465; hypothetical protein FLJ11259; fibro; mAb
 428471; X57348; Hs.184510; stralitin; lung, headnk, colon, panc; diag
 428645; AA431400; Hs.98729; ESTs, Weakly similar to 201720; lung; s.m.
 428651; AF196478; Hs.188401; annexin A10; blad, stom, panc; diag
 428667; AI375550; Hs.346868; nucleolar protein p40; homolog; fibro, uter; diag
 428722; U76456; Hs.190787; tissue inhibitor of metallopro; glio; diag
 428728; NM_016625; Hs.191381; hypothetical protein; ovar, lung, BPH; CTL+s.m.
 428771; AB028992; Hs.193143; KIAA1069 protein; lung; CTL+s.m.
 428784; Y12851; Hs.193470; purinergic receptor P2X, ligand; glio, mela; mAb
 428800; M57627; Hs.193717; interleukin 10; fibro; diag
 428801; AW277121; Hs.254881; ESTs; pros; diag
 428804; AK000713; Hs.193736; hypothetical protein FLJ20706; mela; diag

- 428810; AF068236; Hs.193788; nitric oxide synthase 2A (indu; lung; s.m.
 428819; AL135623; Hs.193914; KIAA0575 gene product; pros; CTL+s.m.
 428824; W23624; Hs.173059; ESTs; panc; diag
 428832; AA578229; Hs.324239; ESTs, Moderately similar to ZN; panc, uter; diag
 428841; AI418430; Hs.104935; ESTs; renal; diag
 428848; NM_000230; Hs.194236; leptin (murine obesity homolog; sarc; diag
 428862; NM_000346; Hs.2316; SRY (sex determining region Y); pros, sarc; CTL+s.m.
 428927; AA441837; Hs.90250; Homo sapiens hypothetical prot; fibro; mAb+diag
 428928; BE409838; Hs.194657; cadherin 1, type 1, E-cadherin; pros, breast, stom, blad; mAb
 428949; AA442153; Hs.104744; hypothetical protein DKFZp434J; sarc; diag
 428957; NM_003881; Hs.194679; WNT1 inducible signaling pathw; cerv; diag
 428959; AF100779; Hs.194680; WNT1 inducible signaling pathw; sarc; diag
 428977; AK001404; Hs.194698; cyclin B2; test; CTL+s.m.
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_H; sarc; diag
 429002; AW248439; Hs.2340; junction plakoglobin; blad; CTL+s.m.
 429010; Y18198; Hs.194725; one cut domain, family member ; panc; diag
 429038; AL023513; Hs.194766; seizure related gene 6 (mouse); lung; mAb
 429058; AF138863; Hs.35254; hypothetical protein FLB6421; esoph; diag
 429065; AJ753247; Hs.29643; Homo sapiens cDNA FLJ13103 fis; lung; diag
 429083; Y09397; Hs.227817; BCL2-related protein A1; mela; diag
 429113; D28235; Hs.196384; prostaglandin-endoperoxide syn; angio, blad, stom; s.m.
 429120; AK001673; Hs.196530; hypothetical protein FLJ10811; test; diag
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolo; ovar; mAb
 429163; AA884766; ; gb:am20a10.s1 Soares_NFL_T_GBC; pros; diag
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; breast, panc, stom, lung, mela; s.m.
 429201; X03178; Hs.198246; group-specific component (vita; panc; diag
 429220; AW207206; Hs.356962; ESTs; breast, pros, BPH; diag
 429228; AI553633; Hs.356828; ESTs; lung, fibro, headnk, esoph; diag
 429259; AA204450; Hs.380088; Plakophilin; lung, headnk; diag
 429290; AF203032; Hs.198760; neurofilament, heavy polypepti; pros; CTL+s.m.
 429299; AI620463; Hs.347408; hypothetical protein MGC13102; pros, cerv; diag
 429329; AA456140; Hs.99235; Homo sapiens pannexin 3 (PANX3; sarc; mAb
 429345; R11141; Hs.199695; hypothetical protein; blad; diag
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (m; headnk, breast, cerv, ovar, blad, lung, esoph, mela, sarc; mAb
 429413; NM_014058; Hs.201877; DESC1 protein; lung, blad; diag
 429415; NM_002593; Hs.202097; procollagen C-endopeptidase en; sarc; diag
 429423; AI016712; Hs.380983; integrin, beta 1 (fibronectin ; angio; mAb
 429432; AI678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag
 429441; AJ224172; Hs.204096; lipophilin B (uteroglobin fami; breast, pros, ovar; diag
 429466; M85835; Hs.12827; ESTs; glio, uter; CTL+s.m.
 429469; M64590; Hs.380791; glycine dehydrogenase (decarbo; test; s.m.
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; blad, lung, headnk, test; diag
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cyto; lung, glio, headnk, mela, sarc; diag
 429504; X99133; Hs.204238; lipocalin 2 (oncogene 24p3) (N; ovar, lung, blad; diag
 429505; AW820035; Hs.278679; a disintegrin and metalloprote; colon, leuk; mAb
 429538; BE182592; Hs.139322; small proline-rich protein 2A; lung, esoph; diag
 429563; BE619413; Hs.2437; eukaryotic translation initiat; lung; diag
 429586; T73510; Hs.209153; angiotensin-like 3; hepC; CTL+s.m.
 429597; NM_003816; Hs.2442; a disintegrin and metalloprote; panc, colon, stom, lung; mAb
 429609; AF002246; Hs.210863; cell adhesion molecule with ho; ovar, mela; diag
 429612; AF062649; Hs.252587; pituitary tumor-transforming 1; lung, blad, headnk; diag
 429655; U48959; Hs.211582; myosin, light polypeptide kina; pros; s.m.
 429663; M68874; Hs.211587; phospholipase A2, group IVA (c; angio, lung; s.m.
 429664; L20433; Hs.211588; POU domain, class 4, transcrip; sarc; CTL+s.m.
 429736; AF125304; Hs.212680; tumor necrosis factor receptor; lung; mAb
 429747; M87507; Hs.2490; caspase 1, apoptosis-related c; colon, stom, fibro; s.m.
 429764; BE245076; Hs.216958; KIAA0194 protein; pros; mAb
 429769; NM_004917; Hs.218366; kallikrein 4 (prostase, enamel; pros; s.m.
 429784; M89796; Hs.30; membrane-spanning 4-domains, s; fibro; mAb
 429823; AA459443; Hs.181400; ESTs; sarc; diag
 429859; NM_007050; Hs.225952; protein tyrosine phosphatase, ; breast; mAb+s.m.
 429918; AW873986; Hs.119383; ESTs; pros, glio; diag
 429921; AA526911; Hs.82772; collagen, type XI, alpha 1; headnk, panc, sarc; CTL
 429983; W92620; Hs.260855; ESTs; blad; diag
 429986; AF092047; Hs.227277; sine oculis homeobox (Drosophi; lung; CTL+s.m.
 430014; H59354; Hs.374303; actinin, alpha 4; renal; diag
 430016; NM_004736; Hs.227656; xenotropic and polytropic retr; ovar; mAb
 430044; AA464510; Hs.152812; ESTs; breast, lung, panc, headnk, ovar, stom, esoph; diag
 430056; X97548; Hs.228059; KRAB-associated protein 1; test; CTL+s.m.
 430129; BE301708; Hs.233955; hypothetical protein FLJ20401; angio; diag
 430130; AL137311; Hs.234074; Homo sapiens mRNA; cDNA DKFZp7; pros; mAb
 430144; AI732722; Hs.98927; ERGL protein; ERGL-53-like pr; pros; diag
 430152; AB001325; Hs.234642; aquaporin 3; blad, fibro; mAb
 430154; AW583058; Hs.234726; serine (or cysteine) proteinas; pros; diag
 430157; BE348706; Hs.278543; ESTs; blad; diag
 430168; AW968343; Hs.145582; DKFZP4341735 protein; blad; diag
 430223; NM_002514; Hs.235935; nephroblastoma overexpressed g; mela; diag
 430226; BE245562; Hs.2551; adrenergic, beta-2-, receptor;; pros; mAb
 430228; AW950939; Hs.6382; ESTs, Highly similar to T00391; glio; diag
 430252; AI638774; Hs.105328; testes development-related NYD; test; CTL+s.m.
 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; test; CTL+s.m.
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551; test; CTL+s.m.
 430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse h; ovar; CTL+s.m.

- 430280; AA361258; Hs.237868; interleukin 7 receptor; mela, lung, panc, stom, esoph, headnk, fibro; mAb+s.m.
 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5_H; test; diag
 430294; AI538226; Hs.32976; guanine nucleotide binding pro; pros; diag
 430337; M36707; Hs.239600; calmodulin-like 3; lung; diag
 430354; AA954810; Hs.239784; human homolog of Drosophila Sc; ovar; diag
 430378; Z29572; Hs.2556; tumor necrosis factor receptor; lung, fibro, breast headnk, blad, breast, colon, stom; diag
 430393; BE185030; Hs.241305; estrogen-responsive B box prot; lung; diag
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; panc; diag
 430407; H23551; Hs.30974; ESTs; panc; diag
 430439; AL133561; Hs.380155; DKFZP434B061 protein; lung, test; diag
 430451; AA836472; Hs.297939; cathepsin B; ovar, lung, headnk, panc, stom; diag
 430454; AW469011; Hs.105635; ESTs; lung; diag
 430476; AA447465; Hs.2563; tachykinin, precursor 1 (subst; sarc; diag
 430487; D87742; Hs.241552; KIAA0268 protein; pros; diag
 430491; AL109791; Hs.241559; Homo sapiens mRNA full length ; ovar; diag
 430498; X02910; Hs.241570; tumor necrosis factor (TNF sup; leuk; diag
 430508; AI015435; Hs.104637; ESTs; lung; mAb+s.m.
 430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; test; CTL+s.m.
 430540; AW245422; Hs.106357; Homo sapiens cDNA: FLJ22105 f; mela; mAb
 430563; AA481269; Hs.348628; ATP-binding cassette, sub-fam1; lung; diag
 430594; AK000790; Hs.246885; hypothetical protein FLJ20783; mela; diag
 430634; AI860651; Hs.26685; calyphosine; ovar; diag
 430637; BE160081; Hs.256290; S100 calcium-binding protein A; mela; diag
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211_H; test; diag
 430676; AF084866; Hs.372585; gb:Homo sapiens envelope prote; test; diag
 430677; Z26317; Hs.359784; desmoglein 2; lung, colon; mAb
 430678; AI458174; Hs.192855; ESTs; lung; diag
 430686; NM_001942; Hs.2633; desmoglein 1; lung, headnk, mela; mAb
 430691; C14187; Hs.157208; aristaless-related homeobox pr; EWS, ovar, panc; diag
 430704; AW813091; Hs.335799; ESTs; stom; diag
 430770; AA765694; Hs.123296; ESTs; mela; diag
 430832; AI073913; Hs.100686; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom, fibro; diag
 430838; N46664; Hs.169395; hypothetical protein FLJ12015; mela; CTL+s.m.
 430890; X54232; Hs.2699; glypican 1; glio, lung, cerv, blad, esoph; mAb
 430985; AA490232; Hs.27323; ESTs, Weakly similar to I78885; lung; mAb
 431009; BE149762; Hs.48956; gap junction protein, beta 6 (; lung, blad, headnk, esoph; mAb
 431053; S40369; Hs.249141; Glutamate receptor subunit; glio; mAb
 431070; AW408164; Hs.249184; transcription factor 19 (SC1); blad; diag
 431089; BE041395; Hs.374629; ESTs, Weakly similar to unknow; blad, lung, pros, angio, fibro; diag
 431099; Y13367; Hs.249235; phosphoinositide-3-kinase, cla; pros; CTL+s.m.
 431103; M57399; Hs.44; pleiotrophin (heparin binding ; sarc, mela; diag
 431124; AF284221; Hs.59506; doublesex and mab-3 related tr; lung; CTL+s.m.
 431151; BE207083; Hs.366053; gb:ba10d10.y1 NIH_MGC_7 Homo s; pros; mAb
 431164; AA493650; Hs.94367; thyroid transcription factor 1; fibro; CTL+s.m.
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endopla; mela, pros, panc, colon, stom; mAb
 431211; M86849; Hs.323733; gap junction protein, beta 2 ; colon, blad, lung, panc, headnk, esoph; mAb
 431217; NM_013427; Hs.250830; Rho GTPase activating protein ; pros; CTL+s.m.
 431221; AA449015; Hs.286145; SRB7 (suppressor of RNA polyme; lung; CTL+s.m.
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A; pros; diag
 431250; BE264649; Hs.251377; taxol resistance associated ge; esoph; diag
 431322; AW970622; Hs.376626; gb:EST382704 MAGE resequenc.; blad, ovar, uter; diag
 431347; AI133461; Hs.251664; insulin-like growth factor 2 (; blad; mAb+diag
 431354; BE046956; Hs.251673; DNA (cytosine-5)-methyltransf; test; CTL+s.m.
 431360; NM_000427; Hs.251680; Ioricin; mela, sarc; diag
 431362; AI874223; Hs.293560; ESTs; angio; diag
 431369; BE184455; Hs.251754; secretory leukocyte protease i; ovar, blad; diag
 431384; BE158000; Hs.334372; gb:MR2-HT0377-150200-202-e03 H; lung; diag
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, s; panc; diag
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gat; ovar, pros, blad; mAb
 431448; AL137517; Hs.306201; hypothetical protein DKFZp5640; blad; mAb
 431457; NM_012211; Hs.256297; integrin, alpha 11; headnk; mAb
 431474; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
 431494; AA991355; Hs.298312; hypothetical protein DKFZp434A; lung; diag
 431512; BE270734; Hs.2795; lactate dehydrogenase A; panc; s.m.
 431548; AI834273; Hs.97111; novel protein; lung, angio, pros; diag
 431553; X78075; Hs.2799; cartilage linking protein 1; sarc; diag
 431579; AW971082; Hs.222886; ESTs, Weakly similar to TRHY_H; pros; diag
 431616; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros, panc, colon ; mAb
 431674; AA098901; Hs.301642; G-protein coupled receptor; ovar; mAb+s.m.
 431723; AW058350; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; fibro; diag
 431728; NM_007351; Hs.268107; multimerin; angio; diag
 431808; M30703; Hs.270833; amphiregulin (schwannoma-deriv; breast, headnk, panc, colon; diag
 431836; AF178532; Hs.271411; beta-site APP-cleaving enzyme ; mela; mAb
 431870; AW449902; Hs.105500; ESTs; renal; diag
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alph; blad, headnk, lung, panc, cerv, stom; mAb
 431938; AA938471; Hs.54431; specific granule protein (28 k; panc; diag
 431939; AW008061; Hs.231994; ESTs; renal, colon; diag
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis; cerv, glio; diag
 431989; AW972870; Hs.291069; ESTs; ovar; diag
 431992; NM_002742; Hs.2891; protein kinase C, mu; pros, glio; s.m.
 432004; BE018302; Hs.2894; placental growth factor, vascu; renal; diag
 432015; AL157504; Hs.159115; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 432023; AW273128; Hs.300268; EST; lung; diag

- 432097; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 432117; AL036195; Hs.2909; prolamine 1; test; CTL+s.m.
 432128; AA127221; Hs.66; ESTs; angio; diag
 432141; BE410964; Hs.272736; nuclear receptor binding prote; test; mAb+s.m.
 432189; AA527941; ; gb.nh30c04.s1 NCI_CGAP_Pr3 Hom; pros; diag
 432199; AI693815; Hs.127179; cryptic gene; panc; diag
 432210; AI567421; Hs.273330; Homo sapiens, clone IMAGE:3544; ovar, lung, blad; diag
 432222; AI204995; ; gb:an03c03.x1 Stratagene schiz; angio, blad, fibro; diag
 432231; AA339977; Hs.274127; CLST 11240 protein; fibro; diag
 432239; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad, lung, headnk, esoph, sarc; s.m.
 432240; AI694767; Hs.129179; Homo sapiens cDNA FLJ13581 fis; pros; diag
 432305; M62402; Hs.274313; insulin-like growth factor bin; cerv; diag
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis; cerv, lung, fibro, pros; diag
 432407; AA221036; ; gb:zr03f12.r1 Stratagene NT2 n; lung, test,colon; diag
 432415; T16971; ; ESTs, Weakly similar to A43932; ovar, pros; diag
 432432; AA541323; Hs.115831; ESTs; uter, pros; diag
 432435; BE218886; Hs.282070; ESTs; pros, uter, colon, stom, fibro; diag
 432441; AW292425; Hs.163484; intron of hepatocyte nuclear f; blad, fibro, pros; diag
 432473; AI202703; Hs.152414; ESTs; pros; diag
 432481; AW451645; Hs.151504; intron of collagen, type XI, a; sarc; diag
 432512; NM_003284; Hs.3017; transition protein 1 (during h; test; CTL+s.m.
 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUIA; fibro, ovar, uter; CTL+s.m.
 432527; AW975028; Hs.102754; ESTs; pros, uter, ovar, cerv; diag
 432542; AW083920; Hs.16098; claudin 2; colon, panc; diag
 432583; AW023624; Hs.162282; potassium channel TASK-4; pota; lung; mAb
 432615; AA557191; Hs.55028; ESTs, Weakly similar to I54374; pros; diag
 432621; AI298501; Hs.21192; ESTs, Weakly similar to T46428; pros; mAb
 432629; AW860548; Hs.280658; ESTs; ovar; diag
 432653; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros, lung; mAb+s.m.
 432666; AW204069; Hs.351118; ESTs, Weakly similar to unname; test; diag
 432706; NM_013230; Hs.286124; CD24 antigen (small cell lung; colon, ovar, pros; mAb+CTL
 432730; AI066520; Hs.131358; ESTs; test; diag
 432731; R31178; Hs.287820; fibronectin 1; panc, fibro; diag
 432788; AA521091; Hs.178499; Homo sapiens cDNA: FLJ23117 fi; lung, ovar; CTL+s.m.
 432800; BE391046; Hs.278962; AIM-1 protein; mela, pros; mAb
 432842; AW674093; Hs.334822; hypothetical protein MGC4485; blad, lung, headnk; CTL+s.m.
 432850; X87723; Hs.3110; angiotensin receptor 2 (AT2); leio; mAb
 432855; AF017988; Hs.279565; secreted frizzled-related prot; panc; diag
 432867; AW016936; Hs.233364; ESTs; stom, colon; diag
 432878; BE386490; Hs.279663; Pirin; mela; CTL+s.m.
 432887; AI926047; Hs.162859; AK056805; Homo sapiens cDNA FL; pros; diag
 432938; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
 432966; AA650114; Hs.325198; ESTs; pros; diag
 433012; NM_004045; Hs.279910; ATX1 (antioxidant protein 1, y; mela; diag
 433013; AI697890; Hs.127337; axin 2 (conductin, axil); colon; CTL+s.m.
 433043; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag
 433068; NM_006456; Hs.288215; sialyltransferase; breast, ovar, mela; s.m.
 433078; AW015188; Hs.121575; Homo sapiens cDNA FLJ12231 fis; blad; diag
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, ; blad, lung, headnk, cerv; mAb
 433147; AF091434; Hs.43080; platelet derived growth factor; ovar, panc, fibro; diag
 433159; AB035898; Hs.150587; kinesin-like protein 2; ovar, uter, colon, blad; diag
 433170; AB037816; Hs.8982; KIAA1395; angio; diag
 433183; AF231338; Hs.222024; transcription factor BMAL2; lung; diag
 433228; F28212; Hs.14953; KIAA1491 protein; test; CTL+s.m.
 433258; AI806626; Hs.207300; ESTs, Weakly similar to ALUB_H; lung; diag
 433285; AW975944; Hs.237396; ESTs; breast, pros; diag
 433293; AF007835; Hs.32417; hypothetical protein MGC2742; fibro, pros, stom, panc; CTL+s.m.
 433323; AA805132; Hs.159142; ESTs; pros; diag
 433334; AI927208; Hs.231958; matrix metalloproteinase 28; panc; s.m.
 433336; AF017986; Hs.31386; secreted frizzled-related prot; ovar, fibro, headnk, lung, panc, blad; diag
 433364; AI075407; Hs.296083; ESTs, Moderately similar to I5; mela; diag
 433365; AF026944; Hs.293797; ESTs; blad; diag
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related c; angio; s.m.
 433388; AI432672; Hs.288539; hypothetical protein FLJ22191; ovar; CTL+s.m.
 433404; T32982; Hs.352670; Homo sapiens cDNA FLJ32064 fis; pros; diag
 433437; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, glio, colon; s.m.
 433444; AW975324; Hs.129816; ESTs; pros; diag
 433466; AA508353; Hs.105314; relaxin 1 (H1); pros; diag
 433485; AI493076; Hs.306098; aldo-keto reductase family 1, ; lung; s.m.
 433495; AW373784; Hs.71; alpha-2-glycoprotein 1, zinc; breast, pros; diag
 433576; BE080715; Hs.161091; ESTs; mela; diag
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene; colon; diag
 433671; AW138797; Hs.132906; 19A24 protein; fibro; mAb
 433701; AW445023; Hs.15155; ESTs; test; diag
 433724; AI827749; Hs.144924; serine/threonine protein kinas; test; CTL+s.m.
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM_); pros, ovar; diag
 433800; AI034361; Hs.135150; lung type-I cell membrane-asso; glio, lung, test; mAb
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homo; test; s.m.
 434011; AW953437; Hs.5486; clone FLB5214; pros; diag
 434105; AW952124; Hs.13094; presenilins associated rhombol; lung; diag
 434217; AW014795; Hs.23349; ESTs; angio; diag
 434262; AF121858; Hs.12169; sorting nexin 8; mela; CTL+s.m.
 434274; AA628539; Hs.57783; ESTs, Moderately similar to AL; test; diag

- 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis; test; diag
 434340; AI193043; Hs.353146; ESTs, Weakly similar to T17226; lung; diag
 434360; AW015415; Hs.127780; ESTs; lung; diag
 434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic re; colon, stom; diag
 434377; AW137148; Hs.306593; intron of periostin (OSF-2os); headnk; diag
 434398; AA121098; Hs.3838; serum-inducible kinase (SNK); angio, breast; CTL+s.m.
 434411; AA632649; Hs.201372; ESTs; stom, leuk; diag
 434414; AI798376; ; gb:tr34b07.x1 NCL CGAP_Ov23 Ho; lung, test, colon; diag
 434423; NM_006769; Hs.3844; LIM domain only 4; panc; diag
 434449; AW953484; Hs.3849; hypothetical protein FLJ22041 ; sarc; diag
 434487; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb+s.m.
 434596; T59538; ; gb:yb65g12.s1 Stratagene ovary; angio; s.m.
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; test; CTL+s.m.
 434609; R76593; ; gb:yi60c11.r1 Soares placenta ; pros; diag
 434636; AA083764; Hs.349208; hypothetical protein MGC3178; angio; diag
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350; test; diag
 434665; AA642125; Hs.74502; gb:nr60c01.s1 NCL CGAP_Lym3 Ho; panc; diag
 434666; AF151103; Hs.112259; T cell receptor gamma locus; pros; mAb+s.m.
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis; panc; diag
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phospho; mela; s.m.
 434846; AW295389; Hs.119768; ESTs; angio; diag
 434876; AF160477; Hs.61460; Ig superfamily receptor LNIR; lung, blad; mAb
 434927; H46612; Hs.293815; Homo sapiens HSPC285 mRNA, par; angio; diag
 434973; AW449285; Hs.313636; EST; pros; diag
 435045; BE297155; Hs.143698; ESTs; test; diag
 435047; AA454985; Hs.54973; cadherin-like protein VR20; pros; mAb
 435066; BE261750; Hs.4747; dyskeratosis congenita 1, dysk; colon; CTL+s.m.
 435080; AI831760; Hs.155111; hypothetical protein FLJ14428; renal; mAb
 435094; AI560129; Hs.289008; EST; ovar, cerv; diag
 435099; AC004770; Hs.4756; flap structure-specific endonu; blad, test, mela; CTL+s.m.
 435140; AA668123; Hs.134170; ESTs; fibro; diag
 435159; AA668879; Hs.116649; ESTs; lung; diag
 435206; AI432364; Hs.160594; ESTs; test; diag
 435243; AW292886; Hs.348932; hypothetical protein dJ434014.; cerv, headnk; diag
 435292; N20514; Hs.172965; ESTs; mela; diag
 435299; AI745458; Hs.343026; ESTs, Weakly similar to T20593; fibro; diag
 435479; AF197137; Hs.155101; ATP synthase, H transporting, ; pros; s.m.
 435496; AW840171; Hs.265398; PAR-6 beta; breast, panc, ovar; diag
 435563; AF210317; Hs.95497; solute carrier family 2 (facil; blad; mAb+s.m.
 435575; AF213457; Hs.44234; triggering receptor expressed ; fibro; mAb+s.m.
 435602; AF217515; Hs.283532; uncharacterized bone marrow pr; test; diag
 435615; Y15065; Hs.4975; potassium voltage-gated channe; glio; mAb
 435652; N32388; Hs.334370; uncharacterized hypothalamus p; panc; diag
 435793; AB037734; Hs.4993; KIAA1313 protein; ovar, lung, uter; diag
 435849; BE305242; Hs.16098; claudin 2; colon, panc; diag
 435876; AW612586; Hs.160271; G protein-coupled receptor 48; pros; mAb
 435897; AF269223; Hs.128322; t-complex 11 (a murine tcp hom; test; diag
 435904; AF261655; Hs.8910; 1,2-alpha-mannosidase IC; blad; s.m.
 435918; AF263538; Hs.86232; growth differentiation factor ; test; diag
 435974; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
 436032; AA150797; Hs.109276; latexin protein; panc, angio; diag
 436063; AK000028; Hs.356100; ribosomal protein S24; pros; diag
 436120; AI248193; Hs.119860; ESTs; fibro; diag
 436199; R38946; Hs.127951; hypothetical protein FLJ14503; renal; diag
 436246; AW450963; Hs.119991; ESTs; blad; diag
 436251; BE515065; Hs.296585; nucleolar protein (KKE/D repea; colon, test, blad; CTL+s.m.
 436278; BE396290; Hs.5097; synaptogyrin 2; pros; mAb
 436291; BE568452; Hs.344037; protein regulator of cytokines; lung, blad, headnk; diag
 436293; AI601188; Hs.306201; ESTs; blad; diag
 436302; AL355841; Hs.99330; hypothetical protein FLJ23588; lung; diag
 436315; BE390513; Hs.27935; hypothetical protein MGC4837; mela; diag
 436396; AI683487; Hs.152213; wingless-type MMTV integration; lung, headnk, pros, panc; diag
 436420; AA443966; Hs.31595; ESTs; angio; mAb
 436476; AA326108; Hs.33829; bHLH protein DEC2; panc; diag
 436511; AA721252; Hs.291502; ESTs; lung; diag
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; lung; diag
 436569; BE439539; Hs.301961; glutathione S-transferase M2 (; blad; s.m.
 436614; AW104388; Hs.149091; ESTs; mela; CTL+s.m.
 436700; AI693690; Hs.301406; hypothetical protein PP3501; mela; mAb
 436729; BE621807; Hs.351316; transmembrane 4 superfamily me; panc, colon, stom, ovar, lung, blad; mAb
 436772; AW975688; Hs.348918; metallothionein 1E (functional; angio; diag
 436775; AA731111; Hs.372225; ESTs; uter, ovar; diag
 436839; AA767346; Hs.372277; ESTs; lung; diag
 436856; AI469355; Hs.127310; ESTs; mela; diag
 436954; AA740151; Hs.130425; ESTs; fibro, uter, ovar; diag
 436972; AA284679; Hs.25640; claudin 3; ovar, lung, pros; mAb
 437052; AA661697; Hs.120591; ESTs; pros; diag
 437099; N77793; Hs.48659; ESTs, Highly similar to S14458; test; diag
 437100; AI761073; Hs.14535; Homo sapiens cDNA: FLJ22314 fi; panc, renal; diag
 437119; AI379921; Hs.177043; XP_171387 similar to rhotekin; fibro; diag
 437145; AF007216; Hs.5462; solute carrier family 4, sodiu; panc, pros, stom; mAb
 437156; AI916600; Hs.121194; Homo sapiens cDNA: FLJ21569 fi; stom, renal, colon; diag
 437181; AI306615; Hs.125343; ESTs, Weakly similar to KIAA07; blad; mAb+s.m.

- 437204; AL110216; Hs.355961; ESTs, Weakly similar to I55214; lung; CTL+s.m.
 437212; AI765021; Hs.210775; ESTs; renal, uter, ovar; diag
 437224; AL117628; Hs.97808; ESTs; test; diag
 437259; AI377755; Hs.120695; ESTs; lung; diag
 437267; AW511443; Hs.258110; ESTs; BPH; diag
 437269; AA334384; Hs.149420; ESTs; angio; diag
 437330; AL353944; Hs.50115; Homo sapiens mRNA; cDNA DKFZp7; sarc; diag
 437381; NM_003684; Hs.5591; MAP kinase-interacting serine; glio; CTL+s.m.
 437390; AI125859; Hs.112607; ESTs; lung; diag
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp5; lung; diag
 437435; AA249439; Hs.27027; hypothetical protein DKFZp762H; lung; diag
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L; test; CTL+s.m.
 437478; AL390172; Hs.317432; branched chain aminotransferase; angio; s.m.
 437553; AI829935; Hs.130497; ESTs, Weakly similar to MAT8_H; blad; mAb
 437571; AA760894; Hs.125350; ESTs; pros; diag
 437623; D63880; Hs.5719; chromosome condensation-relate; test; diag
 437740; AA810265; Hs.122915; ESTs; mela; diag
 437802; AI475995; Hs.122910; ESTs; panc; diag
 437862; AW978107; Hs.5884; Homo sapiens mRNA; cDNA DKFZp5; mela; CTL+s.m.
 437908; AI082424; Hs.351043; ESTs; test; diag
 437915; AI637993; Hs.202312; Homo sapiens clone N11 Ntera2D; lung, headnk, ovar, blad, uter; diag
 437931; AI249468; Hs.124434; ESTs; blad; diag
 437935; AW939591; Hs.5940; mucin 13, epithelial transmembr; colon, stom, uter, panc; mAb+s.m.
 437938; AI950087; Hs.369628; gb:WQ05C02.X1 NCI_CGAP_Kid12 H; renal, ovar, uter, cerv, blad; diag
 437939; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 437960; AI669586; Hs.369312; ESTs; uter, ovar; diag
 438167; R28363; Hs.24286; chemokine binding protein 2 (C; ovar, breast, uter; mAb
 438199; AW016531; Hs.122147; hypothetical protein FLJ13189; breast; diag
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nucl; mela; mAb+s.m.
 438233; W52448; Hs.56147; ESTs; pros, cerv; diag
 438274; AI918906; Hs.55080; ESTs; headnk; diag
 438403; AA806607; Hs.292206; ESTs; lung; mAb
 438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.
 438450; AI050866; Hs.65853; nodal, mouse, homolog; test; diag
 438456; AA913381; Hs.279763; ESTs; test; diag
 438552; AJ245820; Hs.6314; type I transmembrane receptor; pros, ovar; diag
 438670; AI275803; Hs.123428; ESTs; fibro; CTL+s.m.
 438702; AI879064; Hs.7164; ESTs; lung; diag
 438707; L08239; Hs.5326; amino acid system N transporte; ovar; mAb
 438746; AI885815; Hs.184727; Human melanoma-associated anti; panc, blad, mela, ovar; mAb+CTL
 438817; AI023799; Hs.163242; ESTs; ovar, uter, blad, renal; diag
 438859; AI559626; Hs.93522; Homo sapiens mRNA for KIAA1647; renal; diag
 438866; U44385; Hs.6441; tissue inhibitor of metallopro; mela; diag
 438873; AI302471; Hs.124292; Homo sapiens cDNA: FLJ23123 f; fibro; diag
 438898; AI819863; Hs.106243; ESTs; lung; diag
 438915; AA280174; Hs.355711; Williams-Beuren syndrome chrom; lung, test, mela; diag
 438929; AW195515; Hs.253177; ESTs; renal; diag
 438956; W00847; Hs.135056; Human DNA sequence from clone; lung; diag
 438966; AW979074; ; gb:EST391184 MAGE resequences.; renal; diag
 438983; AF085884; Hs.20029; proacrosin binding protein sp3; test; CTL+s.m.
 438993; AA828995; ; gb:od77b08.s1 NCI_CGAP_Ov2 Hom; ovar; mAb+s.m.
 439053; BE244588; Hs.6456; chaperonin containing TCP1, su; test; diag
 439092; AA830149; ; gb:oc44f08.s1 NCI_CGAP_GCB1 Ho; pros; diag
 439176; AI446444; Hs.190394; ESTs, Weakly similar to B28096; pros; diag
 439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic; breast, ovar, uter, pros, blad, panc, colon, fibro, mela; mAb
 439221; AA737106; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582; mela, fibro; diag
 439239; AI031540; Hs.235331; ESTs; blad; diag
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag
 439310; AF086120; Hs.102793; ESTs; mela; diag
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; colon, breast, ovar, uter, cerv, pros, lung, headnk, blad, mela; mAb+s.m.
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secreto; fibro, uter; diag
 439366; AF100143; Hs.6540; fibroblast growth factor 13; pros; CTL+s.m.
 439382; BE247684; Hs.103070; ESTs; angio; diag
 439394; AA149250; Hs.56105; ESTs; lung; diag
 439410; AA632012; Hs.188746; ESTs; angio; diag
 439453; BE264974; Hs.6566; thyroid hormone receptor inter; lung, esoph, ovar; mAb+s.m.
 439496; BE616501; Hs.32343; Homo sapiens, Similar to RIKEN; mela, esoph; diag
 439559; AW970780; Hs.59483; leucine-rich repeat-containing; ovar, stom, mela, colon; mAb
 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog; ovar, uter; mAb
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC0048; lung, headnk, cerv; diag
 439702; AW085525; Hs.55964; ESTs; mela; diag
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar, lung, headnk; diag
 439735; AI635386; Hs.142846; hypothetical protein; pros; diag
 439737; AI751438; Hs.41271; Homo sapiens mRNA full length; panc; diag
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length; panc, fibro, breast; diag
 439755; AW748482; Hs.77873; B7 homolog 3; sarc; mAb
 439759; AL359055; Hs.67709; Homo sapiens mRNA full length; colon, stom, panc, leuk, lung; diag
 439778; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
 439780; AL109688; ; gb:Homo sapiens mRNA full leng; blad, esoph; diag
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length; ovar, uter, cerv, breast, pros; diag
 439864; AI720078; Hs.291997; ESTs, Weakly similar to A47582; test; diag
 439867; AA847510; Hs.161292; ESTs; panc; diag

- 5 439920; H05430; Hs.288433; neurotrimin; panc; mAb+diag
 439926; AW014875; Hs.137007; ESTs; blad, esoph, lung, cerv; diag
 439963; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.
 440042; A1073387; Hs.133898; ESTs; ovar; CTL+s.m.
 440086; NM_005402; Hs.6906; v-ral simian leukemia viral on; angio; diag
 440099; AL080058; Hs.6909; DKFZP564G202 protein; panc; diag
 440119; AA865455; Hs.125331; ESTs, Moderately similar to un; test; diag
 440138; AB033023; Hs.318127; hypothetical protein FLJ10201; lung; CTL+s.m.
 10 440151; AA868167; ; gb:ak38e07.s1 Soares_testis_NH; sarc; diag
 440207; A1371978; Hs.128326; ESTs; test; diag
 440209; H05049; Hs.247837; neurexin 3; fibro; diag
 440210; AW674562; Hs.122128; ESTs; glio; diag
 440225; BE295782; Hs.159; tumor necrosis factor receptor; glio; mAb
 15 440238; AW451970; Hs.155644; paired box gene 2; ovar; diag
 440260; A1972867; Hs.7130; copine IV; pros; diag
 440273; A1805392; Hs.325335; Homo sapiens cDNA: FLJ23523 fi; lung, fibro; diag
 440274; R24595; Hs.7122; scrapie responsive protein 1; sarc; diag
 440311; A1733079; Hs.125407; ESTs, Moderately similar to AL; renal; diag
 20 440325; NM_003812; Hs.7164; a disintegrin and metalloprote; lung; mAb
 440333; A1378424; Hs.288761; hypothetical protein FLJ21749; pros; CTL+s.m.
 440449; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
 440452; A1925136; Hs.55150; ESTs, Weakly similar to CAYP_H; fibro; diag
 440457; BE387593; Hs.21321; Homo sapiens clone FLB9213 PRO; mela; diag
 25 440484; BE328156; Hs.150356; ESTs; panc; diag
 440529; AW207640; Hs.16478; Homo sapiens cDNA: FLJ21718 fi; pros; diag
 440659; AF134160; Hs.7327; claudin 1; lung; mAb
 440704; M69241; Hs.162; insulin-like growth factor bin; lung, glio, ovar; diag
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN; test; diag
 30 440801; AA906366; Hs.370038; ESTs; pros; diag
 440819; A1809444; Hs.202108; ESTs; pros; diag
 440901; AA909358; Hs.128612; ESTs; ovar; pros; diag
 440943; AW082298; Hs.146161; hypothetical protein MGC2408; lung; diag
 440983; M20681; Hs.7594; solute carrier family 2 (facil; test; mAb
 35 441020; W79283; Hs.35962; ESTs; lung, panc; diag
 441031; A1110684; Hs.7645; fibrinogen, B beta polypeptide; lung, panc, colon; CTL+s.m.
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis; panc, ovar, stom, uter, lung; diag
 441134; W29092; Hs.346950; cellular retinoic acid-binding; sarc; diag
 441247; AW118681; Hs.128051; Homo sapiens thymic stromal ly; pros; diag
 40 441321; H17182; Hs.7771; B-cell associated protein; test; diag
 441345; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 441350; AB020690; Hs.7782; paraneoplastic antigen MA2; panc; mAb+CTL
 441377; BE218239; Hs.202656; ESTs; uter, endo, lung; diag
 441384; AA447849; Hs.288660; retinoic acid induced 3; ovar; mAb+s.m.
 45 441392; AW451831; Hs.222119; ESTs, Weakly similar to S30433; renal; diag
 441457; AW996651; Hs.43838; ESTs; angio; diag
 441495; AW294603; Hs.127039; ESTs; blad; diag
 441525; AW241867; Hs.127728; ESTs; lung; diag
 441553; AA281219; Hs.121296; ESTs; lung, test, ovar; CTL+s.m.
 50 441633; AW958544; Hs.112242; normal mucosa of esophagus spe; blad, lung, cerv, headnk, colon, panc; diag
 441790; AW294909; Hs.132208; ESTs; lung; diag
 441801; AW242799; Hs.86366; ESTs; blad; diag
 441835; AB036432; Hs.184; advanced glycosylation end pro; fibro; mAb
 441859; AW194364; Hs.380444; interleukin-4 induced gene-1 p; ovar, mela, fibro; mAb
 55 441878; A1801869; Hs.127982; ESTs; test; diag
 442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482; fibro, angio; CTL+s.m.
 442082; R41823; Hs.7413; calyntenin-2; breast, pros, ovar; diag
 442104; L20971; Hs.188; phosphodiesterase 4B, cAMP-spe; angio; CTL+s.m.
 442108; AW452649; Hs.343259; ESTs; lung; diag
 60 442242; AV647908; Hs.90424; Homo sapiens cDNA: FLJ23285 fi; BPH; diag
 442323; AW016669; Hs.29190; ESTs; breast; diag
 442333; A1650877; Hs.129302; ESTs; test; diag
 442432; BE093589; Hs.38178; hypothetical protein FLJ23468; blad, lung, panc, esoph, mela; CTL+s.m.
 442438; AA995998; Hs.370007; gb:os26b03.s1 NCL_CGAP_Kid5 Ho; uter, ovar, renal; diag
 65 442441; A1820662; Hs.129598; ESTs; breast; diag
 442503; AF147078; Hs.375031; p53-responsive gene 5; mela; diag
 442506; BE566411; Hs.41726; ESTs; angio; diag
 442573; H93366; Hs.7567; branched chain aminotransferas; ovar, panc, angio, test; s.m.
 442577; AA292998; Hs.163900; ESTs; blad, panc, colon, stom, ovar; diag
 70 442580; A1733682; Hs.130239; ESTs; breast; diag
 442609; AL020996; Hs.8518; selenoprotein N; mela; diag
 442613; A1004002; Hs.130522; Kv channel-interacting protein; glio; diag
 442622; NM_000435; Hs.8546; Notch (Drosophila) homolog 3; ovar; mAb
 442711; AF151073; Hs.8645; hypothetical protein; angio, mela, sarc; diag
 75 442739; NM_007274; Hs.8679; cytosolic acyl coenzyme A thio; mela; s.m.
 442757; A1739528; Hs.28345; ESTs; mela; diag
 442818; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
 442821; BE391929; Hs.8752; transmembrane protein 4; ovar; diag
 442832; AW206560; Hs.253569; ESTs; pros, fibro; diag
 442896; R37725; Hs.283093; ESTs; panc; diag
 80 442994; A1026718; Hs.16954; ESTs; blad, fibro; diag
 443054; A1745185; Hs.84520; yes-associated protein 65 kDa; blad; diag
 443162; T49951; Hs.9029; DKFZP434G032 protein; blad, lung; CTL+s.m.
 443171; BE281128; Hs.9030; TONDU; blad, ovar; diag

- 443184; AI638728; Hs.135159; ESTs; sarc; diag
 443211; AI128388; Hs.143655; ESTs; blad, ovar, lung, headnk, stom, colon; diag
 443216; W80487; Hs.324521; hypothetical protein DC50; test; diag
 443257; AI334040; Hs.11614; HSPC065 protein; fibro; CTL+s.m.
 443400; R28424; Hs.250648; ESTs; lung; diag
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; test; CTL+s.m.
 443537; D13305; Hs.203; cholecystokinin B receptor; test; mAb
 443648; AI085377; Hs.143610; ESTs; lung, headnk; diag
 443709; AI082692; Hs.134662; ESTs; fibro; diag
 443715; AI583187; Hs.9700; cyclin E1; lung, stom, ovar, colon; CTL+s.m.
 443785; AW449952; Hs.190125; basic-helix-loop-helix-PAS pro; glio, uter, ovar; CTL+s.m.
 443802; AW504924; Hs.9805; KIAA1291 protein; sarc; diag
 443883; AA114212; Hs.9930; serine (or cysteine) proteinase; sarc; s.m.
 443885; H91806; Hs.15284; ESTs; mela; diag
 443892; AI889572; Hs.246875; ESTs; lung; diag
 443950; NM_001425; Hs.9999; epithelial membrane protein 3; mela; mAb
 443968; AA287702; Hs.10031; KIAA0955 protein; angio; diag
 443983; H04482; Hs.163724; ESTs; mela; mAb
 443991; NM_002250; Hs.10082; potassium intermediate/small c; pros, colon, uter; mAb
 444009; AI380792; Hs.135104; ESTs; angio; diag
 444151; AW972917; Hs.128749; alpha-methylacyl-CoA racemase; pros; mAb
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like ; test; CTL+s.m.
 444163; AI126098; ; FGENSEH predicted RNaseH domain; blad; s.m.
 444301; AK000136; Hs.10760; asporin (LRR class 1); panc; diag
 444325; AW152618; Hs.16757; ESTs; esoph; diag
 444330; AI597655; Hs.49265; ESTs; angio; diag
 444342; NM_014398; Hs.10887; similar to lysosome-associated; hepC, lung, fibro, blad, esoph; diag
 444378; R41339; Hs.47860; neurotrophic tyrosine kinase, ; lung, glio; mAb+s.m.
 444409; AI792140; Hs.49265; ESTs; angio; diag
 444444; AI149332; Hs.14855; ESTs; blad; diag
 444471; AB020684; Hs.11217; KIAA0877 protein; glio, lung, colon ; mAb
 444476; AF020038; Hs.11223; isocitrate dehydrogenase 1 (NA; blad; s.m.
 444484; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ovar, uter, breast, cerv, blad, headnk; mAb
 444649; AW207523; Hs.371001; ESTs; blad; diag
 444670; H58373; Hs.332938; hypothetical protein MGC5370; sarc; diag
 444754; T83911; Hs.11881; transmembrane 4 superfamily me; panc, omuc, stom, lung, colon; mAb+s.m.
 444809; BE207568; Hs.208219; oculospanin; mela; mAb
 444823; BE262989; Hs.12045; putative protein; test; diag
 444863; AW384082; Hs.104879; serine (or cysteine) proteinase; mela; s.m.
 444895; AI674383; Hs.22891; solute carrier family 7 (catio; ovar; mAb+s.m.
 444995; AJ272265; Hs.12230; secreted phosphoprotein 2, 24k; hepC, panc; diag
 445019; AI205540; Hs.281295; ESTs; headnk, lung, colon; diag
 445070; NM_000677; Hs.258; adenosine A3 receptor; glio, renal; mAb
 445076; AI206888; Hs.154131; ESTs; test; diag
 445084; H38914; Hs.250848; hypothetical protein FLJ14761; sarc; mAb
 445093; AI207197; Hs.156905; ESTs; test; diag
 445109; AF039916; Hs.12330; ectonucleoside triphosphate di; pros; s.m.
 445119; AF035121; Hs.12337; kinase insert domain receptor ; angio; mAb
 445160; AI299144; Hs.101937; sine oculis homeobox (Drosophi; sarc; CTL+s.m.
 445182; AW189787; Hs.361778; ESTs; blad; diag
 445247; AW274290; Hs.153997; ESTs; mela; diag
 445279; R41900; Hs.22245; ESTs; angio; diag
 445363; NM_005993; Hs.12570; tubulin-specific chaperone d; test; diag
 445413; AA151342; Hs.12677; CGI-147 protein; pros, colon, uter, ovar, lung, panc ; diag
 445418; AW139377; Hs.127179; cryptic gene; panc; diag
 445424; AB028945; Hs.12696; cortactin SH3 domain-binding p; pros ; diag
 445443; AV653838; Hs.295131; ESTs; lung; diag
 445654; X91247; Hs.13046; thioredoxin reductase 1; lung; s.m.
 445684; AK001696; Hs.13109; Ran binding protein 11; angio; diag
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; angio; CTL+s.m.
 445784; AI253155; Hs.146065; ESTs; mela; CTL+s.m.
 445885; AI734009; Hs.127699; KIAA1603 protein; pros, fibro; diag
 445900; AF070526; Hs.125036; Homo sapiens clone 24787 mRNA ; renal, leuk; mAb
 445911; AI985987; Hs.145645; ESTs, Moderately similar to AL; blad; diag
 445982; BE410233; Hs.13501; pescadillo (zebrafish) homolog; mela; diag
 446057; AI420227; Hs.366053; Trp-p8 transient receptor pote; pros; mAb
 446082; AI274139; Hs.156452; ESTs; blad; diag
 446098; AW072215; Hs.208470; ESTs; angio; diag
 446100; AW967109; Hs.13804; hypothetical protein DJ462023; pros; diag
 446102; AW168067; Hs.317694; ESTs; lung; diag
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083; test; mAb
 446269; AW263155; Hs.14559; hypothetical protein FLJ10540; lung, headnk; CTL+s.m.
 446291; BE397753; Hs.14623; interferon, gamma-inducible p; mela; diag
 446292; AF081497; Hs.279682; Rh type C glycoprotein; lung, cerv; mAb
 446293; AI420213; Hs.149722; LIM domain transcription facto; ovar, test; diag
 446320; AF126245; Hs.14791; acyl-Coenzyme A dehydrogenase ; pros; s.m.
 446332; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag
 446342; BE298665; Hs.14846; solute carrier family 7 (catio; uter, colon, pros, mela; mAb
 446428; AW082270; Hs.12496; ESTs, Weakly similar to ALU4_H; fibro; diag
 446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); lung, test; diag
 446608; N75217; Hs.175622; ESTs; uter, fibro; diag
 446626; AW292180; Hs.156142; ESTs; pros; diag

- 5 446636; AC002563; Hs.15767; citron (rho-interacting, serin; lung; CTL+s.m.
446644; NM_003272; Hs.21065; transmembrane 7 superfamily me; mela; mAb
446673; NM_016361; Hs.15871; LPAP for lysophosphatidic acid; blad; diag
446727; AB011095; Hs.16032; KIAA0523 protein; angio; CTL+s.m.
10 446733; AA863360; Hs.26040; ESTs, Weakly similar to fatty ; breast; s.m.
446755; AW451473; Hs.16134; serine/threonine kinase 10; mela; CTL+s.m.
446791; A1632278; Hs.195922; ESTs; test; diag
446839; BE091926; Hs.16244; mitotic spindle coiled-coil re; test; diag
446856; A1814373; Hs.164175; ESTs; lung; diag
446868; AV660737; Hs.348297; ESTs; panc; diag
446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G; lung; mAb
446932; AA961459; Hs.125644; ESTs; fibro; diag
446967; A1699629; Hs.156781; ESTs; fibro; diag
15 446979; A1654443; Hs.197683; ESTs; test; diag
446984; AB020722; Hs.16714; Rho guanine exchange factor (G; angio; CTL+s.m.
446989; AK001898; Hs.16740; hypothetical protein FLJ11036; lung, headnk; diag
446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; panc, fibro; diag
446999; AA151520; Hs.351416; hypothetical protein MGC4485; headnk; diag
20 447004; AW296968; Hs.157539; FGENESH predicted secreted pro; glio; diag
447078; AW885727; Hs.9914; ESTs; lung; diag
447126; AW150632; Hs.170307; Rat guanine nucleotide exchang; angio; diag
447164; AF026941; Hs.17518; vipirin; similar to inflammat; colon, lung, breast, stom, hepC, esoph, mela; diag
447178; AW594641; Hs.192417; ESTs; mela; diag
25 447188; H65423; Hs.17631; hypothetical protein DKFZp434E; test; diag
447210; AF035269; Hs.17752; phosphatidylserine-specific ph; pros, mela; s.m.
447289; AW247017; Hs.36978; melanoma antigen, family A, 3; lung, mela; mAb+CTL
447334; AA515032; Hs.91109; ESTs; blad; diag
447343; AA256641; Hs.236894; ESTs, Highly similar to S02392; lung, blad, panc, headnk, mela; mAb+s.m.
30 447350; A1375572; Hs.172634; v-erb-a avian erythroblastic l; breast, ovar, uter; diag
447377; X77343; Hs.334334; transcription factor AP-2 alpha; breast, lung, mela; CTL+s.m.
447395; A1418412; Hs.184793; Homo sapiens cDNA: FLJ21880 fi; panc; diag
447437; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
447499; AW262580; Hs.147674; protocadherin beta 16; pros, glio, ovar ; mAb+s.m.
35 447532; AK000614; Hs.18791; hypothetical protein FLJ20607; lung, blad; CTL+s.m.
447534; AW953935; Hs.288655; ESTs; lung, test; diag
447578; AA912347; Hs.136585; ESTs, Weakly similar to JC5314; ovar; s.m.
447595; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
447604; AW089933; Hs.301342; hypothetical protein MGC4342; mela; diag
40 447636; Y10043; Hs.19114; high-mobility group (nonhiston; lung; CTL+s.m.
447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient; test; diag
447749; T53260; Hs.8297; ESTs; renal; diag
447761; AF061573; Hs.19492; protocadherin 8; EWS, glio; mAb
447768; X86400; Hs.19520; FXFD domain-containing ion tra; renal; mAb
45 447818; W79940; Hs.355279; Homo sapiens clone 24670 mRNA ; renal; diag
447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022; renal, ovar, uter; diag
447881; BE620886; Hs.355279; GCN1 (general control of amino; renal; diag
447937; AL109716; Hs.20034; Homo sapiens mRNA full length ; mela; mAb
447993; AW139525; Hs.170362; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
50 448030; N30714; Hs.325960; membrane-spanning 4-domains, s; panc, leuk, renal, stom lung; mAb
448045; AJ297436; Hs.20166; prostate stem cell antigen; blad, panc, pros; mAb
448105; AW591433; Hs.298241; Transmembrane protease, serine; breast, panc, colon, lung, ovar, stom; mAb+diag+s.m.
448133; AA723157; Hs.73769; folate receptor 1 (adult); ovar, fibro; mAb
448140; AF146761; Hs.20450; BCM-like membrane protein prec; fibro, mela, leuk; mAb
55 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase.; test; CTL+s.m.
448181; AF272833; Hs.279763; hypothetical protein FLJ10504; test; diag
448204; A1475124; Hs.170561; ESTs; sarc; diag
448231; A1701916; Hs.202509; ESTs; angio; diag
448258; BE386983; Hs.343214; hypothetical protein FLJ20396; mela, ovar; mAb
60 448262; AW880830; Hs.186273; ESTs; blad; diag
448275; BE514434; Hs.20830; kinesin-like 2; ovar, esoph, mela; diag
448278; W07369; Hs.11782; ESTs; lung; diag
448290; AK002107; Hs.20843; Homo sapiens cDNA FLJ11245 fis; pros; diag
448321; NM_005883; Hs.20912; adenomatous polyposis coli lik; glio; CTL+s.m.
65 448357; N20169; Hs.108923; RAB38, member RAS oncogene fam; lung, mela; diag
448410; AK000227; Hs.21126; hypothetical protein FLJ20220; mela; diag
448437; AW470125; Hs.220529; gb:wx60c04.x1 NCL_CGAP_Pan1 Ho; panc, colon; diag
448499; BE613280; Hs.77550; p53-regulated DDA3; glio; diag
448569; BE382657; Hs.21486; signal transducer and activato; panc, headnk, fibro, cerv, mela, renal; CTL+s.m.
70 448588; A1970276; Hs.156905; KIAA1676; test; CTL+s.m.
448595; AB014544; Hs.21572; KIAA0644 gene product; breast, glio; mAb
448664; A1879317; Hs.334691; splicing factor 3a, subunit 1.; mela; CTL+s.m.
448674; W31178; Hs.154140; ovary-specific acidic protein; angio; diag
448692; AW013907; Hs.167531; methylcrotonoyl-Coenzyme A car; pros, pros; s.m.
75 448706; AW291095; Hs.21814; Interleukin 20 receptor, alpha; pros, uter, blad, colon; mAb
448719; AA033627; Hs.21858; trinucleotide repeat containin; mela, sarc; CTL+diag
448775; AB025237; Hs.388; nudix (nucleoside diphosphate) ; test; diag
448811; A1590371; Hs.199460; ESTs; esoph, panc; mAb
448939; BE267795; Hs.22595; hypothetical protein FLJ10637; test; CTL+s.m.
80 448966; AW372914; Hs.86149; phosphoinositol 3-phosphate-bi; mela; CTL+s.m.
448981; A1968719; Hs.195387; ESTs; test; diag
448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros, cerv, colon, lung, stom, blad, headnk, ovar, breast; mAb
448993; A1471630; Hs.355952; KIAA0144 gene product; lung, blad; diag
448999; AF179274; Hs.22791; transmembrane protein with EGF; pros, glio ; mAb

- 5 449003; X76342; Hs.389; alcohol dehydrogenase 7 (class; lung, headnk; s.m.
449019; A1949095; Hs.67776; ESTs, Weakly similar to T22341; blad, lung; diag
449027; AJ271216; Hs.22880; dipeptidylpeptidase III; blad, colon, ovar; s.m.
449040; NM_012191; Hs.22919; putative tumor suppressor; lung; CTL+s.m.
449078; AK001256; Hs.22975; KIAA1576 protein; mela; diag
449101; AA205847; Hs.23016; G protein-coupled receptor; lung, headnk; mAb
449109; AW270992; Hs.120949; ESTs, Weakly similar to ALU7_H; sarc; diag
449156; AF103907; Hs.171353; prostate cancer antigen 3, non; pros; mAb+CTL
10 449207; AL044222; Hs.23255; nucleoporin 155kD; lung; diag
449228; AJ403107; Hs.148590; protein related with psoriasis; lung; diag
449230; BE613348; Hs.356392; melanoma cell adhesion molecule; lung, cerv, headnk, blad, ovar, colon; mAb
449317; AW293413; Hs.132906; 19A24 protein; mela; mAb
449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN; headnk, lung, angio; CTL+s.m.
15 449322; A1638616; Hs.196566; ESTs; test; diag
449338; H73444; Hs.394; adrenomedullin; renal; diag
449394; AA004368; Hs.18160; Homo sapiens cDNA FLJ11550 fis; angio; mAb
449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fi; test; diag
449448; D60730; Hs.57471; ESTs; blad, lung, headnk, breast; diag
20 449467; AW205006; Hs.197042; ESTs; lung; diag
449494; AW237014; Hs.315369; aquaporin 4; fibro; diag
449569; A1656634; Hs.195389; ESTs; test; diag
449592; A1655494; Hs.195718; ESTs; panc; diag
449618; A1076459; Hs.15978; KIAA1272 protein; angio; diag
25 449625; NM_014253; Hs.349094; odz (odd Oz/ten-m, Drosophila); pros; diag
449650; AF055575; Hs.23838; calcium channel, voltage-depen; pros; mAb
449680; A1033821; Hs.12160; ESTs; renal; diag
449691; AW265634; Hs.133100; ESTs; glio, esoph, lung, blad ; diag
449697; H06350; Hs.135056; Human DNA sequence from clone ; lung; diag
30 450096; A1682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
450098; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
450149; AW969781; Hs.132863; Zic family member 2 (odd-paire; sarc; CTL+s.m.
450152; A1138635; Hs.22968; intron of VEGFR; renal; diag
450377; AB033091; Hs.355925; KIAA1265 protein; ovar, colon; diag
35 450382; AA397658; Hs.60257; Homo sapiens cDNA FLJ13598 fis; pros; diag
450400; A1694722; Hs.279744; ESTs; panc; diag
450431; AW136797; Hs.266041; ESTs; test; diag
450451; AW591528; Hs.202072; ESTs; uter, endo; diag
450506; NM_004460; Hs.418; fibroblast activation protein.; panc, esoph; diag
40 450534; A1570189; Hs.25132; KIAA0470 gene product; angio; CTL+s.m.
450581; AF081513; Hs.25195; TGF-beta 4; uter, cerv, test; diag
450635; AW403954; Hs.25237; mesenchymal stem cell protein ; blad; mAb
450642; R39773; Hs.7130; copine IV; pros; diag
450656; AA010539; Hs.18912; unnamed protein product; fibro, uter; CTL+s.m.
45 450663; H43540; Hs.25292; ribonuclease HI, large subunit; mela; s.m.
450676; A1147155; Hs.279727; ESTs; sarc; diag
450684; AA872605; Hs.25333; interleukin 1 receptor, type I; blad, lung, headnk; mAb
450690; AA296696; Hs.333418; FXFD domain-containing ion tra; mela; diag
450693; AW450461; Hs.203965; ESTs; pros, uter; diag
50 450719; A1096837; Hs.21349; ESTs, Weakly similar to RB88_H; test; diag
450737; AW007152; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
450785; AA852713; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
450832; AW970602; Hs.105421; ESTs; lung; diag
55 451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN; pros, uter, glio; diag
451035; AU076785; Hs.430; plastin 1 (I isoform); panc; diag
451050; AW937420; Hs.351869; ESTs; mela; diag
451099; R52795; Hs.25954; interleukin 13 receptor, alpha; glio, fibro, mela; mAb
451106; BE382701; Hs.25980; N-MYC oncogene; test, ovar; CTL+s.m.
451110; A1955040; Hs.265398; PAR-6 beta (partitioning def; breast, ovar, lung, colon; CTL+s.m.
60 451181; A1796330; Hs.207461; ESTs; panc; diag
451253; H48299; Hs.26126; claudin 10; lung, ovar, panc; mAb
451291; R39288; Hs.6702; ESTs; lung; diag
451295; A1557212; Hs.17132; ESTs, Moderately similar to I5; panc; diag
65 451320; AW118072; Hs.350251; diacylglycerol kinase, zeta (1; lung; s.m.
451346; NM_006338; Hs.26312; glioma amplified on chromosome; ovar; mAb
451386; AB029006; Hs.26334; spastic paraplegia 4 (autosoma; lung; diag
451398; A1793124; Hs.144479; ESTs; breast, ovar; diag
451411; AA017492; Hs.135655; EST; pros; diag
451497; H83294; Hs.284122; Wnt inhibitory factor-1; uter, fibro, pros, colon, sarc; diag
70 451541; BE279383; Hs.26557; plakophilin 3; lung, blad, ovar; diag
451592; A1805416; Hs.213897; ESTs; lung, headnk; diag
451635; AA018899; Hs.127179; cryptic gene; panc; diag
451663; A1872360; Hs.209293; ESTs; pros; diag
451720; AW970985; Hs.290853; ESTs; pros; diag
451743; AW074266; Hs.336428; ESTs; lung; diag
75 451820; AW058357; Hs.199248; ESTs; panc; mAb
451844; T61430; ; gb:yc06a03.s1 Stratogene lung ; blad; diag
451982; F13036; Hs.27373; Homo sapiens mRNA; cDNA DKFZp5; pros, blad; mAb
451999; AW176401; Hs.380623; DEAD/H (Asp-Glu-Ala-Asp/His) b; test; CTL+s.m.
80 452046; AB018345; Hs.27657; KIAA0802 protein; lung, uter; CTL+s.m.
452208; AA024792; Hs.31895; hypothetical protein MGC4093; renal; diag
452240; A1591147; Hs.61232; ESTs; blad, lung, headnk, panc, cerv; diag
452243; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
452244; N33530; Hs.176674; ESTs; mela; diag

- 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S; test; CTL+s.m.
 452295; BE379936; Hs.28866; programmed cell death 10; lung; diag
 452298; AI039243; Hs.278585; ESTs; angio; diag
 452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590; lung, panc, blad, stom, esoph, fibro, colon; s.m.
 452316; AA298484; Hs.61265; ESTs, Moderately similar to G7; blad; diag
 452340; NM_002202; Hs.505; ISL1 transcription factor, LIM; panc, pros; CTL+s.m.
 452353; C18825; Hs.29191; epithelial membrane protein 2; pros, breast; mAb
 452355; N54926; Hs.29202; G protein-coupled receptor 34; glio, fibro, panc; mAb
 452367; U71207; Hs.29279; eyes absent (Drosophila) homolog; lung, pros, ovar, uter; CTL+s.m.
 452416; AA026115; Hs.114777; ESTs; fibro; diag
 452461; N78223; Hs.108106; transcription factor; blad, lung, headnk, ovar, glio, stom, colon, cerv; CTL+s.m.
 452571; W31518; Hs.34665; ESTs; stom, lung, panc, colon, fibro; diag
 452594; AU076405; Hs.29981; solute carrier family 26 (sulf; ovar; mAb
 452613; AA461599; Hs.23459; ESTs; lung; diag
 452679; Z42387; Hs.83883; transmembrane, prostate androg; pros, colon, panc, pros; mAb
 452705; H49805; Hs.246005; ESTs; panc; diag
 452717; AW160399; Hs.30376; hypothetical protein; pros; diag
 452721; AJ269529; Hs.301871; solute carrier family 37 (glyc; pros; mAb
 452732; BE300078; Hs.80449; Homo sapiens, clone IMAGE:3535; blad; diag
 452744; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; mela; diag
 452792; AB037765; Hs.30652; KIAA1344 protein; pros, uter, breast; diag
 452795; AW392555; Hs.18878; hypothetical protein FLJ21620; renal, headnk, colon, lung, panc; CTL
 452796; AB011100; Hs.30656; KIAA0528 gene product; test; diag
 452833; BE559681; Hs.30736; KIAA0124 protein; lung, mela; CTL+s.m.
 452865; AI924046; Hs.119567; ESTs, Weakly similar to A47582; lung; diag
 452899; M96739; Hs.30956; nescent helix loop helix 1; sarc; CTL+s.m.
 452924; AW580939; Hs.97199; complement component C1q recep; angio; diag
 452933; AW391423; Hs.288555; Homo sapiens cDNA: FLJ22425 fi; angio; CTL+s.m.
 452934; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 452955; AW390282; Hs.31130; transmembrane 7 superfamily me; pros; mAb+s.m.
 453006; AI362575; Hs.303171; ESTs; pros; diag
 453028; AB006532; Hs.31442; RecQ protein-like 4; blad, lung, test; CTL+s.m.
 453085; AW954243; Hs.351573; KIAA0251 protein; angio; diag
 453096; AW294631; Hs.351270; ESTs; pros; diag
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog; lung, headnk, colon; mAb
 453107; NM_016113; Hs.279746; vanilloid receptor-like protei; mela; mAb
 453134; AA032211; Hs.118493; ESTs; blad; diag
 453142; AA033648; Hs.7473; Homo sapiens gap junction prot; fibro; mAb
 453160; AI263307; Hs.356901; H2B histone family, member L; lung, panc, pros; diag
 453210; AL133161; Hs.32360; hypothetical protein FLJ10867; lung; CTL+s.m.
 453216; AL137566; Hs.32405; progesterone receptor (PR); blad; mAb+s.m.
 453256; AI565587; Hs.32556; KIAA0379 protein; mela; diag
 453310; X70697; Hs.553; solute carrier family 6 (neuro; fibro; mAb
 453321; AI984381; Hs.232521; ESTs; blad; diag
 453323; AF034102; Hs.32951; solute carrier family 29 (nuc; ovar; CTL+s.m.
 453331; AI240665; Hs.352537; ESTs; breast, lung, panc, esoph; mAb+diag+s.m.
 453344; BE349075; Hs.44571; ESTs; mela; diag
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; test; CTL+s.m.
 453365; AA035211; Hs.17404; SOX7 SRY (sex determining regi; angio, blad; CTL+s.m.
 453370; AI470523; Hs.139336; ATP-binding cassette, sub-fami; pros; mAb
 453389; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; renal, ovar, blad; mAb+s.m.
 453392; U23752; Hs.32964; SRY (sex determining region Y); ovar, lung, glio, sarc; CTL+s.m.
 453459; BE047032; Hs.257789; ESTs; ovar, cerv, blad, uter, panc, angio, lung; diag
 453464; AI884911; Hs.32989; receptor (calcitonin) activity; pros; mAb
 453633; AA357001; Hs.34045; hypothetical protein FLJ20764; lung, esoph, test; diag
 453637; NM_002589; Hs.34073; BH-protocadherin (brain-heart); headnk; mAb
 453642; AI370936; Hs.34074; dipeptidylpeptidase VI; glio; mAb
 453779; N35187; Hs.43388; 28kD interferon responsive pro; mela; diag
 453789; AA628517; Hs.118502; ESTs; angio; diag
 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1; glio, lung, uter, headnk, cerv, panc, pros, sarc; mAb
 453883; AI638516; Hs.347524; cofactor required for Sp1 tran; blad, lung; diag
 453884; AA355925; Hs.36232; KIAA0186 gene product; lung, ovar, test, esoph; diag
 453912; AL121031; Hs.356843; SWI/SNF related, matrix associ; mela; diag
 453922; AF053306; Hs.36708; budding uninhibited by benzimid; colon, stom, lung, test; CTL+s.m.
 453935; AI633770; Hs.42572; ESTs; panc; diag
 453941; U39817; Hs.36820; Bloom syndrome; lung, cerv, headnk; CTL+s.m.
 453964; AI961486; Hs.249196; ESTs; lung; diag
 453966; BE148734; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 453985; N44545; Hs.251865; ESTs; test; diag
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 famit; lung, headnk; s.m.
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; lung; diag
 454066; X00356; Hs.37058; calcitonin/calcitonin-related; lung; diag
 454071; AI041793; Hs.42502; ESTs; breast; diag
 454077; AC005952; Hs.37062; insulin-like 3 (Leydig cell); test; diag
 454098; W27953; Hs.217493; Plakophilin; lung; diag
 454117; BE410100; Hs.40368; adaptor-related protein comple; mela; CTL+s.m.
 454360; L78207; Hs.54470; ATP-binding cassette, sub-fami; glio; mAb
 454429; BE273437; Hs.301406; hypothetical protein PP3501; mela; mAb
 454439; AW819152; Hs.154320; DKFZP566O1646 protein; lung; diag
 454478; AW805749; Hs.372783; superoxide dismutase 2, mitoch; mela; s.m.
 455601; AI368680; Hs.816; SRY (sex determining region Y); lung, cerv, esoph; s.m.
 456034; AW450979; ; gb:Ul-H-BI3-ala-a-12-O-Ul.s1 N; blad, fibro; diag
 456062; AI866286; Hs.71962; ESTs, Weakly similar to B36298; fibro, ovar, uter; diag

456177; NM_012391; Hs.79414; prostate epithelium-specific E; breast, pros; diag
 456266; L29073; Hs.198726; cold shock domain protein A; panc; CTL+s.m.
 456321; NM_001327; Hs.87225; cancer/testis antigen; lung; CTL
 456553; AA721325; Hs.189058; ESTs, Highly similar to Simila; panc; diag
 456723; Z43902; Hs.4748; adenylate cyclase activating p; glio; mAb+s.m.
 456736; AW248217; Hs.1619; achaete-scute complex (Drosoph); lung; diag
 456759; BE259150; Hs.127792; delta (Drosophila)-like 3; glio, lung; mAb
 456847; AI360456; Hs.86088; ESTs; test; diag
 456938; X52509; Hs.161640; tyrosine aminotransferase; breast; s.m.
 456977; AK000252; Hs.169758; hypothetical protein FLJ20245; angio; diag
 457200; U33749; Hs.197764; thyroid transcription factor 1; fibro; CTL+s.m.
 457211; AW972565; Hs.32399; ESTs, Weakly similar to S51797; mela, pros; CTL+s.m.
 457292; AI921270; Hs.281462; hypothetical protein FLJ14251; blad; mAb
 457313; AF047002; Hs.241520; transcriptional coactivator; test; CTL+s.m.
 457411; AW085961; Hs.130093; iroquois-class homeobox protein; breast, fibro; diag
 457465; AW301344; Hs.122908; DNA replication factor; test, mela; diag
 457498; AI732230; Hs.191737; ESTs; pros; diag
 457561; AA331517; Hs.286055; chimerin (chimaerin) 2; glio; mAb
 457590; AI612809; Hs.5378; hypothetical protein MGC10724; ovar; diag
 457869; AU077186; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
 458092; W67353; Hs.350558; KIAA0251 protein; lung; diag
 458124; AW005548; Hs.124590; ESTs; fibro; diag
 458435; AI418718; Hs.144121; ESTs, Weakly similar to T46916; glio; diag
 458471; AV648609; Hs.194240; ESTs; renal, panc, hepC; diag
 458933; AI638429; Hs.24763; RAN binding protein 1; lung, test; diag
 459373; BE408266; Hs.301406; hypothetical protein PP3501; mela; mAb
 459578; AW612538; Hs.304491; EST; mela; diag
 459702; AI204995; ; gb:an03c03.x1 Stratagene schiz; blad, fibro; diag
 459705; BE082764; Hs.270252; ESTs, Weakly similar to androg; fibro; mAb+s.m.

TABLE 3B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
103739	49403_2	AA115173 AA075709 AA076354 AA083101 AA076396 AA085391 AA070684 AA083368 AA075779 AA075221 AA076395 AA650486 AA083500
108282	108971_1	AA065143 AA065142
113230	2327174_1	AI820546 AI821336 T61430
118417	35983_1	AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594
		AI818326 AF080230 S46404 AI970376 AA463952 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614951
		N29986 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611
		AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833
		AA207155 BI004756 AA206262 AI365204 H77608 AW590511
	121335	AA404418 AI217248
	126872	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	322521	AF147347 T55503 T55426
	322975	C16391 C16413
	323332	AI829520 AI791832 AI791823 AA229315 AA228414 AA229211
	323817	AA410943 BF366582 AA334202 AA332882 BF371899 AW948953
	324261	AL044891 AI908240 AA393080 AW748403 BE069341 BF330573
	406685	M18728
	409051	AA075419 AA082953 AA080912 AA062835 AA071252 AA084926 AA078992 AA113913 AA081881 AA070343 AA083821 AA062836 AA113892
		AA075318 AA076594 AA078900 AA1134801 AA063293 AA083403 AW974305
	409123	AA070050 AA070823 AA063403
	409745	BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722
		BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762
		BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
	411880	BE088101 T05990 AW872477
	413804	BE168256 BE168190 T64682
	414221	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	417886	AA210987 D57294 AA214584 AA207006 D56572
	427260	AA401424 AA400100 AA663848
	427298	AA933717 BF061897 AW628327 AA641788 AA400495
	427521	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165
		AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
	429163	AW974271 AA592975 AA447312 AA884766
	432189	AA527941 AA635266 AI810608 AI620190
	432222	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	432407	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104
		AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279
		BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849
		AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859
		BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
		AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
	432415	BG166382 AW161086 N42363 BE935013 BE934998 BG291451 AV700520 BG152773 AI224956 AI079635 AW054706 AA843979 AI744193 F04060
		T23457 F04044 AA723859 AA977643 AA283764 AI123609 N21561 BF055052 BE856661 AI804220 AA843394 AI472045 AI740490 AA578830
		H09495 AI283334 AA609495 AI122773 AW162543 AW161798 BF940077 AI808825 AI360866 AI123189 R40236 R20726 AW975899 BE764052
		N31709 N31708 AI031947 AW194138
	434414	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422
		AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298

AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175
 BF854337
 AF147374 T59538 T59589 T59598 T59542
 AF147390 R76593 R76594
 AW979074 AA834841 AA828650
 AI926361 AA834879 AA828995
 AW978407 AA830149 M85983 AW503637 BF352096
 AL109688 R23665 R26578
 AA868167 F21558 F31418 F35624
 BG403189 AI148521 AI184746 AI126098 R05933 BI057330
 AI820546 AI821336 T61430
 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354

TABLE 3C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
325372	5866920	Minus	1117061-1117304
325544	6682452	Plus	171228-171286
327036	6531965	Plus	319951-320040
327075	6531965	Plus	4041318-4041431
327414	5867750	Plus	102461-102586
328700	5868264	Plus	764089-764203
330211	6013592	Plus	59158-59215
332798	Dunham, I. et.al.	Minus	232147-231974
333769	Dunham, I. et.al.	Plus	7696625-7696707
333904	Dunham, I. et.al.	Minus	8217374-8217261
334223	Dunham, I. et.al.	Minus	12734365-12734269
334447	Dunham, I. et.al.	Plus	14308764-14308824
335115	Dunham, I. et.al.	Minus	21388250-21388146
335809	Dunham, I. et.al.	Plus	26310772-26310909
335824	Dunham, I. et.al.	Plus	26376860-26376942
335825	Dunham, I. et.al.	Plus	26378175-26378268
335936	Dunham, I. et.al.	Minus	27360474-27360400
336034	Dunham, I. et.al.	Plus	29014404-29014590
336152	Dunham, I. et.al.	Minus	30156053-30155870
336536	Dunham, I. et.al.	Plus	988418-989185
338008	Dunham, I. et.al.	Plus	7697068-7697236
338033	Dunham, I. et.al.	Plus	8092128-8092271
338158	Dunham, I. et.al.	Minus	11794465-11794343
338255	Dunham, I. et.al.	Minus	15242294-15242231
400494	9714719	Plus	169845-170272
400517	9796686	Minus	49996-50346
400651	8117978	Minus	81488-81646
400665	8118496	Plus	16879-17023
400773	8131629	Minus	44116-44238,48208-48321
400844	9188605	Plus	24746-24872,25035-25204
400846	9188605	Plus	39310-39474
400881	2842777	Minus	91446-91603,92123-92265
401093	8516137	Minus	22335-23166
401234	9929642	Plus	120173-120337
401424	8176894	Plus	24223-24428
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
401704	3097841	Plus	24712-25374
401732	1200312	Plus	19346-19525,19625-19708,19897-19973,2006
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
401797	6730720	Plus	6973-7118
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
402145	8018280	Plus	113086-114800
402199	8576116	Minus	84187-84744
402230	9966312	Minus	29782-29932
402239	7690131	Plus	38175-38304,42133-42266
402260	3399665	Minus	113765-113910,115653-115765,116808-11694
402265	3287673	Plus	21059-21168
402305	7328724	Plus	40832-41362
402420	9796339	Plus	129750-129919
402424	9796344	Minus	64925-65073
402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402550	7652009	Minus	80413-80673
402604	9909420	Plus	20393-20767
402605	9909420	Minus	47680-47973

	402606	9909429	Minus	81747-82094
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	402777	9588235	Plus	126786-126948
5	402860	9588237	Minus	76423-76560
	402888	9930892	Minus	54727-54901
	402992	7767907	Minus	42137-42515
	402994	2996643	Minus	4727-4969
	403046	3540153	Minus	55707-55859,56369-56511
10	403047	3540153	Minus	59793-59968
	403071	8954241	Plus	136688-137096
	403088	8954241	Plus	169894-170193,170504-170806
	403171	9838164	Minus	74502-74703
	403328	8469086	Minus	120428-120703
15	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
	403409	9438598	Plus	6860-7054,12573-12771
	403433	9719611	Minus	72225-72437
	403478	9958258	Plus	116458-116564
20	403715	7239669	Plus	85128-85292
	403740	7630882	Plus	86504-87227
	403776	7770611	Minus	1414-1513,1624-1756
	403903	7710671	Minus	101165-102597
	404029	7671252	Plus	108716-111112
25	404049	3688074	Minus	75765-78155
	404210	5006246	Plus	169926-170121
	404240	5002624	Minus	116132-116407,116653-116922
	404253	9367202	Minus	55675-56055
	404286	2326514	Plus	51086-51301
30	404298	9944263	Minus	73591-73723
	404403	7272157	Minus	72053-72238
	404440	7528051	Plus	80430-81581
	404866	9366919	Minus	11743-11929
	404877	1519284	Plus	1095-2107
35	404927	7342002	Plus	68690-69563
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	405001	6015406	Minus	104646-104819
	405025	7107727	Plus	105267-105343,106184-106294,106387-10653
	405121	8102330	Minus	35816-36004,36587-36684
40	405238	7249119	Minus	51728-51836
	405239	7249119	Plus	144345-144464,144690-144836,151750-15188
	405451	7622517	Minus	145949-146227
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405546	1054740	Plus	124010-124183
45	405547	1054740	Plus	124361-124520,124914-125050
	405646	4914350	Plus	741-969
	405704	4204244	Plus	138842-139051
	405770	2735037	Plus	61057-62075
	405849	7651817	Minus	17705-18287
50	405932	7767812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
	406137	9166422	Minus	30487-31058
	406173	7230224	Plus	12925-13213
	406348	9255985	Minus	71754-71944
55	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406434	9256651	Minus	17803-17931
	406467	9795551	Plus	182212-182958
	406506	7711374	Minus	6843-8077
60	406547	7711513	Minus	172780-174358

Table 4A lists about 425 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues. These genes were selected from a starting collection of about 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 75th percentile value amongst non-malignant adult tissues. Certain predicted protein domains are noted.

Table 5A lists about 231 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected similarly as for Table 1. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 50th percentile value amongst non-malignant adult tissues. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

TABLE 4A: ABOUT 425 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES

75 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: Unigene number
 Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 80 UniGene Title: Unigene gene title
 R1: Ratio of 90th percentile of tumor to 75th percentile of normal body tissue

Pkey	ExAccn	UniGeneID	Pred.Prot.Domains	UniGeneTitle	R1
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5	419551	AW582256	Hs.91011	TM=M;SS=M	anterior gradient 2 (Xenopus laevis	9.7
	426174	AA547959	Hs.115838		Homo sapiens similar to Echinoidin	7.0
	409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	6.8
	428471	X57348	Hs.184510	14-3-3;TM=M;SS=N	stratiferin	6.4
	417931	W95642	Hs.82961	trefoil;TM=N;SS=M	trefoil factor 3 (intestinal)	6.3
10	447966	AA340605	Hs.105887	Jacalin;TM=N;SS=M	ESTs, Weakly similar to Homolog of	6.1
	406387				Target Exon	6.0
	421814	L12350	Hs.108623	EGF,isp_1,vwc,TSPN,isp_3;	thrombospondin 2	5.8
	406867	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	5.8
	426104	AI204418	Hs.190080		ESTs	5.8
15	421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	5.8
	422511	AU076442	Hs.117938	Collagen,none	collagen, type XVII, alpha 1	5.7
	426539	AB011155	Hs.170290	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	5.6
	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXD domain-containing ion transpor	5.5
	419329	AY007220	Hs.288998	S_100;TM=M;SS=N	S100-type calcium binding protein A	5.4
20	418344	AA216387			gb:nc16b02.s1 NCI_CGAP_Pr1 Homo sap	5.2
	407116	AA130986	Hs.271627		ESTs	5.1
	417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midkine (neurite growth-promoting f	5.1
	419452	U33635	Hs.90572	ig,ptkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	5.1
	421552	AF026692	Hs.105700	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 4	5.1
25	409453	AI885516	Hs.95612	cadherin,cadherin,Cadheri	ESTs	5.1
	409632	W74001	Hs.55279	serpin;TM=N;SS=N	serine (or cysteine) proteinase inh	5.1
	417515	L24203	Hs.82237	zf-B_box,zf-UBR1;TM=M;SS=	ataxia-telangiectasia group D-assoc	5.0
	411573	AB029000	Hs.70823	Sulfatase;TM=M;SS=N	KIAA1077 protein	5.0
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regulato	5.0
30	422087	X58968	Hs.111301	fn2,hemopexin,Peptidase_M	matrix metalloproteinase 2 (gelatin	5.0
	421143	AB024536	Hs.102171	ig,LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily containi	4.9
	408491	AI089063	Hs.7882		ESTs	4.9
	417944	AU077196	Hs.82985	vwc,Collagen,COLFI;TM=N;S	collagen, type V, alpha 2	4.9
	409062	AL157488	Hs.50150		Homo sapiens mRNA; cDNA DKFZp564B18	4.9
35	422281	M36803	Hs.346935	hemopexin;TM=N;SS=M	hemopexin	4.9
	425308	M97639	Hs.155585	ig,kringle,ptkinase,Fz;TM=	receptor tyrosine kinase-like orpha	4.8
	408349	BE546947	Hs.44276	homeobox;TM=M;SS=N	homeo box C10	4.8
	449019	AI949095	Hs.67776		ESTs, Weakly similar to T22341 hypo	4.8
	435561	AA351978	Hs.4943	MAGE,Cys_knot,EGF,Jaminin	hepatocellular carcinoma associated	4.8
40	410687	U24389	Hs.65436	Lysyl_oxidase;TM=N;SS=M	lysyl oxidase-like 1	4.8
	429455	AI472111	Hs.278694	lectin_c	CD209 antigen	4.8
	414407	AA147026	Hs.76704		ESTs	4.8
	419390	AI701162	Hs.331904	PMP22_Claudin,PMP22_Claud	hypothetical protein MGC11138	4.7
	453902	BE502341	Hs.3402		ESTs	4.7
45	411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	4.7
	450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	4.7
	449717	AB040935	Hs.23954	Glyco_transf_25;TM=N;SS=N	cerebral cell adhesion molecule	4.6
	451529	AI917901	Hs.208641	actin,none	ESTs	4.6
	435370	AI964074	Hs.225838	EGF,fn3,fibrinogen_C,toxi	ESTs	4.6
50	411761	AI733848	Hs.71935	zf-C2H2;TM=M;SS=N	putative zinc finger protein from E	4.6
	424223	AJ243706	Hs.143323	PHD,ARID,jmjC,jmjN,zf-C5H	putative DNA/chromatin binding moti	4.6
	426935	NM_000088	Hs.172928	vwc,Collagen,COLFI;TM=M;S	collagen, type I, alpha 1	4.5
	408796	AA688292	Hs.170345	hormone_rec,zf-C4	ESTs	4.5
	407230	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	4.4
55	422830	AC007954	Hs.121371		hypothetical protein DKFZp434P0111	4.4
	447528	AI612027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	4.4
	430168	AW968343	Hs.145582	efhand,efhand	DKFZP43411735 protein	4.4
	423225	AA852604	Hs.125359	ig,Ribosomal_S19;TM=M;SS=	Thy-1 cell surface antigen	4.4
	414822	AA156542	Hs.72127	homeobox,HLH	ESTs	4.4
60	452683	AI089575	Hs.374574	homeobox,none	progesterone membrane binding prote	4.4
	444784	D12485	Hs.11951	Somatomedin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	4.4
	453957	AL080235	Hs.35861	TM=Y;SS=M	Ras-induced senescence 1 (RIS1)	4.4
	413859	AW992356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	4.3
	440369	AW176150	Hs.132449		downstream of breast cancer antigen	4.3
65	418140	BE613836	Hs.83551	TM=M;SS=M	microfibrillar-associated protein 2	4.3
	441384	AA447849	Hs.288660	7tm_3,none	retinoic acid induced 3	4.3
	424464	R68537	Hs.17962	homeobox,none	ESTs	4.3
	423582	BE000831	Hs.23837	TGFb_propeptide,TGF-beta,	Homo sapiens cDNA FLJ11812 fis, clo	4.3
	432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	4.2
70	433320	D60647	Hs.250879	rrm	ESTs, Highly similar to CTXN RAT CO	4.2
	429165	AW009886	Hs.118258		prostate cancer associated protein	4.2
	416984	H38765	Hs.80706	Flavodoxin_2;TM=M;SS=N	diaphorase (NADH/NADPH) (cytochrome	4.2
	448913	AA194422	Hs.22564	rrm,zf-RanBP,ptkinase,GST_	myosin VI	4.2
	430154	AW583058	Hs.234726	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	4.2
75	400496			TM=Y;SS=N	ENSP00000224716*:GTP-binding protei	4.2
	442599	AF078037	Hs.324051	SH3,ank;TM=M;SS=N	RelA-associated inhibitor	4.2
	448520	AB002367	Hs.21355	ptkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	4.2
	431309	AW451711	Hs.313760	homeobox,none	ESTs, Weakly similar to I38022 hypo	4.2
	426485	NM_006207	Hs.170040	ig;TM=N;SS=M	platelet-derived growth factor rece	4.2
80	435858	AF254260	Hs.283009	bZIP;TM=M;SS=N	tufelin 1	4.2
	446051	BE048061	Hs.37054	Ephrin_A_deamin,dsrm,z-al	ephrin-A3	4.2
	451982	F13036	Hs.27373	NA;NA	Homo sapiens mRNA; cDNA DKFZp564O17	4.2
	450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	4.1
	431890	X17033	Hs.271986	vwa,Integrin_A,FG-GAP;TM=	integrin, alpha 2 (CD49B, alpha 2 s	4.1
	434449	AW953484	Hs.3849	efhand,FKBP;TM=M;SS=N	hypothetical protein FLJ22041 simil	4.1
	422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	4.1

5	423057	AW961597	Hs.130816		ESTs, Moderately similar to I38022	4.1
	452063	R53185	Hs.32366	HLH;TM=M;SS=N	ESTs, Weakly similar to TWST_HUMAN	4.1
	450680	AF131784	Hs.25318	ras,none	Homo sapiens clone 25194 mRNA seque	4.1
	418283	S79895	Hs.83942	Peptidase_C1;TM=N;SS=M	cathepsin K (pseudodysostosis)	4.1
	416361	AW204907	Hs.6872		ESTs, Weakly similar to CA13_HUMAN	4.1
	426255	BE262530	Hs.2006	GST_C,GST_N;TM=M;SS=N	glutathione S-transferase M3 (brain	4.1
	408113	T82427	Hs.194101	7tm_3,none	Homo sapiens cDNA: FLJ20869 fis, cl	4.1
10	407792	AI077715	Hs.39384	TM=M;SS=Y	putative secreted ligand homologous	4.1
	422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	4.1
	429359	W00482	Hs.2399	hemopexin,Peptidase_M10;T	matrix metalloproteinase 14 (membra	4.1
	442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	4.0
	448826	AI580252	Hs.255565		ESTs, Weakly similar to putative p1	4.0
	419648	T73661	Hs.91877	TM=N;SS=M	thyroid hormone responsive SPOT14 (4.0
15	421485	AA243499	Hs.104800	TM=Y;SS=M	hypothetical protein FLJ10134	4.0
	440273	AI805392	Hs.325335		Homo sapiens cDNA: FLJ23523 fis, cl	4.0
	417363	AW129357	Hs.329700		ESTs	4.0
	451277	AK001123	Hs.26176	TM=Y;SS=M	hypothetical protein FLJ10261	4.0
	421823	N40850	Hs.28625		ESTs	4.0
20	452239	AW379378	Hs.356289		protein tyrosine phosphatase, recep	4.0
	444286	AI625304	Hs.201008		ESTs	4.0
	451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	4.0
	451304	M92642	Hs.26208	Collagen,TSPN;TM=M;SS=M	collagen, type XVI, alpha 1	4.0
	429556	AW139399	Hs.314807	TM=M;SS=N	ESTs	4.0
25	441094	U33819	Hs.7647	zf-C2H2,LIM,PHD,TFIIS;TM=	MYC-associated zinc finger protein	4.0
	407788	BE514982	Hs.38991	efhand,S_100,S_100,efhand	S100 calcium-binding protein A2	4.0
	451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	3.9
	437762	T78028	Hs.154679	C2,none	synaptotagmin I	3.9
	433399	N46406	Hs.84700	START;TM=M;SS=N	similar to phosphatidylcholine tran	3.9
30	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	3.9
	404578	AF183810	Hs.26102	zf-C2H2,rubredoxin;TM=M;S	trichorhinophalangeal syndrome I gene	3.9
	443883	AA114212	Hs.9930	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	3.9
	445084	H38914	Hs.250848	TM=Y;SS=M	hypothetical protein FLJ14761	3.9
	453880	AI803166	Hs.135121	HSP70,none	ESTs, Weakly similar to I38022 hypo	3.9
35	424125	M31669	Hs.1735	TGF-beta,TGFb_propeptide;	inhibin, beta B (activin AB beta po	3.9
	437377	AL359573	Hs.124940	ras;TM=M;SS=N	GTP-binding protein	3.9
	422562	AI962060	Hs.118397	Zn_carbOpept,F5_F8_type_C	AE-binding protein 1	3.9
	422320	AI745249	Hs.23650	TM=Y;SS=N	ESTs, Weakly similar to AAB47496 NG	3.9
	433078	AW015188	Hs.121575	asp	Homo sapiens cDNA FLJ12231 fis, clo	3.9
40	411894	M57609	Hs.72916	zf-C2H2;TM=N;SS=M	GLI-Kruppel family member GLI3 (Gre	3.9
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	3.9
	418113	AI272141	Hs.83484	HMG_box,homeobox;TM=M;SS=	SRY (sex determining region Y)-box	3.9
	418753	BE217818	Hs.87016		hypothetical protein FLJ22938	3.8
	452679	Z42387	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.8
45	421030	AW161357	Hs.101174	tubulin-binding;TM=N;SS=M	microtubule-associated protein tau	3.8
	431567	N51357	Hs.260855	TM=M;SS=N	Homo sapiens cDNA: FLJ21410 fis, cl	3.8
	426363	M58524	Hs.2025	TGF-beta,TGFb_propeptide;	transforming growth factor, beta 3	3.8
	447151	AI022813	Hs.92679	kinesin;TM=M;SS=M	Homo sapiens clone CDABP0014 mRNA s	3.8
	448717	R67419	Hs.21851	HLH,homeobox,none	Homo sapiens cDNA FLJ12900 fis, clo	3.8
50	425867	D60385	Hs.12079	cadherin;TM=Y;SS=M	calysentin-2	3.8
	423940	NM_012429	Hs.277728	CRAL_TRIO;TM=M;SS=N	SEC14 (S. cerevisiae)-like 2	3.8
	426742	AA383828	Hs.181131		ESTs	3.8
	435818	AA700553	Hs.368614	arf,ras,RecR,none	ESTs	3.8
	420005	AW271106	Hs.133294		ESTs	3.8
55	410867	X63556	Hs.750	EGF,TB,wnt,EB,TIL;TM=N;SS	fibrillin 1 (Marfan syndrome)	3.8
	402531	AB037745	Hs.104696	TM=M;SS=M	KIAA1324 protein	3.8
	449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	3.8
	424806	AA382523	Hs.105689	TM=Y;SS=N	MSTP031 protein	3.8
	443933	AI091631	Hs.203845	ion_trans;TM=Y;SS=M	two pore potassium channel KT3.3	3.8
60	432952	AA813887	Hs.188173		Homo sapiens cDNA FLJ12187 fis, clo	3.8
	424036	AA770688	Hs.348495	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member L	3.7
	453828	AW970960	Hs.293821	Pep_M12B_propep,Repolysi	ESTs	3.7
	407112	AA070801	Hs.51615	hormone_rec,zf-C4	ESTs, Weakly similar to ALU7_HUMAN	3.7
	445669	AI570830	Hs.174870		ESTs	3.7
65	446091	AW022192	Hs.200197	homeobox,none	ESTs	3.7
	424651	AI493206	Hs.120785		ESTs	3.7
	409178	BE393948	Hs.50915	trypsin;TM=M;SS=Y	kallikrein 5	3.7
	417059	AL037672	Hs.81071	TM=N;SS=Y	extracellular matrix protein 1	3.7
70	431194	D43704	Hs.250712	Ca_channel_B,RepB_protein	calcium channel, voltage-dependent,	3.7
	430397	AI924533	Hs.105607	HCO3_cotransp;TM=Y;SS=N	bicarbonate transporter related pro	3.7
	418969	W33191	Hs.28907	SH3;TM=M;SS=N	hypothetical protein FLJ20258	3.7
	427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	3.7
	424012	AW368377	Hs.137569	SAM,P53;TM=M;SS=N	tumor protein 63 kDa with strong ho	3.7
	418840	AI821614	Hs.185831		ESTs	3.7
75	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamini	cadherin, EGF LAG seven-pass G-type	3.7
	433430	AI863735	Hs.369982	thyroglobulin_1,IGFBP,zf-	ESTs	3.7
	422491	AA338548	Hs.117546	TM=M;SS=Y	neuronatin	3.7
	435114	AA775483	Hs.288936	ODC_AZ,Ribosomal_L9_N;TM=	mitochondrial ribosomal protein L9	3.7
	416899	BE262645	Hs.80420	IL8;TM=M;SS=M	small inducible cytokine subfamily	3.7
80	422110	AI376736	Hs.121555	kazal,none	secreted protein, acidic, cysteine-	3.7
	448560	BE613183	Hs.23213	zf-RanBP,MDM2,Ndr	ESTs	3.6
	414945	BE076358	Hs.77687	UPAR_LY6;TM=M;SS=M	lymphocyte antigen 6 complex, locus	3.6
	422119	AI277829	Hs.111862	WD40;TM=M;SS=N	KIAA0590 gene product	3.6
	447335	BE617695	Hs.286192	TM=M;SS=N	hypothetical protein FLJ20940	3.6

5	450663	H43540	Hs.25292	RNase_HII;TM=N;SS=M	ribonuclease HI, large subunit	3.6
	417387	AW021102	Hs.21509	zf-C2H2,none	ESTs	3.6
	450825	AC005954	Hs.25527	PDZ,Guanylate_kin;TM=N;SS	tight junction protein 3 (zona occl	3.6
	439755	AW748482	Hs.77873	ig;TM=Y;SS=M	B7 homolog 3	3.6
	439873	BE159253	Hs.300638		ESTs	3.6
	439039	AI656707	Hs.48713		ESTs	3.6
	419235	AW470411	Hs.288433	pkinae,none	neurotrimin	3.6
	445033	AV652402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	3.6
10	404394	AF332975	Hs.307004	EGF,m1,vwc,vwd,MAM,Kerat	Zonadhesin	3.6
	452222	AW806287	Hs.21432	Sema,TIG,PSI,GDI	SEX gene	3.6
	422961	Y13620	Hs.122607	TM=M;SS=N	B-cell CLL/lymphoma 9	3.6
	420988	AW006352	Hs.159643		ESTs, Weakly similar to T32554 hypo	3.6
	439680	AW245741	Hs.58461	zf-C2H2,TFIIS,KRAB;TM=M;S	ESTs, Weakly similar to A35659 krue	3.6
15	426815	D59505	Hs.351344	ig,SET,PHD,zf-CXXC,Adap_c	ESTs, Weakly similar to K1CI_HUMAN	3.6
	437446	AA788946	Hs.101302	fn3,vwa,Collagen,TSPN;TM=	ESTs, Moderately similar to CA1C RA	3.6
	421690	AW162667	Hs.106857	efhand;TM=M;SS=N	calbindin 2, (29kD, calretinin)	3.5
	453939	AA418160	Hs.86043		Homo sapiens cDNA FLJ13558 fis, clo	3.5
	426158	NM_001982	Hs.199067	Furin-like,pkinae,Recep_	v-erb-b2 avian erythroblastic leuke	3.5
20	439246	AI498072	Hs.351474	ank,pkinae,UPF0073;TM=N;	membrane-associated tyrosine- and t	3.5
	410653	BE383768	Hs.65238	zf-C3HC4,AIP3;TM=M;SS=N	95 kDa retinoblastoma protein bindi	3.5
	412703	AW984744			gb:RC1-HN0015-040400-011-d03 HN0015	3.5
	427871	AW992405	Hs.352406	TM=M;SS=N	Homo sapiens, clone IMAGE:3507281,	3.5
	444273	AI903474	Hs.230	LRR,LRRNT;TM=M;SS=M	fibromodulin	3.5
25	434936	AI285970	Hs.183817	UCH-2	ESTs	3.5
	457869	AJ077186	Hs.108885	vwa,Collagen;TM=M;SS=M	Homo sapiens, alpha-1 (VI) collagen	3.5
	422575	AK000546	Hs.118552	PTR2;TM=Y;SS=M	hypothetical protein FLJ20539	3.5
	428343	AL043021	Hs.12705	WD40;TM=N;SS=M	ESTs	3.5
	426716	NM_006379	Hs.171921	ig,Sema,PSI;TM=N;SS=M	sema domain, immunoglobulin domain	3.5
30	423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	3.5
	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	3.5
	407926	AW956382	Hs.59771	TYA;TM=N;SS=M	ESTs	3.5
	447041	AL135480	Hs.250705		Homo sapiens cDNA FLJ11685 fis, clo	3.5
	419073	AW372170	Hs.183918	death,ZU5;TM=N;SS=M	Homo sapiens cDNA FLJ12797 fis, clo	3.5
35	446945	AI193115	Hs.16611	TM=M;SS=N	tumor protein D52-like 1	3.5
	416322	BE019494	Hs.79217	P5CR,NAD_Gly3P_dh,Octopin	pyrroline-5-carboxylate reductase 1	3.5
	447347	AA570056	Hs.122730	NA;NA	ESTs, Moderately similar to KIAA121	3.5
	448984	AW751955	Hs.22753	TM=M;SS=N	hypothetical protein FLJ22318	3.5
	421778	AA428000	Hs.283072	NA;NA	actin related protein 2/3 complex,	3.5
40	423363	BE544348	Hs.127562	homeobox;TM=M;SS=N	homeo box C11	3.5
	432545	X52486	Hs.3041	cyclin,none	uracil-DNA glycosylase 2	3.5
	408495	W68796	Hs.237731		ESTs	3.5
	406851	AA609784	Hs.352392	ig,MHC_II_beta;TM=M;SS=Y	major histocompatibility complex, c	3.5
	418736	T18979	Hs.87908	helicase_C,AT_hook,SNF2_N	Snf2-related CBP activator protein	3.4
45	410197	NM_005518	Hs.59889	HMG_CoA_synt;TM=N;SS=N	3-hydroxy-3-methylglutaryl-Coenzyme	3.4
	453597	BE281130	Hs.33713	KH-domain,Ribosomal_S3_C,	myo-inositol 1-phosphate synthase A	3.4
	417259	AW903838	Hs.81800	EGF,ig,lectin_c,sushi,Xli	chondroitin sulfate proteoglycan 2	3.4
	453985	N44545	Hs.251865	PH,none	ESTs	3.4
	412634	U55984	Hs.356531		heat shock 90kD protein 1, alpha	3.4
	407204	R41933	Hs.140237	histone,histone	ESTs, Weakly similar to ALU1_HUMAN	3.4
50	444371	BE540274	Hs.239	Fork_head;TM=M;SS=N	forkhead box M1	3.4
	447334	AA515032	Hs.91109		ESTs	3.4
	426530	U24578	Hs.278625	A2M,NTR,ANATO,A2M_N,preny	complement component 4A	3.4
	419749	X73608	Hs.93029	kazal,thyroglobulin_1;TM=	sparc/osteonectin, cwcv and kazal-I	3.4
55	423595	R82826	Hs.220702	homeobox,none	ESTs	3.4
	406673	M34996	Hs.198253	ig,MHC_II_alpha;TM=M;SS=M	major histocompatibility complex, c	3.4
	434241	AF119913		TM=N;SS=M	Homo sapiens PRO3077 mRNA, complete	3.4
	412490	AW803564	Hs.288850		Homo sapiens cDNA: FLJ22528 fis, cl	3.4
	452277	AL049013	Hs.28783	ank;TM=M;SS=N	KIAA1223 protein	3.4
60	431457	NM_012211	Hs.256297	FG-GAP,vwa;TM=Y;SS=M	integrin, alpha 11	3.4
	421777	BE562088	Hs.108196	TM=M;SS=N	HSPC037 protein	3.4
	453082	H18835	Hs.31608	ion_trans;TM=Y;SS=M	hypothetical protein FLJ20041	3.4
	414085	AA114016	Hs.75746	aldedh;TM=N;SS=M	aldehyde dehydrogenase 1 family, me	3.4
	440300	N39760	Hs.8859	TM=M;SS=N	Homo sapiens, Similar to RIKEN cDNA	3.4
65	400290	H18836	Hs.31608	Cys_knot	hypothetical protein FLJ20041	3.4
	433339	AF019226	Hs.8036	ras,arf;TM=M;SS=N	glioblastoma overexpressed	3.4
	419301	AA236166	Hs.132957	TM=Y;SS=M	tenomodulin protein	3.4
	414792	BE314949	Hs.87128	TM=Y;SS=M	hypothetical protein FLJ23309	3.4
	451428	AW083384	Hs.11067		ESTs, Highly similar to T46395 hypo	3.4
70	432210	AI567421	Hs.273330	EGF,kazal,laminin_EGF,lam	Homo sapiens, clone IMAGE:3544662,	3.4
	452242	R50956	Hs.159993		glycosyltransferase	3.4
	450676	AI147155	Hs.279727		ESTs	3.4
	413014	AW250533	Hs.75139	TM=M;SS=N	partner of RAC1 (arfpapin 2)	3.4
	427919	AA173942	Hs.326416	CTF_NFI,none	Homo sapiens mRNA; cDNA DKFZp564H19	3.4
75	424005	AB033041	Hs.137507	TM=Y;SS=N	vang (van gogh, Drosophila)-like 2	3.4
	422072	AB018255	Hs.111138	RhoGAP;TM=M;SS=N	KIAA0712 gene product	3.4
	440995	T57773	Hs.10263		ESTs	3.4
	426150	NM_003658	Hs.167218	homeobox;TM=N;SS=M	BariH-like homeobox 2	3.3
	416877	BE386266	Hs.85658	zf-C2H2;TM=M;SS=N	hypothetical protein FLJ23436	3.3
80	452191	AU076408	Hs.28309	UDPG_MGDP_dh,UDPG_MGDP_dh	UDP-glucose dehydrogenase	3.3
	450273	AW296454	Hs.24743	rrm,none	hypothetical protein FLJ20171	3.3
	456177	NM_012391	Hs.79414	Ets,SAM_PNT;TM=M;SS=N	prostate epithelium-specific Ets tr	3.3
	423062	NM_003655	Hs.5637	chromo;TM=N;SS=M	ESTs	3.3
	421848	X15880	Hs.108885	vwa,Collagen;TM=M;SS=M	collagen, type VI, alpha 1	3.3

5	433577	AW007080	Hs.284192		ESTs	3.3
	409636	AA305729	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	3.3
	404730	AA486704	Hs.33287	CTF_NFI:none	Nuclear factor I/B	3.3
	422940	BE077458		Sec7,PH,ANF_receptor,lig_	gb:RC1-BT0606-090500-015-b04 BT0606	3.3
	410001	AB041036	Hs.57771	trypsin;TM=M;SS=M	kalikrein 11	3.3
	427461	AA531527	Hs.332040	TM=Y;SS=M	hypothetical protein MGC13010	3.3
	453468	W00712	Hs.32990	TM=M;SS=N	DKFZP566F084 protein	3.3
	443807	W52930	Hs.9822	HAT;TM=N;SS=M	HCNP protein; XPA-binding protein 2	3.3
10	456034	AW450979			gb:UI-HI3-ala-a-12-0-UI.s1 NCI_CG	3.3
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	3.3
	412755	BE144306	Hs.179891		ESTs, Weakly similar to P4HA_HUMAN	3.3
	429690	AW956329	Hs.23721	sugar_lr,Ribosomal_S25	ESTs	3.3
	423472	AF041260	Hs.129057	TM=M;SS=N	breast carcinoma amplified sequence	3.3
15	424118	BE269041	Hs.140452	perilipin;TM=N;SS=M	cargo selection protein (mannose 6	3.3
	437275	AW976035	Hs.292396	Frizzled,Fz	ESTs, Weakly similar to A47582 B-ca	3.3
	437464	AA323296	Hs.97837		Homo sapiens mRNA; cDNA DKFZp547J04	3.3
	433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	3.3
	434931	AW968941	Hs.166254		hypothetical protein DKFZp5661133	3.3
20	451691	AI809278	Hs.208152	C2	ESTs	3.3
	430433	AA478883	Hs.273766	VW,none	ESTs	3.3
	429343	AK000785	Hs.199480	VHS,ENTH,UIM;TM=N;SS=M	Homo sapiens, Similar to epsin 3, c	3.3
	450835	BE262773	Hs.25584	ArfGap;TM=N;SS=M	hypothetical protein FLJ10767	3.3
	414591	AI888490	Hs.248107		ESTs, Weakly similar to ALU8_HUMAN	3.3
25	452579	AA131657	Hs.23830	CN_hydrolase	ESTs	3.3
	409960	BE261944	Hs.355264		hexokinase 1	3.3
	406850	AI624300	Hs.172928	vwc, Collagen, COLFI;TM=M;S	collagen, type I, alpha 1	3.3
	453874	AW591783	Hs.36131	homeobox,none	collagen, type XIV, alpha 1 (unduli	3.2
	425964	AW889928	Hs.9071		progesterone membrane binding prote	3.2
30	428412	AA428240	Hs.126083		ESTs	3.2
	430316	NM_000875	Hs.239176	fn3,Furin-like, pkinase, Re	insulin-like growth factor 1 recept	3.2
	440087	W28969	Hs.7718	KOW,Ribosomal_S4e,S4,rm;	hypothetical protein FLJ22678	3.2
	449933	AW157098	Hs.324104	DUF176,efhand;TM=M;SS=N	Human DNA sequence from clone RP1-6	3.2
	441128	AA570256	Hs.348504	TM=Y;SS=M	ESTs, Weakly similar to T23273 hypo	3.2
35	434182	W20309	Hs.8107	G-gamma;TM=M;SS=N	G-protein gamma-12 subunit	3.2
	422737	M26939	Hs.119571	Collagen, COLFI;TM=N;SS=M	collagen, type III, alpha 1 (Ehlers	3.2
	408202	AA227710	Hs.43658	OLF;TM=M;SS=N	DKFZP586L151 protein	3.2
	424971	AA479005	Hs.154036	PH;TM=M;SS=N	tumor suppressing subtransferable c	3.2
	407869	AI827976	Hs.24391	efhand;TM=M;SS=N	hypothetical protein FLJ13612	3.2
40	444734	NM_001360	Hs.11806	ERG4_ERG24;TM=Y;SS=M	7-dehydrocholesterol reductase	3.2
	426991	AK001536	Hs.214410		Homo sapiens cDNA FLJ10674 fis, clo	3.2
	414081	AW969976	Hs.365706	gla;TM=N;SS=Y	matrix Gla protein	3.2
	408795	AW749126	Hs.170345	hormone_rec,zf-C4	hypothetical protein FLJ13710	3.2
45	452345	AA293279	Hs.29173	DSPc;TM=M;SS=N	hypothetical protein FLJ20515	3.2
	437879	BE262082	Hs.5894	TM=N;SS=N	hypothetical protein FLJ10305	3.2
	407872	AB039723	Hs.40735	Fz,Frizzled,7tm_2,DUF81;T	frizzled (Drosophila) homolog 3	3.2
	427289	AI097346	Hs.323878	aminotran_5,SDF,none	phosphoserine aminotransferase	3.2
	432375	BE536069	Hs.2962	efhand,S_100;TM=N;SS=M	S100 calcium-binding protein P	3.2
	429415	NM_002593	Hs.202097	CUB,NTR;TM=N;SS=M	procollagen C-endopeptidase enhance	3.2
50	412774	AA120865	Hs.380149	hormone_rec,zf-C4	ESTs	3.2
	445942	T80334	Hs.13479	TM=M;SS=N	hypothetical protein FLJ20847	3.2
	439456	AI752409	Hs.109314	zf-C2H2;TM=N;SS=M	hypothetical protein FLJ20980	3.2
	414774	X02419	Hs.77274	kringle,trypsin,plant_thi	plasminogen activator, urokinase	3.2
	433336	AF017986	Hs.31386	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 2	3.2
55	439905	AW799755	Hs.110953	HLH;TM=M;SS=N	retinoic acid induced 1	3.2
	420251	AW374968	Hs.379829		Human DNA sequence from clone RP5-1	3.2
	413004	T35901	Hs.75117	TM=M;SS=N	interleukin enhancer binding factor	3.2
	418686	Z36830	Hs.87268	annexin;TM=M;SS=N	annexin A8	3.2
	410279	BE271977	Hs.61809	ras;TM=M;SS=N	hypothetical protein FLJ14117	3.2
60	424391	BE550112	Hs.158549		ESTs, Weakly similar to T2D3_HUMAN	3.2
	440409	AW294316	Hs.125608	thiored	ESTs	3.2
	452689	F33868	Hs.284176	transferrin,KH-domain,rm	transferrin	3.2
	418154	BE165866	Hs.352403	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	3.2
	434384	AA631910	Hs.370133		ESTs	3.2
65	413436	AF238083	Hs.68061	DAGKc;TM=M;SS=N	sphingosine kinase 1	3.2
	431663	NM_016569	Hs.267182	T-box;TM=M;SS=N	TBX3-Iso protein	3.2
	432874	W94322	Hs.279651	SH3;TM=M;SS=Y	melanoma inhibitory activity	3.2
	436252	AI539519	Hs.142827		Homo sapiens cDNA FLJ11562 fis, clo	3.2
70	421044	AF061871	Hs.101302	fn3,vwa, Collagen, TSPN;TM=	Human DNA sequence from clone RP1-2	3.2
	419102	AA234098	Hs.42424		ESTs, Weakly similar to 2004399A ch	3.2
	419359	AL043202	Hs.90073	CAS_CSE1;TM=M;SS=N	chromosome segregation 1 (yeast hom	3.2
	441859	AW194364	Hs.9877	Amino_oxidase,FAD_binding	interleukin-4 induced gene-1 protei	3.1
	426418	M90464	Hs.169825	Collagen,C4,VPR;TM=N;SS=M	collagen, type IV, alpha 5 (Alport	3.1
	413076	U10564	Hs.75188	pkinae;TM=M;SS=N	wee1 (S. pombe) homolog	3.1
75	407874	AI766311	Hs.289047	COQ7	Homo sapiens cDNA FLJ14059 fis, clo	3.1
	448019	AW947164	Hs.195641		ESTs, Moderately similar to I38022	3.1
	427024	AA397572	Hs.348902	vwc,W2,MA3,MIF4G	chromosome 11 open reading frame 14	3.1
	410281	AF076612	Hs.166186	LEA,perilipin;TM=M;SS=N	Homo sapiens clone 23928 mRNA seque	3.1
	447205	BE617015	Hs.11006		ESTs, Moderately similar to T17372	3.1
80	434433	AW629759			gb:hh70e05.y1 NCI_CGAP_GU1 Homo sap	3.1
	439737	AI751438	Hs.41271	C1q, Collagen,none	Homo sapiens mRNA full length inser	3.1
	450157	AW961576	Hs.60178	PH,Band_41,RhoGEF,none	ESTs	3.1
	445989	H97754	Hs.11108		ESTs	3.1
	442213	N36110	Hs.305971	sugar_lr;TM=Y;SS=M	solute carrier family 2 (facilitate	3.1

	402496				Target Exon	3.1
	438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	3.1
	439335	AA742697	Hs.62492	TM=N;SS=M	NM_052863:Homo sapiens secretoglobi	3.1
5	412276	BE262621	Hs.73798	MIF,sugar_tr,none	macrophage migration inhibitory fac	3.1
	416950	AL049798	Hs.80552		dermatopontin	3.1
	456157	AW979153	Hs.336881	transmembrane4,none	ESTs	3.1
	452753	AA028049	Hs.277728	CRAL_TRIO,none	SEC14 (S. cerevisiae)-like 2	3.1
10	414420	AA043424	Hs.76095	TM=M;SS=N	immediate early response 3	3.1
	446229	AI744964	Hs.14449	TM=M;SS=N	KIAA1609 protein	3.1
	453143	AA382234	Hs.356289	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	3.1
	411441	AL042355	Hs.70202	WD40;TM=M;SS=N	WD repeat domain 10	3.1
	422921	BE062045	Hs.351625	AAA,hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23260 fis, cl	3.1
	444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	3.1
15	436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	3.1
	427890	AA435761	Hs.373623	RFX_DNA_binding,none	ESTs	3.1
	444838	AV651680	Hs.208558	integrin_A,FG-GAP,none	ESTs	3.1
	427876	AI494291	Hs.369171		ESTs	3.1
	413040	AA193338	Hs.12321	Na_Ca_Ex;TM=Y;SS=M	sodium calcium exchanger	3.1
20	427515	T79526	Hs.179516	EMP24_GP25L;TM=Y;SS=M	integral type I protein	3.1
	451092	AI207256	Hs.13766	filament;TM=N;SS=N	Homo sapiens mRNA for FLJ00074 prot	3.1
	442222	AI061301	Hs.164773	trypsin,krangle,UPAR_LY6	ESTs	3.1
	452613	AA461599	Hs.23459		ESTs	3.1
	447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	3.1
25	412890	T85247	Hs.351875	COX6C;TM=M;SS=M	cytochrome c oxidase subunit VIc	3.1
	418313	BE244231	Hs.84038	TM=Y;SS=N	CGI-06 protein	3.1
	440006	AK000517	Hs.6844	AAA,NB-ARC,PAAD_DAPIN;NA;	NALP2 protein; PYRIN-Containing APA	3.1
	434042	AI589941	Hs.8254		Homo sapiens, Similar to tumor diff	3.1
	420576	AA297634	Hs.54925		KIAA1858 protein	3.1
30	432269	NM_002447	Hs.2942	pkinese,Sema,PSI,TIG,A4_E	macrophage stimulating 1 receptor (3.1
	424927	AW973666	Hs.153850		hypothetical protein C321D2.4	3.1
	440100	BE382685	Hs.158549		ESTs, Weakly similar to T2D3_HUMAN	3.1
	452408	AA306477	Hs.29379	TM=M;SS=N	hypothetical protein FLJ10687	3.1
	441362	BE614410	Hs.23044	TM=N;SS=N	RAD51 (S. cerevisiae) homolog (E co	3.1
35	418444	AI902899	Hs.85155	zf-CCCH;TM=M;SS=N	butyrate response factor 1 (EGF-res	3.1
	423464	NM_016240	Hs.128856	Collagen;TM=Y;SS=N	CSR1 protein	3.1
	424604	AW865388	Hs.151076	TM=M;SS=N	KIAA1243 protein	3.1
	420059	AF161486	Hs.94769	ras,none	RAB23, member RAS oncogene family	3.1
	453271	AA903424	Hs.6786	LIM;TM=M;SS=N	ESTs	3.1
40	411274	NM_002776	Hs.69423	trypsin;TM=M;SS=N	kallikrein 10	3.1
	434095	AA011117	Hs.3745	EGF,F5_F8_type_C;TM=N;SS=	milk fat globule-EGF factor 8 prote	3.1
	403439			ank;TM=M;SS=N	NM_031419*:Homo sapiens molecule po	3.1
	413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Repro	kruppel-related zinc finger protein	3.1
45	411756	BE294350	Hs.71891	pkinese,F5_F8_type_C;TM=Y	discoidin domain receptor family, m	3.1
	409007	AL122107	Hs.49599		Homo sapiens mRNA; cDNA DKFZp434G08	3.1
	452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	3.1
	414359	M62194	Hs.75929	cadherin,Cadherin_C_term;	cadherin 11, type 2, OB-cadherin (o	3.1
	433212	BE218049	Hs.121820		ESTs	3.1
	449123	D50920	Hs.23106	TM=M;SS=N	KIAA0130 gene product	3.1
50	431176	AI026984	Hs.293662	MCPsignal,laminin_B,lamin	ESTs	3.0
	419245	AI732742	Hs.87440		ESTs	3.0
	434493	AA635305	Hs.375591		ESTs	3.0
	449177	BE616694	Hs.288042		hypothetical protein FLJ14299	3.0
	430449	AA352723	Hs.241471	WH1;TM=M;SS=N	RNB6	3.0
55	452887	AI702223	Hs.107253	K-box;TM=N;SS=M	hypothetical protein DKFZp761F241	3.0
	451678	AA374181	Hs.26799		DKFZP564D0764 protein	3.0
	445457	AF168793	Hs.12743	Carn_acyltransf;TM=M;SS=N	camitine O-octanoyltransferase	3.0
	407597	AA043925	Hs.339352	fn3,lg;TM=Y;SS=M	Homo sapiens brother of CDO (BOC) m	3.0
	431629	AU077025	Hs.265827	TM=M;SS=Y	interferon, alpha-inducible protein	3.0
60	432302	AA345857	Hs.274307	TIG;TM=M;SS=N	KIAA1442 protein	3.0
	442549	AI751601	Hs.8375	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	3.0
	437959	AI472068	Hs.375604	elF5_elF2B,W2;TM=M;SS=N	KIAA1856 protein	3.0
	447400	AK000322	Hs.18457	zf-C3HC4;TM=Y;SS=M	hypothetical protein FLJ20315	3.0
	411734	AW374954	Hs.71779		Homo sapiens DNA from chromosome 19	3.0
65	443547	AW271273	Hs.356487	fn3,none	hypothetical protein FLJ12666	3.0
	417000	BE277919	Hs.306019	TM=Y;SS=M	ESTs, Weakly similar to ALU7_HUMAN	3.0
	416987	D86957	Hs.80712	GTP_CDC;TM=N;SS=M	KIAA0202 protein	3.0
	424494	U78575	Hs.149255	PIP5K;TM=N;SS=M	phosphatidylinositol-4-phosphate 5-	3.0
	414496	W73853	Hs.355424	pkinese,F5_F8_type_C,adh_	ESTs	3.0
70	413336	AI569936	Hs.296178	Occludin;TM=M;SS=N	hypothetical protein FLJ22637	3.0
	434314	BE392921	Hs.3797	ras,arf;TM=M;SS=N	RAB26, member RAS oncogene family	3.0
	401038			TM=M;SS=N	C11000425:gij4507721[ref]NP_003310.	3.0
	418245	AA088767	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.0
	407688	W25317	Hs.37616		Human D9 splice variant B mRNA, com	3.0
75	456906	AF117646	Hs.156637	zf-C3HC4,Cbl_N,Cbl_N2,Cbl	Cas-Br-M (murine) ectropic retrovir	3.0
	424744	AW175781	Hs.152720	TM=M;SS=N	M-phase phosphoprotein 6	3.0
	452195	AA994712	Hs.116878		ESTs	3.0
	415988	BE407713	Hs.78943	Pept_C1-like;TM=N;SS=M	bleomycin hydrolase	3.0
	418399	AF131781	Hs.84753	TM=N;SS=N	hypothetical protein FLJ12442	3.0
80	420568	F09247	Hs.247735	cadherin,lipocalin;TM=M;S	protocadherin alpha 10	3.0
	404661			TM=M;SS=N	C9000306:gij12737280[ref]XP_006682	3.0
	414152	NM_003248	Hs.75774	EGF,TSPN,isp_3;TM=M;SS=M	thrombospondin 4	3.0
	421307	BE539976	Hs.103305	chromo	Homo sapiens mRNA; cDNA DKFZp434B04	3.0
	444868	BE560471	Hs.12101	TM=N;SS=M	hypothetical protein	3.0

450214	BE439763	Hs.227571	RGS;TM=M;SS=N	regulator of G-protein signalling 4	3.0
452664	AA398859	Hs.18397	TM=M;SS=M	hypothetical protein FLJ23221	3.0
422105	AI929700	Hs.111680	TM=M;SS=N	endosulfine alpha	3.0
422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	3.0
434067	H18913	Hs.124023		Homo sapiens cDNA FLJ14218 fis, clo	3.0
412676	NM_000165	Hs.74471	connexin,Connexin43;TM=Y;	gap junction protein, alpha 1, 43kD	3.0
426801	AA486846	Hs.271795		ESTs, Weakly similar to I38022 hypo	3.0
421983	AI252640	Hs.110364	pro_isomerase,none	peptidylprolyl isomerase C (cycloph	3.0
429299	AI620463	Hs.347408	TM=Y;SS=N	hypothetical protein MGC13102	3.0
408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	3.0
438746	AI885815	Hs.184727	transferrin,Guanylate_kin	Human melanoma-associated antigen p	3.0

TABLE 4B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
418344	245371_1	AA216387 T63548 AA228676
412703	1243670_1	AW984759 AW984744
434241	63414_1	AF119913 AI207698 R57074
422940	58443_1	BC012771 BG397153 BF366196 AA337277 AA319285 AW843252
456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
434433	111338_1	AA633408 AW749955 AW629759 AI651005

TABLE 4C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406387	9256180	Plus	116229-116371,117512-117651
400496	9743564	Plus	41515-41695
402496	9797769	Minus	8615-9103
403439	9719679	Plus	91463-91632
401038	7232177	Minus	4277-4469
404661	9797073	Plus	33374-33675,33769-34008

TABLE 5A: ABOUT 231 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES THAT MAY ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
R1: Ratio of 90th percentile tumor to 50th percentile of normal body tissue

Pkey	ExAccn	UniGeneID	Pred.Prot.Domains	UniGeneTitle	R1
409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	20.5
421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	16.3
419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXD domain-containing ion transpor	13.7
417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midkine (neurite growth-promoting f	13.7
414521	D28124	Hs.76307	DAN;TM=M;SS=M	neuroblastoma, suppression of tumor (DAN)	13.7
438091	AW373062	Hs.351546	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	13.4
413815	AL046341	Hs.75562	pkinase,F5_F8_type_C;TM=Y	discoidin domain receptor family, m	13.2
439180	AI393742	Hs.199067	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	13.2
431441	U81961	Hs.2794	ASC;TM=Y;SS=N	sodium channel, nonvoltage-gated 1	12.5
452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	12.4
452239	AW379378	Hs.356289		protein tyrosine phosphatase, recep	12.1
441384	AA447849	Hs.288660	7tm_3,none	retinoic acid induced 3	11.9
419223	X60111	Hs.1244	transmembrane4;TM=Y;SS=M	CD9 antigen (p24)	11.7
413859	AW992356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	11.5
410687	U24389	Hs.65436	Lysyl_oxidase;TM=N;SS=M	lysyl oxidase-like 1	11.2
422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	10.1
419452	U33635	Hs.90572	ig,pkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	9.9
427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	9.9
444784	D12485	Hs.11951	Somatostatin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	9.9
436972	AA284679	Hs.25640	PMP22_Claudin;TM=Y;SS=M	claudin 3	9.7
412926	AI879076	Hs.75061	MARCKS;TM=N;SS=M	macrophage myristoylated alanine-ri	9.5
425280	U31519	Hs.1872	PEPCK;TM=M;SS=N	phosphoenolpyruvate carboxykinase 1	9.5
432636	AA340864	Hs.278562	PMP22_Claudin;TM=Y;SS=M	claudin 7	9.4
423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	9.4
424206	NM_003734	Hs.198241	Cu_amine_oxid,Cu_amine_ox	amine oxidase, copper containing 3	9.4
444797	AB018333	Hs.12002	SH3,SAM;TM=M;SS=N	KIAA0790 protein	9.0

	402559	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphat.type 2B	9.0
	443932	AW888222	Hs.9973	SH2,WW,PID,none	tensin	8.9
	421143	AB024536	Hs.102171	ig,LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily containi	8.8
5	433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	8.7
	410668	BE379794	Hs.159651	death,TNFR_c6;TM=Y;SS=M	hypothetical protein	8.7
	433662	W07162	Hs.150826	ras,ABC_tran,arf;TM=M;SS=	RAB25 RAB25, member RAS oncogene fa	8.6
	421853	AL117472	Hs.108924	SH3,Sorb;TM=M;SS=N	SH3-domain protein 5 (ponsin)	8.6
10	425335	BE394327	Hs.296267	efhand,kazal,arf,ras,7tm_	folistatin-like 1	8.5
	400290	H18836	Hs.31608	Cys_knot	hypothetical protein FLJ20041	8.5
	438089	W05391	Hs.351546	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	8.4
	426158	NM_001982	Hs.199067	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	8.3
	447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	8.2
	439941	AI392640	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	8.2
15	439318	AW837046	Hs.6527	7tm_2,CytC_asm,GPS;TM=Y;S	G protein-coupled receptor 56	8.1
	442213	N36110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	8.1
	412649	NM_002206	Hs.74369	integrin_A,FG-GAP;TM=M;SS	integrin, alpha 7	8.1
	448913	AA194422	Hs.22564	rrm,zf-RanBP,pkinase,GST_	myosin VI	8.1
	420166	AW732276	Hs.95583	transmembrane4;TM=Y;SS=M	transmembrane 4 superfamily member	8.0
20	407102	AA007629	Hs.348601	transport_prot,SWIB,ASC	glycerol-3-phosphate dehydrogenase	7.9
	452516	AA058630	Hs.29759	TM=N;SS=M	RNA POLYMERASE I AND TRANSCRIPT REL	7.9
	413076	U10564	Hs.75188	pkinase;TM=M;SS=N	wee1 (S. pombe) homolog	7.9
	443604	C03577	Hs.9615	efhand;TM=M;SS=N	myosin regulatory light chain 2, sm	7.7
	429002	AW248439	Hs.2340	Armadillo_seg;TM=M;SS=N	junction plakoglobin	7.6
25	432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	7.6
	426359	AA376409	Hs.10862	adenylatekinase,none	Homo sapiens cDNA: FLJ23313 fis, cl	7.5
	417733	AL048678	Hs.82503	NA;NA	H.sapiens mRNA for 3'UTR of unknown	7.5
	451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	7.4
	443951	F13272	Hs.356835	PMP22_Claudin,none	ferritin, light polypeptide	7.4
	409960	BE261944	Hs.355264		hexokinase 1	7.3
30	423184	NM_004428	Hs.1624	Ephrin;TM=M;SS=M	ephrin-A1	7.3
	405121	X04385	Hs.110802	Cys_knot,TGF-beta,vwa,vcv	von Willebrand factor (VWF), mRNA	7.1
	438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	7.1
35	417771	AA804698	Hs.82547		retinoic acid receptor responder (t	7.0
	424118	BE269041	Hs.140452	perilipin;TM=N;SS=M	cargo selection protein (mannose 6	7.0
	402705	X67951	Hs.180909	AhpC-TSA;TM=M;SS=M	peroxiredoxin 1 (PRDX1)	7.0
	417115	AW952792	Hs.334612	Sm,pkinase;TM=N;SS=N	small nuclear ribonucleoprotein pol	7.0
	442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	6.9
40	447216	R75812	Hs.169248	cytochrome_c;NA;NA	p75NTR-associated cell death execut	6.9
	422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	6.9
	414657	AA424074	Hs.76780	TM=M;SS=N	protein phosphatase 1, regulatory (6.9
	447528	AI612027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	6.9
	436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	6.9
	428013	AF151020	Hs.181444	TM=Y;SS=M	hypothetical protein	6.9
45	444143	AW747996	Hs.160999	Bcl-2,none	ESTs, Moderately similar to A56194	6.8
	414443	AU077268	Hs.76144	ig,pkinase;TM=Y;SS=N	platelet-derived growth factor rece	6.7
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regulato	6.7
	448479	H96115	Hs.21293	UDPGP;TM=M;SS=N	UDP-N-acteylglucosamine pyrophospho	6.6
	410552	X66945	Hs.748	ig,pkinase,SH2,SH3,C2,PH,	fibroblast growth factor receptor 1	6.6
50	414883	AA926960	Hs.348669	CKS;TM=N;SS=N	CDC28 protein kinase 1	6.6
	417426	NM_002291	Hs.82124	laminin_EGF,laminin_Nterm	laminin, beta 1	6.6
	428179	AI127772	Hs.279696	pkinase,PX,pkinase_C;TM=N	serum/glucocorticoid regulated kina	6.6
	443195	BE148235	Hs.193063	Aa_trans,none	Homo sapiens cDNA FLJ14201 fis, clo	6.5
	424512	X53002	Hs.149846	integrin_B,EGF;TM=Y;SS=M	integrin, beta 5	6.5
55	421733	AL119671	Hs.1420	ig,pkinase;TM=Y;SS=M	fibroblast growth factor receptor 3	6.5
	428950	BE311879	Hs.194673	DED;TM=M;SS=N	phosphoprotein enriched in astrocyt	6.5
	450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	6.5
	416078	AL034349	Hs.79005		protein tyrosine phosphatase, recep	6.5
60	408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	6.4
	428373	AI751656	Hs.183986	ig;TM=Y;SS=M	poliovirus receptor-related 2 (herp	6.4
	449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	6.4
	406621	X57809	Hs.181125	ig,HSP70,Ppx-GppA;TM=M;SS	immunoglobulin lambda locus	6.4
	431629	AU077025	Hs.265827	TM=M;SS=Y	interferon, alpha-inducible protein	6.4
	428169	AI928984	Hs.182793	photoRC,UPF0118;TM=Y;SS=N	golgi phosphoprotein 2	6.4
65	443337	Y07604	Hs.9235	NDK;TM=N;SS=N	non-metastatic cells 4, protein exp	6.4
	451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	6.4
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	6.4
	426539	AB011155	Hs.170299	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	6.3
	417208	S67773	Hs.81665	ig,pkinase;TM=Y;SS=M	v-kit Hardy-Zuckerman 4 feline sarc	6.3
70	438278	BE409248	Hs.57988	TFIIS,RNA_POL_M_15KD,UPF0	hypothetical protein FLJ22357 simil	6.3
	429455	AI472111	Hs.278694	lectin_c	CD209 antigen	6.3
	431685	AW296135	Hs.267659	CH,DAG_PE-bind,PH,RhoGEF,	vav 3 oncogene	6.3
	445033	AV652402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	6.3
	411756	BE294350	Hs.71891	pkinase,F5_F8_type_C;TM=Y	disoidin domain receptor family, m	6.3
75	453902	BE502341	Hs.3402		ESTs	6.3
	418005	AI186220	Hs.83164	Collagen,TSPN;TM=M;SS=M	collagen, type XV, alpha 1	6.2
	449924	W30681	Hs.146233	SH3,none	Homo sapiens cDNA: FLJ22130 fis, cl	6.2
	426520	BE545684	Hs.343566	aa_permeases,pyridoxal_de	KIAA0251 protein	6.2
80	453064	R40334	Hs.89463		potassium large conductance calcium	6.2
	448520	AB002367	Hs.21355	pkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	6.2
	452683	AI089575	Hs.374574	homeobox,none	progesterone membrane binding prote	6.2
	402575	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphat. type 2B	6.2
	444672	Z95636	Hs.116659	laminin_EGF,laminin_G,EGF	laminin, alpha 5	6.2
	450440	AB024334	Hs.25001	14-3-3;TM=M;SS=N	tyrosine 3-monooxygenase/tryptophan	6.2

5	432314	AA533447	Hs.285173	Xlink,none	ESTs	6.1
	438564	AA381553	Hs.198253	Ig,MHC,II_alpha,none	major histocompatibility complex, c	6.1
	444252	R21135	Hs.54985		ESTs	6.1
	425184	BE278288	Hs.155048	ig;TM=Y;SS=M	Lutheran blood group (Auberger b an	6.1
	431890	X17033	Hs.271986	vwa,integrin_A,FG-GAP;TM=	integrin, alpha 2 (CD49B, alpha 2 s	6.1
	449475	AI348027	Hs.129826	transmembrane4;TM=Y;SS=M	hypothetical protein PP1057	6.1
	449538	AI559444	Hs.104679	TM=M;SS=M	ESTs	6.0
	414496	W73853	Hs.355424	pkinase,F5_F8_type_C,adh_	ESTs	6.0
10	414217	AI309298	Hs.279898	NA;NA	Homo sapiens cDNA: FLJ23165 fis, cl	6.0
	445333	BE537641	Hs.44278	ras,arf,TK;TM=N;SS=M	hypothetical protein FLJ12538 simil	5.9
	431183	NM_006855	Hs.250696	ER_lumen_recept;TM=M;SS=M	KDEL (Lys-Asp-Glu-Leu) endoplasmic	5.9
	409645	AI142265	Hs.55498	polyprenyl_synt;TM=M;SS=N	geranylgeranyl diphosphate synthase	5.9
	412276	BE262621	Hs.73798	MIF,sugar_tr,none	macrophage migration inhibitory fac	5.9
15	416137	BE279513	Hs.278607	pkinase,UBA,ThiF;TM=M;SS=	ubiquitin activating enzyme E1-like	5.9
	412969	AI373162	Hs.75103	14-3-3;TM=N;SS=M	tyrosine 3-monooxygenase/tryptophan	5.9
	414504	AW069181	Hs.115175	pkinase,SAM;TM=M;SS=N	sterile-alpha motif and leucine zip	5.9
	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamini	cadherin, EGF LAG seven-pass G-type	5.9
	436415	BE265254	Hs.343258	Peptidase_M24,Furin-like,	proliferation-associated 2G4, 38kD	5.9
20	413900	AW409747	Hs.75612	TPR,PDZ,WW,Guanylate_kin;	stress-induced-phosphoprotein 1 (Hs	5.9
	441455	AJ271671	Hs.7854	Zip;TM=Y;SS=M	zinc/iron regulated transporter-lik	5.9
	444006	BE395085	Hs.334762	Idl_recept_a,PKD,MHC_I;TM	type I transmembrane protein Fn14	5.8
	408269	AW888219	Hs.44077	CH;TM=M;SS=N	parvin, alpha	5.8
	411372	AI147861	Hs.213289	Glyco_transf_11,EGF,Idl_r	low density lipoprotein receptor (f	5.8
25	450825	AC005954	Hs.25527	PDZ,Guanylate_kin;TM=N;SS=	tight junction protein 3 (zona ocl	5.8
	456534	X91195	Hs.100623	LIM,PDZ,pkinase;TM=N;SS=M	phospholipase C, beta 3, neighbor p	5.7
	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.7
	446812	AL042279	Hs.16206	pkinase	uncharacterized hypothalamus protei	5.7
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	5.7
30	405484	XM_093451		TM=N;SS=M	C3002124*.gii12737280[ref]XP_006682	5.7
	425367	BE271188	Hs.155975	TM=M;SS=Y	protein tyrosine phosphatase, recep	5.7
	444607	AW405635	Hs.293687	PI-PLC-X,PH,PI-PLC-Y	ESTs	5.7
	421456	AW579842	Hs.104557	zf-C2H2,DUF18,efhand,C2,P	hypothetical protein FLJ10697	5.6
	412810	M21574	Hs.74615	ig,pkinase,DUF11;TM=M;SS=	platelet-derived growth factor rece	5.6
35	450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	5.6
	453880	AI803166	Hs.135121	HSP70,none	ESTs, Weakly similar to I38022 hypo	5.6
	439578	AW263124	Hs.350547	WD40;TM=M;SS=N	nuclear receptor co-repressor/HDAC3	5.6
	450954	AI904740	Hs.25691	TM=Y;SS=M	receptor (calcitonin) activity modi	5.6
	414555	N98569	Hs.76422	phoslip;TM=M;SS=Y	phospholipase A2, group IIA (platel	5.6
40	409963	AA133590	Hs.377830	MBOAT,none	calcium/calmodulin-dependent protei	5.6
	450463	AW952018	Hs.201398	C1q,Collagen;TM=M;SS=Y	G protein coupled receptor interact	5.6
	425177	AF127577	Hs.155017	TM=N;SS=M	nuclear receptor interacting protei	5.5
	445496	AB007860	Hs.12802	SH3,ank,PH,ArfGap;TM=M;SS	development and differentiation enh	5.5
	428981	BE313077	Hs.93135	rm	ESTs, Weakly similar to ALU2_HUMAN	5.5
45	424441	X14850	Hs.147097	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member X	5.5
	415662	AW972481	Hs.170610	pkinase,none	ESTs, Highly similar to G01887 MEK	5.5
	422105	AI929700	Hs.111680	TM=M;SS=N	endosulfine alpha	5.5
	429556	AW139399	Hs.314807	TM=M;SS=N	ESTs	5.5
50	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	5.5
	425205	NM_005854	Hs.155106	TM=Y;SS=N	receptor (calcitonin) activity modi	5.5
	444633	AF111713	Hs.12284	ig;TM=Y;SS=M	junctional adhesion molecule 1	5.5
	431565	AF161470	Hs.260622	TM=Y;SS=N	butyrate-induced transcript 1	5.5
	429655	U48959	Hs.211582	pkinase,fn3,ig,none	myosin, light polypeptide kinase	5.5
55	431886	L77964	Hs.271980	pkinase;TM=M;SS=N	mitogen-activated protein kinase 6	5.5
	453143	AA382234	Hs.356289	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	5.4
	451863	AL120634	Hs.331803	cpn60_TCP1,E1-E2_ATPase,C	ATPase, Ca transporting, plasma mem	5.4
	422293	X94453	Hs.114366	aldedh,aakinese;TM=M;SS=N	pyrroline-5-carboxylate synthetase	5.4
	432179	X75208	Hs.2913	EPH_lbd,fn3,pkinase,SAM;T	EphB3	5.4
	408048	NM_007203	Hs.42322	Paralemmn;TM=N;SS=N	A kinase (PRKA) anchor protein 2	5.4
60	448153	Y10805	Hs.20521	NusG;TM=N;SS=M	HMT1 (hnRNP methyltransferase, S. c	5.4
	421251	Z28913	Hs.102948	LIM,PDZ;TM=N;SS=M	enigma (LIM domain protein)	5.4
	439039	AI656707	Hs.48713	pkinase,none	ESTs	5.4
	409882	AJ243191	Hs.56874	HSP20;TM=N;SS=M	heat shock 27kD protein family, mem	5.4
65	451295	AI557212	Hs.17132	pkinase,DAG_PE-bind,pkina	ESTs, Moderately similar to I54374	5.4
	442549	AI751601	Hs.8375	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	5.4
	445930	AF055009	Hs.13456	DAGKc,DAGKa,ank,WD40,bZIP	Homo sapiens clone 24747 mRNA seque	5.4
	453082	H18835	Hs.31608	ion_trans;TM=Y;SS=M	hypothetical protein FLJ20041	5.4
	426432	AF001601	Hs.169857	Arylesterase;TM=M;SS=N	paraooxase 2	5.4
	415753	U52819	Hs.78781	PDGF;TM=M;SS=M	vascular endothelial growth factor	5.4
70	450778	U81375	Hs.25450	Nucleoside_tran;TM=Y;SS=M	solute carrier family 29 (nucleosid	5.4
	414739	U83867	Hs.77196	efhand,SH3,spectrin;TM=N;	spectrin, alpha, non-erythrocytic 1	5.3
	421233	AA209534	Hs.284243	transmembrane4;TM=Y;SS=M	tetraspan NET-6 protein	5.3
	414774	X02419	Hs.77274	kringle,trypsin,plant_thi	plasminogen activator, urokinase	5.3
	414368	W70171	Hs.75939	PRK,CoaE;TM=N;SS=N	uridine monophosphate kinase	5.3
75	446051	BE048061	Hs.37054	Ephrin_A_deamin,dsm,z-al	ephrin-A3	5.3
	423619	T48691	Hs.249159	7tm_1,7tm_2;TM=Y;SS=M	adrenergic, alpha-2A-, receptor	5.3
	440188	AK001812	Hs.7036	ROK;TM=M;SS=N	N-Acetylglucosamine kinase	5.3
	414135	NM_004419	Hs.2128	Rhodanese,DSPc,Y_phosphat	dual specificity phosphatase 5	5.3
80	444838	AV651680	Hs.208558	integrin_A,FG-GAP,none	ESTs	5.3
	447918	AI129320	Hs.115175	pkinase,SAM,none	ESTs, Highly similar to JC5818 gamm	5.3
	405517	AF000974	Hs.119498	LIM;TM=M;SS=N	thyroid hormone receptor interactor 6	5.3
	413588	AA971014	Hs.75432	IMPDH_C,CBS,IMPDH_N;TM=M;	IMP (inosine monophosphate) dehydro	5.2
	411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	5.2
	416157	NM_003243	Hs.342874	zona_pellucida;TM=Y;SS=M	transforming growth factor, beta re	5.2

5	407744	AB020629	Hs.38095	ABC_tran,PRK;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.2
	446108	AL036596	Hs.42322	Paralemmin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.2
	422034	AC006486	Hs.333069	Ets;TM=M;SS=N	Ets2 repressor factor	5.2
	417098	AB017385	Hs.173859	Frizzled,Fz,7tm_2,toxin_2	frizzled (Drosophila) homolog 7	5.2
	430526	AF181862	Hs.242407	7tm_3;TM=Y;SS=M	G protein-coupled receptor, family	5.2
	414176	BE140638	Hs.75794	7tm_1,CRCB;TM=Y;SS=N	EDG-2 (endothelial differentiation	5.2
	416710	AI268325	Hs.54890	Peptidase_M49,EGF,ig,Neur	hypothetical protein FLJ23590	5.2
	417896	AA379770	Hs.82890	DAD;TM=Y;SS=M	defender against cell death 1	5.2
10	413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Repro	kruppel-related zinc finger protein	5.2
	421837	AF135168	Hs.108802	AAA,cdc48_N,cdc48_2,NB-AR	N-ethylmaleimide-sensitive factor	5.2
	429379	NM_014840	Hs.200598	kinase,RIO1;TM=M;SS=N	KIAA0537 gene product	5.2
	429619	AL120751	Hs.211568		eukaryotic translation initiation f	5.2
	437275	AW976035	Hs.292396	Frizzled,Fz	ESTs, Weakly similar to A47582 B-ce	5.1
	421071	AI311238	Hs.104476	TM=Y;SS=M	ESTs, Weakly similar to CGHU1E coll	5.1
15	448581	NM_002709	Hs.21537		protein phosphatase 1, catalytic su	5.1
	452568	AA805634	Hs.300870	PI3_PI4_kinase;TM=M;SS=M	Homo sapiens mRNA; cDNA DKFZp547M07	5.1
	452069	AB028949	Hs.183994	Metallophos;TM=M;SS=N	KIAA1026 protein	5.1
	437175	AW968078	Hs.87773	kinase,kinase_C,none	protein kinase, cAMP-dependent, cat	5.1
20	437056	AI147061		spectrin,SH3,PH,CH	gb:ok33a11.s1 Soares_NSF_F8_9W_OT_P	5.1
	450998	BE387614	Hs.25797	rrm;TM=M;SS=N	splicing factor 3b, subunit 4, 49kD	5.1
	444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	5.1
	448528	BE613248	Hs.172084	PHD;TM=M;SS=N	Homo sapiens, clone IMAGE:3627860,	5.1
	452345	AA293279	Hs.29173	DSPC;TM=M;SS=N	hypothetical protein FLJ20515	5.1
25	443412	W84893	Hs.9305		angiotensin receptor-like 1	5.1
	412853	M34175	Hs.74626	Adaptin_N,Alpha_adaptinC2	adaptor-related protein complex 2,	5.1
	439866	AA280717	Hs.6727	rrm,NTF2;TM=M;SS=N	Ras-GTPase activating protein SH3 d	5.1
	439975	AW328081	Hs.6817	Ham1p_like;TM=M;SS=N	inosine triphosphatase (nucleoside	5.1
	435523	T62849	Hs.11090	TM=Y;SS=M	membrane-spanning 4-domains, subfam	5.1
30	433423	BE407127	Hs.8997	HSP70,ig,Ppx-GppA;TM=M;SS	heat shock 70kD protein 1A	5.1
	412641	M16660	Hs.74335	HSP90,HATPase_c;TM=M;SS=N	heat shock 90kD protein 1, beta	5.1
	431236	AV656840	Hs.285115	fn3;TM=Y;SS=M	interleukin 13 receptor, alpha 1	5.1
	438552	AJ245820	Hs.6314		type I transmembrane receptor (seiz	5.0
	422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	5.0
35	427502	AI811865	Hs.71133	TM=M;SS=N	Homo sapiens, clone IMAGE:3161564,	5.0
	414166	AW888941	Hs.75789	DEAD,helicase_C,rrm,Ndr,C	N-myc downstream regulated	5.0
	424954	NM_000546	Hs.1846	P53,WD40,IRK;TM=M;SS=N	tumor protein p53 (Li-Fraumeni synd	5.0
	422089	AA523172	Hs.103135	REJ,PLAT,PKD,WSC,LRR	ESTs, Weakly similar to SFR4_HUMAN	5.0
	426636	BE242634	Hs.2055	ThiF,UBACT;TM=M;SS=N	ubiquitin-activating enzyme E1 (A1S	5.0
40	410793	AW581906	Hs.66392	SH3,efhand,C2,PH,RhoGEF,M	intersectin 1 (SH3 domain protein)	5.0

TABLE 5B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
437056	428504_3	AW976398 AI147061 AA765223 AA743380 AI803927

TABLE 5C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405484	5922025	Plus	199214-199579,199672-199920,200262-20049

TABLE 6A: 777 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL ADULT TISSUES

Table 6A lists 777 genes up-regulated in colon cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" colon cancer level was set to the 90th percentile amongst 95 colon cancers. The "average" normal adult tissue level was set to the 90th percentile amongst 209 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the 209 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	447033	AI357412	Hs.157601	ESTs	31.35
	409041	AB033025	Hs.50081	KIAA1199 protein	29.00
5	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	26.41
	422330	D30783	Hs.115263	epiregulin	24.38
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	23.55
10	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	22.70
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	21.60
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	21.15
	415989	AI267700	Hs.317584	ESTs	20.95
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.35
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	18.68
15	421470	R27496	Hs.1378	annexin A3	18.05
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.30
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.15
	450531	AW301032	Hs.203800	ESTs	16.60
20	432867	AW016936	Hs.233364	ESTs	16.35
	443211	AI128388	Hs.143655	ESTs	15.80
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	15.10
	406964	M21305		gb:Human alpha satellite and satellite 3	15.00
	410355	S58544	Hs.153057	sperm associated antigen 1	14.70
25	441377	BE218239	Hs.202656	ESTs	14.45
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	14.35
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	14.35
	440304	BE159984	Hs.125395	ESTs	14.25
	426427	M86699	Hs.169840	TTK protein kinase	13.60
30	451561	N52812	Hs.177403	ESTs	12.80
	434032	AW009951	Hs.206892	ESTs	12.75
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	12.65
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfami	12.55
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.40
35	446232	AI281848	Hs.194691	retinoic acid induced 3	12.25
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	12.18
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.85
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	11.80
	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	11.65
40	452461	N78223	Hs.108106	transcription factor	11.42
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	11.35
	400534				11.00
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	10.75
	453688	AW381270	Hs.194110	hypothetical protein PRO2730	10.75
45	426890	AA393167	Hs.41294	ESTs	10.60
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	10.50
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	10.40
50	425761	AW664214	Hs.196729	ESTs	10.25
	404567				10.15
	428536	AI143139	Hs.2288	visinin-like 1	10.10
	414972	BE263782	Hs.77695	KIAA0008 gene product	10.05
	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.95
55	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	9.90
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.85
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	9.85
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	9.78
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	9.73
60	420900	AL045633	Hs.44269	ESTs	9.68
	438639	AI278360	Hs.31409	ESTs	9.55
	439521	AI808955	Hs.58248	ESTs	9.55
	445676	AI247763	Hs.16928	ESTs	9.50
	408489	AI082437	Hs.26690	ESTs	9.50
65	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	9.37
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.00
	423349	AF010258	Hs.127428	homeo box A9	8.96
	400195	NA		NA	8.90
	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	8.90
70	418895	AA894638	Hs.14600	ESTs	8.85
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.80
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.75
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	8.65
	414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	8.64
75	445436	AI224105	Hs.151408	ESTs	8.50
	403776				8.50
	433447	U29195	Hs.3281	neuronal pentraxin II	8.50
	407168	R45175	Hs.117183	ESTs	8.31
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	8.30
80	422505	AL120862	Hs.124165	ESTs	8.25
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.20
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	8.15
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	409687	T51125	Hs.8493	ESTs	8.05

	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.93
	406360	NA		NA	7.80
5	443450	N66045	Hs.133529	ESTs	7.75
	414422	AA147224	Hs.337232	ESTs	7.75
	442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	7.70
	438604	AA811896	Hs.44604	ESTs	7.60
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	7.55
	400250	NA		NA	7.53
10	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.50
	404996				7.50
	450459	AI697193	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	7.45
	445019	AI205540	Hs.281295	ESTs	7.30
15	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.25
	448816	AB033052	Hs.22151	KIAA1226 protein	7.25
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	7.25
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	7.20
	433859	AW896758	Hs.273789	ESTs	7.20
20	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	7.20
	456120	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.20
	419751	AW195581	Hs.93121	KIAA0761 protein	7.16
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	7.15
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	7.15
25	421373	AA808229	Hs.167771	ESTs	7.10
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.00
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.96
	444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E (OABP	6.95
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.95
	413573	AI733859	Hs.149089	ESTs	6.95
30	442660	AW138174	Hs.130651	ESTs	6.93
	427878	C05766	Hs.181022	CGI-07 protein	6.90
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.85
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp58611518 (f	6.82
35	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.80
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	6.75
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	6.75
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	6.71
	401644				6.70
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	6.70
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	6.69
	406747	AI925153	Hs.217493	annexin A2	6.65
45	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.60
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	6.60
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	6.55
	427072	H38046	Hs.303193	ESTs	6.55
	452588	AA889120	Hs.110637	homeo box A10	6.53
50	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.50
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	6.50
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	6.50
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	6.50
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.50
55	410908	AA121686	Hs.10592	ESTs	6.47
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	6.47
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.45
	452838	U65011	Hs.30743	preferentially expressed antigen in meta	6.42
	451389	N73222	Hs.279009	matrix Gla protein	6.40
60	438202	AW169287	Hs.22588	ESTs	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	6.37
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.36
	436539	AI005457	Hs.275048	ESTs	6.35
65	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	6.34
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	6.32
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	6.31
	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.30
	413597	AW302885	Hs.117183	ESTs	6.30
70	429529	AA454190	Hs.24283	ESTs, Moderately similar to reduced expr	6.30
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.25
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.20
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.20
	438050	BE262816	Hs.6061	protein kinase, AMP-activated, beta 1 no	6.20
75	416857	AA188775	Hs.292453	ESTs	6.20
	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	6.18
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.15
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.15
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.15
80	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	6.11
	424745	AA214618	Hs.152759	activator of S phase kinase	6.10
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.10
	454438	AA224053	Hs.172405	cell division cycle 27	6.08
	407771	AL138272	Hs.62713	ESTs	6.08

	416057	AI927382	Hs.29857	ESTs	6.05
	442917	AA314907	Hs.85950	ESTs	6.00
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	6.00
5	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	5.96
	412246	AI160873	Hs.69233	zinc finger protein	5.96
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.95
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.95
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	5.95
10	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.90
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	5.87
	408908	BE296227	Hs.250822	serine/threonine kinase 15	5.86
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	5.86
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	5.85
15	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.85
	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.85
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	5.85
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.85
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.82
20	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	459309	AA040620	Hs.5672	hypothetical protein AF140225	5.80
	410060	NM_001448	Hs.58367	glypican 4	5.79
	423806	AA331247	Hs.86617	ESTs	5.77
25	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	5.75
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	5.75
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.75
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	5.75
	442957	AI949952	Hs.49397	ESTs	5.75
30	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	5.70
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	409757	NM_001898	Hs.123114	cystatin SN	5.69
35	433687	AA743991		gb:ny57g01.s1 NCI_CGAP_Pr18 Homo sapiens	5.68
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.60
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.60
	438777	AA825487	Hs.142179	ESTs	5.60
	417235	AA810278	Hs.24250	ESTs	5.60
40	451177	AI969716	Hs.13034	ESTs	5.60
	415227	AW821113	Hs.72402	ESTs	5.58
	436217	T53925	Hs.107	fibrinogen-like 1	5.56
	452881	AW135220	Hs.241921	ESTs	5.55
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.55
45	426235	AI631964	Hs.34447	ESTs	5.55
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	5.53
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	5.52
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
50	453884	AA355925	Hs.36232	KIAA0186 gene product	5.47
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.47
	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	5.47
	420218	AW958037	Hs.286	ribosomal protein L4	5.45
	421155	H87879	Hs.102267	lysyl oxidase	5.45
55	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	5.45
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.45
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	5.44
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	5.42
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.41
60	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	5.41
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	5.35
	430217	N47863	Hs.336901	ribosomal protein S24	5.33
	417372	T99755	Hs.334728	ESTs	5.30
	415139	AW975942	Hs.48524	ESTs	5.30
65	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	5.29
	424086	AI351010	Hs.102267	lysyl oxidase	5.27
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.27
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	5.26
	452131	AI860677	Hs.72325	Human DNA sequence from clone RP1-187J11	5.25
70	436016	AA806465	Hs.121536	Human DNA sequence from clone RP11-472E5	5.25
	449347	AV649748	Hs.295901	KIAA0493 protein	5.25
	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.25
	453921	AI824009	Hs.44577	ESTs	5.25
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.25
75	421076	AW007988	Hs.233299	ESTs, Weakly similar to I38022 hypotheti	5.25
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	5.24
	433384	AI021992	Hs.124244	ESTs	5.23
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	5.21
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.20
80	441795	N58115	Hs.21137	AD024 protein	5.20
	449416	AI651016	Hs.246311	ESTs	5.20
	418379	AA218940	Hs.137516	fidgetin-like 1	5.20
	426753	T89832	Hs.170278	ESTs	5.18
	422109	S73265	Hs.1473	gastrin-releasing peptide	5.17

	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	5.17
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	5.17
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	5.15
5	427728	AJ245600	Hs.180545	Homo sapiens mRNA for hypothetical prote	5.15
	447713	AI420733	Hs.207083	ESTs	5.15
	425739	T19016	Hs.159410	molybdopterin synthase sulfurylase	5.15
	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	5.15
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	5.13
10	441139	AW449009	Hs.126647	ESTs	5.13
	451121	AW973795	Hs.128927	Homo sapiens cDNA FLJ13903 fis, clone TH	5.10
	435202	AI971313	Hs.170204	KIAA0551 protein	5.10
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	5.10
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	5.09
	422805	AA436989	Hs.121017	H2A histone family, member A	5.07
15	411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	5.06
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	5.06
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	5.05
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.05
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.05
20	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.05
	441675	AI914329	Hs.5461	ESTs	5.00
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.00
	401480	NA	NA	NA	5.00
25	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	4.95
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	4.92
	414718	H95348	Hs.107987	ESTs	4.91
	419139	AI123517	Hs.269940	ESTs	4.90
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	4.90
30	425420	BE536911	Hs.234545	hypothetical protein NUF2R	4.90
	408758	NM_003686	Hs.47504	exonuclease 1	4.90
	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDN	4.90
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	4.90
	433927	AI557019	Hs.116467	small nuclear protein PRAC	4.89
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	4.88
35	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	4.87
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	4.87
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	4.86
	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	4.85
40	418396	AI765805	Hs.26691	ESTs	4.85
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.84
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	4.80
	406414				4.75
	430178	AW449612	Hs.152475	ESTs	4.71
45	411901	AA166730	Hs.6966	Human DNA sequence from clone RP1-187J11	4.70
	404025	NA	NA	NA	4.70
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	4.68
	436662	AI582393	Hs.126695	ESTs	4.68
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	4.68
50	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	4.65
	431041	AA490967	Hs.197955	KIAA0704 protein	4.65
	417860	AW408557	Hs.235498	hypothetical protein FLJ14075	4.65
	410658	AW105231	Hs.192035	ESTs	4.65
	425895	AI269484	Hs.161427	zinc finger protein 215	4.65
55	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	4.65
	436397	AA715013	Hs.169835	ESTs	4.60
	439225	AA192669	Hs.45032	ESTs	4.60
	423197	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	4.60
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.60
60	412723	AA648459	Hs.335951	hypothetical protein AF301222	4.59
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	4.59
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.58
	430704	AW813091	Hs.335799	ESTs	4.56
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	4.55
65	433326	AI379486	Hs.159430	ESTs	4.55
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	4.55
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	4.55
	423343	AA324643	Hs.246106	ESTs	4.55
	416467	H57585	Hs.37467	ESTs	4.55
70	408867	AA437199	Hs.656	cell division cycle 25C	4.54
	419423	D26488	Hs.90315	KIAA0007 protein	4.54
	414132	AI801235	Hs.48480	ESTs	4.53
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	4.53
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	4.50
75	451009	AA013140	Hs.115707	ESTs	4.50
	431064	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	4.50
	432725	AL137496	Hs.9001	ESTs	4.50
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	4.50
80	410486	AW235094	Hs.69233	zinc finger protein	4.50
	428532	AF157326	Hs.184786	TBP-interacting protein	4.50
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.50
	408390	AF123050	Hs.44532	diubiquitin	4.49
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	4.47
	434294	AJ271379	Hs.76194	ribosomal protein S5	4.47

	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.46
	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypotheti	4.45
	410142	AA081924	Hs.124918	KIAA1795 protein	4.45
5	434894	AW977850	Hs.23856	hypothetical protein MGC5297	4.45
	420092	AA814043	Hs.88045	ESTs	4.45
	400115	NA		NA	4.45
	430967	H16791	Hs.31445	ESTs	4.41
	438078	AI016377	Hs.131693	ESTs	4.41
10	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	4.40
	429774	AI522215	Hs.50883	KIAA1804 protein	4.40
	426214	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	4.40
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.40
	450480	X82125	Hs.25040	zinc finger protein 239	4.40
15	421211	AA284966	Hs.266308	mosaic serine protease	4.40
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	4.40
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	4.37
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT	4.35
	410568	AW162948	Hs.64542	cleavage and polyadenylation specific fa	4.35
20	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	4.35
	448243	AW369771	Hs.52620	integrin, beta 8	4.35
	438069	N80701	Hs.33790	ESTs	4.35
	446152	AI292036	Hs.150028	ESTs	4.34
	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	4.32
25	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.30
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.30
	422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	4.30
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.30
	439619	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	4.30
30	458076	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	4.30
	450192	AA263143	Hs.24596	RAD51-interacting protein	4.29
	443232	AF161521	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	4.28
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibito	4.26
	434217	AW014795	Hs.23349	ESTs	4.26
35	409723	AW885757	Hs.257862	ESTs	4.25
	417956	AA210704	Hs.190465	ESTs	4.25
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	4.25
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.24
40	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	4.22
	424583	AF017445	Hs.150926	fucose-1-phosphate guanylyltransferase	4.20
	429436	AA452934	Hs.279813	hypothetical protein	4.20
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila inaD-like	4.20
	448912	D83781	Hs.22559	KIAA0197 protein	4.20
	442671	AI005668	Hs.134779	EST	4.20
45	411893	R82845	Hs.273789	ESTs	4.20
	456281	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.20
	421106	AA877124	Hs.172844	ESTs	4.20
	451401	AI793163		gb:on52g03.y5 NCI_CGAP_Co8 Homo sapiens	4.20
	404516	NA		NA	4.20
50	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	4.20
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.20
	419229	AI827237	Hs.282884	ESTs	4.18
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	4.16
	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	4.16
55	433159	AB035898	Hs.150587	kinesin-like protein 2	4.15
	419247	S65791	Hs.89764	fragile X mental retardation 1	4.15
	432491	AA662910	Hs.42635	hypothetical protein DKFz434K2435	4.15
	422093	AF151852	Hs.111449	CGI-94 protein	4.15
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	4.15
60	446999	AA151520	Hs.334822	hypothetical protein MGC4485	4.15
	414538	AW612228	Hs.107987	ESTs	4.14
	453931	AL121278	Hs.25144	ESTs	4.12
	427718	AI798680	Hs.25933	ESTs	4.11
	453863	X02544	Hs.572	orosomucoid 1	4.10
65	440209	H05049	Hs.22269	neurexin 3	4.10
	435148	AI918049	Hs.124961	ESTs	4.10
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.10
	448692	AW013907	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	4.10
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	4.10
70	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.10
	457059	BE561665	Hs.177677	exosome component Rrp40	4.10
	407162	N63855	Hs.142634	zinc finger protein	4.10
	406117				4.10
	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	4.09
75	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	4.08
	448666	NM_014953	Hs.323346	KIAA1008 protein	4.07
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	4.07
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	4.07
	456030	AA136106	Hs.184852	KIAA1553 protein	4.05
80	434082	AI373481	Hs.131715	hypothetical protein PRO1777	4.05
	443646	AI085198	Hs.164226	ESTs	4.05
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.05
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	4.05
	432619	AW291722	Hs.278526	related to the N terminus of tre	4.05

	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.05
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	4.04
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	4.04
5	424176	AL137273	Hs.142307	hypothetical protein	4.04
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.04
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.03
	435420	AI928513	Hs.59203	ESTs	4.03
	406666	V00495	Hs.184411	albumin	4.02
10	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	4.00
	449448	D60730	Hs.57471	ESTs	4.00
	421037	AI684808	Hs.197653	ESTs	4.00
	448310	AI480316		gb:tm26h09.x1 Soares_NFL_T_GBC_S1 Homo s	4.00
	408155	AB014528	Hs.43133	KIAA0628 gene product	4.00
	413841	M34276	Hs.75576	plasminogen	3.98
15	400110	NA		NA	3.98
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.97
	443715	AI583187	Hs.9700	cyclin E1	3.97
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.97
20	450164	AI239923	Hs.30098	ESTs	3.97
	451592	AI805416	Hs.213897	ESTs	3.95
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome delta	3.95
	426199	AA371865	Hs.97090	ESTs	3.95
	414148	BE084049		gb:PM0-BT0651-270400-003-f02 BT0651 Homo	3.95
25	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	3.94
	449532	W74653	Hs.271593	ESTs, Moderately similar to A47582 B-cel	3.93
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.93
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.92
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.91
30	416185	AW975861	Hs.47367	KIAA1785 protein	3.91
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.90
	432596	AJ224741	Hs.278461	matrilin 3	3.90
	451229	AW967707	Hs.48473	ESTs	3.90
	413583	AL120806	Hs.5888	ESTs	3.90
35	432702	AW973953	Hs.293744	ESTs	3.90
	437207	T27503	Hs.15929	hypothetical protein FLJ12910	3.90
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.90
	423697	BE088697	Hs.131834	Homo sapiens mRNA; cDNA DKFZp434B0328 (f	3.90
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	3.90
40	432289	AI860145	Hs.55118	ESTs	3.89
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.88
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.88
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.88
	410094	BE147897	Hs.58593	general transcription factor IIF, polype	3.88
45	441826	AW503603	Hs.129915	phosphotriesterase related	3.87
	444059	R69743	Hs.116774	integrin, alpha 1	3.86
	426262	AI792141	Hs.196270	folate transporter/carrier	3.85
	452641	AW952893	Hs.237825	signal recognition particle 72kD	3.85
50	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	3.85
	448315	AW280912	Hs.20797	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.85
	411343	U77949	Hs.69563	CDC6 (cell division cycle 6, S. cerevisi	3.85
	409734	BE161664	Hs.56155	hypothetical protein	3.85
	454014	AW016670	Hs.233275	ESTs	3.84
	453116	AI276680	Hs.146086	ESTs	3.83
55	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	3.82
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.82
	435040	AI932350	Hs.152825	ESTs	3.81
	426249	F05422	Hs.168352	nucleoporin-like protein 1	3.81
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	3.81
60	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.81
	437631	AA764749	Hs.267245	hypothetical protein FLJ14803	3.80
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	3.80
	405769				3.80
	438295	AI394151	Hs.37932	ESTs	3.80
65	453628	AW243307	Hs.83937	hypothetical protein	3.80
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	3.80
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.76
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	3.75
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.75
70	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.75
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.74
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	3.74
	418413	R95735	Hs.117753	ESTs, Weakly similar to A48666 cell prol	3.73
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	3.73
75	406667	M12523	Hs.184411	albumin	3.72
	436411	AW674352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	3.72
	417246	AI760098	Hs.21411	ESTs	3.72
	410664	NM_006033	Hs.65370	lipase, endothelial	3.71
	432686	BE223007	Hs.152460	Homo sapiens cDNA FLJ12909 fis, clone NT	3.70
80	442881	AI023175	Hs.167022	ESTs	3.70
	432356	AA831032	Hs.111670	ESTs, Highly similar to JC2257 prolyl ol	3.70
	450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	3.70
	405460	NA		NA	3.70
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.70

	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-1	3.70
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	3.69
	439857	AA847194	Hs.232002	ESTs	3.69
5	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.69
	444471	AB020684	Hs.11217	KIAA0877 protein	3.69
	419559	Y07828	Hs.91096	ring finger protein	3.69
	437641	AA811452	Hs.291911	ESTs	3.68
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.67
10	417791	AW965339	Hs.111471	ESTs	3.66
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.66
	432023	AW273128	Hs.330144	EST	3.66
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.65
	450600	BE079478	Hs.24880	ESTs	3.65
15	420595	AA278865	Hs.88523	ESTs	3.65
	404477	NA	NA	NA	3.65
	457003	S78234	Hs.172405	cell division cycle 27	3.65
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	3.65
	452220	BE158006	Hs.212296	ESTs	3.65
20	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	3.65
	457465	AW301344	Hs.122908	DNA replication factor	3.64
	436149	AI754308	Hs.159452	ESTs	3.63
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	3.63
	427920	Z11502	Hs.181107	annexin A13	3.63
25	424841	AB001106	Hs.151413	glia maturation factor, beta	3.63
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.62
	411975	AI916058	Hs.144583	ESTs	3.61
	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	3.61
	429528	H09604	Hs.13268	ESTs	3.61
30	449722	BE280074	Hs.23960	cyclin B1	3.60
	428389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheti	3.60
	419945	AW290975	Hs.118923	ESTs	3.60
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	3.60
	420585	AW505139	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	3.60
35	407809	AW082279	Hs.244106	ESTs	3.60
	457708	AA805443	Hs.179909	hypothetical protein FLJ22995	3.60
	427943	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.60
	428771	AB028992	Hs.193143	KIAA1069 protein	3.60
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	3.59
40	418688	T85017	Hs.1192	KIAA0074 protein	3.59
	436961	AW375974	Hs.156704	ESTs	3.58
	430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1	3.58
	415245	N59650	Hs.27252	ESTs	3.57
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.55
45	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	3.55
	401165	NA	NA	NA	3.55
	415382	AI743539	Hs.72465	ESTs, Weakly similar to non-lens beta ga	3.55
	433968	AL157518	Hs.90421	PRO2463 protein	3.55
	421528	AB037837	Hs.105461	hypothetical protein FLJ20357	3.55
50	443325	BE398006	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.55
	444355	BE383686	Hs.191621	ESTs, Moderately similar to ALU6_HUMAN A	3.55
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.55
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.55
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	3.55
55	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.54
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.54
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.53
	432542	AW083920	Hs.16098	claudin 2	3.53
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.52
60	423441	R68649	Hs.278359	absent in melanoma 1 like	3.51
	452940	AA029722	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.51
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	3.50
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.48
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.48
65	449915	NM_004529	Hs.404	myeloid/lymphoid or mixed-lineage leukem	3.47
	427975	AI536065	Hs.122460	ESTs	3.46
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	3.45
	404253				3.45
	435567	AW504944	Hs.162990	Homo sapiens cDNA FLJ14193 fis, clone NT	3.45
70	432158	W33165	Hs.22983	UDP-glucose:glycoprotein glucosyltransfe	3.45
	417315	AI080042	Hs.336901	ribosomal protein S24	3.45
	419140	AI982647	Hs.215725	ESTs	3.44
	446901	AI347274		gb:tc05d02.x1 NCL_CGAP_Co16 Homo sapiens	3.43
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.42
75	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.42
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	3.41
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.41
	419131	AA406293	Hs.41167	ESTs	3.41
	430264	AA470519		gb:nc71f10.s1 NCL_CGAP_Pr1 Homo sapiens	3.40
80	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	3.40
	453531	AA417940	Hs.271400	ESTs, Weakly similar to JC5795 CDEP prot	3.40
	444826	AI674482	Hs.148441	ESTs	3.40
	445354	AV653485	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA,	3.40
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.40

	418939	AW630803	Hs.89497	lamin B1	3.40
	418134	AA397769	Hs.86617	ESTs	3.40
	430544	AA481066	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	3.39
5	427927	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.39
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.39
	410406	AI969703	Hs.1466	glycerol kinase	3.38
	408494	AA554714	Hs.187578	Homo sapiens cDNA FLJ11639 fis, clone HE	3.38
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypotheti	3.38
10	446432	AI377320	Hs.150058	ESTs	3.36
	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	3.35
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.35
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	3.35
	421039	NM_003478	Hs.101299	cullin 5	3.35
15	407819	R42185	Hs.274803	ESTs	3.35
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	3.35
	433361	AW469373	Hs.300141	ribosomal protein L39	3.35
	435022	AW183385	Hs.54627	ESTs, Weakly similar to FTDH_HUMAN 10-FO	3.35
	447164	AF026941	Hs.17518	Homo sapiens clg5 mRNA, partial sequence	3.35
20	454018	AW016892	Hs.100855	ESTs	3.35
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	3.35
	453941	U39817	Hs.36820	Bloom syndrome	3.34
	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.33
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.33
25	438008	AA775026	Hs.203802	ESTs	3.33
	421246	AW582962	Hs.102897	CGI-47 protein	3.33
	451707	AW051061	Hs.60973	ESTs	3.33
	457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0	3.31
	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.31
30	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.31
	438746	AI885815	Hs.184727	ESTs	3.30
	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	3.30
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	3.30
	458855	AW361299	Hs.107000	hypothetical protein FLJ11294	3.30
35	417221	AW379029	Hs.118338	ESTs, Weakly similar to unnamed protein	3.30
	424770	AA425562	Hs.11065	Homo sapiens HDCME13P mRNA, partial cds	3.30
	417720	AA205625	Hs.208067	ESTs	3.29
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	3.29
	452862	AW378065	Hs.8687	ESTs	3.28
40	414343	AL036166	Hs.323378	coated vesicle membrane protein	3.28
	437222	AL117588	Hs.12778	ESTs	3.28
	422665	AJ011812	Hs.119018	transcription factor NRF	3.28
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.28
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	3.27
45	447829	AI433029	Hs.164104	ESTs	3.27
	427576	BE242611	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.27
	456132	BE219771	Hs.237146	hypothetical protein FLJ12752	3.26
	407305	AA715284		gb:nv35f03.r1 NCL_CGAP_Br5 Homo sapiens	3.26
50	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.26
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	3.25
	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypotheti	3.25
	453320	AW450240	Hs.257274	ESTs	3.25
	451797	AW663958	Hs.333513	small inducible cytokine subfamily E, me	3.25
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	3.25
55	410659	AI080175	Hs.68826	ESTs	3.25
	446202	AI279706	Hs.149474	ESTs	3.25
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	3.25
	439262	AA832333	Hs.333045	ESTs	3.25
	401823	NA		NA	3.25
60	441264	AA927170	Hs.23290	ESTs	3.25
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.24
	408321	AW405882	Hs.44205	cortistatin	3.24
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	3.24
	404519				3.24
65	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.23
	422660	AW297582	Hs.103267	hypothetical protein FLJ22548 similar to	3.23
	427961	AW293165	Hs.143134	ESTs	3.22
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	3.22
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.21
70	458652	AW375610	Hs.117102	hypothetical protein FLJ13046 similar to	3.21
	426472	BE246138	Hs.30853	ESTs	3.21
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.21
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.21
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.20
75	443162	T49951	Hs.9029	DKFZP434G032 protein	3.20
	431678	AW072372	Hs.267446	hypothetical protein FLJ11184	3.20
	430439	AL133561	Hs.241426	DKFZP434B061 protein	3.20
	407201	N31998	Hs.164256	hypothetical protein FLJ20657	3.20
	437905	AW363121	Hs.175596	ESTs, Weakly similar to T26935 hypotheti	3.20
80	434160	BE551196	Hs.114275	ESTs	3.20
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	3.20
	412966	BE243311	Hs.8024	IK cytokine, down-regulator of HLA II	3.19
	414386	X00442	Hs.75990	haptoglobin	3.19
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	3.18

	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.18
	433764	AW753676	Hs.39982	ESTs	3.17
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypotheti	3.17
5	429616	AI982722	Hs.120845	ESTs	3.17
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.16
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.16
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.16
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.15
10	443830	AI142095	Hs.143273	ESTs	3.15
	413516	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo	3.15
	433527	AW235613	Hs.133020	ESTs	3.15
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.15
	457453	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.15
15	427687	AW003867	Hs.1570	histamine receptor H1	3.15
	455068	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.15
	441720	AI346487	Hs.28739	ESTs	3.15
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	3.15
	445921	AW015211	Hs.146181	ESTs	3.15
20	429957	AW204530	Hs.99500	ESTs	3.15
	403137				3.14
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	3.14
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	3.14
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.14
25	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.14
	439277	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	3.13
	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	3.13
	406668	T62745	Hs.184411	albumin	3.13
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	3.13
30	437594	AA761431	Hs.74335	heat shock 90kD protein 1, beta	3.13
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.13
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	3.13
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	3.11
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	3.11
35	441790	AW294909	Hs.132208	ESTs	3.11
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	3.10
	449664	R06212	Hs.127733	ESTs	3.10
	435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.10
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.10
40	402963				3.10
	428967	AW978441	Hs.296100	ESTs	3.10
	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo	3.10
	407502	U52096		gb:Human zinc finger protein (kr-znf1) m	3.10
45	426853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	3.10
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.10
	421056	AI076890	Hs.146847	TRAF family member-associated NFKB activ	3.10
	420617	AK001652	Hs.99423	ATP-dependent RNA helicase	3.10
	421841	AA908197	Hs.108850	MAK-related kinase	3.10
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	3.10
50	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	3.10
	433037	NM_014158	Hs.279938	HSPC067 protein	3.09
	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	3.09
	457726	AI217477	Hs.194591	ESTs	3.09
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	3.08
55	433013	AI697890	Hs.127337	axin 2 (conductin, axil)	3.08
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.08
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL_HUMAN SORTI	3.07
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.07
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	3.07
60	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	3.07
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.07
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	3.06
	436554	AI985810	Hs.301173	ESTs	3.06
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	3.06
65	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	3.06
	445413	AA151342	Hs.12677	CGI-147 protein	3.06
	452909	NM_015368	Hs.30985	pannexin 1	3.06
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	3.05
	425942	AU077195	Hs.164036	glucosamine (N-acetyl)-6-sulfatase (Sanf	3.05
70	406333				3.05
	428454	U55936	Hs.184376	synaplosomal-associated protein, 23kD	3.05
	411864	AW948147		gb:RC0-MT0013-280300-031-e03 MT0013 Homo	3.05
	458632	AI744445	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.05
	448292	BE281316	Hs.47334	hypothetical protein FLJ14495	3.05
75	459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypotheti	3.05
	402167				3.05
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	3.05
	437828	AW976806	Hs.73149	paired box gene 8	3.05
	404232				3.05
80	418164	AI761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	3.05
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.05
	452787	AW294022	Hs.222707	KIAA1718 protein	3.05
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.05
	410718	AI920783	Hs.191435	ESTs	3.04

419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.04
446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.03
425492	AL021918	Hs.158174	zinc finger protein 184 (Krueppel-like)	3.02
452834	AI638627	Hs.105685	KIAA1688 protein	3.02
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.02
416568	H64844	Hs.138558	ESTs	3.02
425834	NM_001639	Hs.1957	amyloid P component, serum	3.02
426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	3.01
412719	AW016610	Hs.129911	ESTs	3.01
439586	AA922936	Hs.110039	ESTs	3.01
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	3.01
429703	T93154	Hs.28705	ESTs	3.00
400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.00
415261	T40928	Hs.8346	ESTs	3.00
419435	AI200540	Hs.14877	ESTs, Weakly similar to (define not ava	3.00
429985	NM_015836	Hs.227274	tryptophanyl tRNA synthetase 2 (mitochon	3.00
423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.00
407182	AA312551	Hs.230157	ESTs	3.00
424202	BE350295	Hs.15032	RAN binding protein 17	3.00
444585	AW170015	Hs.6594	ESTs	3.00
420552	AK000492	Hs.98806	hypothetical protein	3.00
451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	3.00
441928	AI370188	Hs.211454	ESTs	3.00
430888	BE155293	Hs.76064	ribosomal protein L27a	3.00
417806	AI867277	Hs.183733	ESTs	3.00
447175	AI365208	Hs.293606	ESTs	3.00
417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	3.00
435447	AI872932		gb:wm72e03.x1 NCL_CGAP_U12 Homo sapiens	3.00
405394				3.00
454975	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.00
441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	3.00
428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.00

TABLE 6B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
411765	125700_1	H43346 AA248302 AA095182
411864	1262055_1	AW948147 BE092318 AW948138 AW948130 AW948148 AW948129 AW948136 AW948152 AW948144 AW948137 AW948160
412359	129085_1	AW837985 AW837938 AA101955 AW837913 AW837935
413516	1374595_1	BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856
414148	142133_1	BE084049 AW292907 AA135984
424492	240008_1	AI133482 AI207619 AA341626
430264	315008_1	AA470519 BE303010 BE302954 BE384120
431064	327472_1	AI903735 AA491283 AI694953 AW976903 AA761362
433687	373061_1	AA743991 AA604852 AW272737
434414	38585_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
		AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
		AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730
		AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957
		N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
		BE081531 H59570
435447	406400_1	AI872932 AA682306 BE220163 W88695 T81307 H91447
436411	419334_1	AW674352 AA715374 Z25205
443613	575391_1	AI079356 W23287
446901	697809_1	AI347274 AW844024
448310	757918_1	AI480316 AW847535
451401	868474_1	AI793163 AW875182 AW875178 AW875176
454403	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093
454975	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
		AW848214
455838	1374605_1	BE145808 BE145807 BE181883

TABLE 6C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	400534	6981826	Minus	278637-279292
	401165	9438376	Minus	168244-168423
	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401644	8576138	Plus	82655-83959
	401823	2262095	Minus	42575-42697,43189-43287,45830-45974
10	402167	8571795	Plus	109122-110357
	402963	5419653	Minus	12950-15959
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403776	7770611	Minus	1414-1513,1624-1756
	404025	7341444	Plus	131740-131905
15	404232	8218045	Minus	71800-71956
	404253	9367202	Minus	55675-56055
	404477	8080699	Plus	113390-113577
	404516	8151967	Plus	114153-114322
	404519	8152000	Plus	12817-13000
20	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405394	6624123	Minus	31900-32373
	405460	7684569	Minus	52223-52389
	405769	3046270	Minus	76844-77193
25	406117	9142932	Plus	54304-54584
	406333	9213235	Plus	64689-64798
	406360	9256107	Minus	7513-7673
	406414	9256407	Plus	49593-49850

30 TABLE 7A: 516 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

Table 7A lists 516 genes up-regulated in colon cancer compared to normal colon. These were selected as for Table 6A except for using all CEP and colon sample in the normal body tissue list as the normal samples in determining the denominator value and the ratio was equal to or greater than 5.0.

35	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title
	R1:	Ratio of tumor to normal colon

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
45	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	57.52
	406667	M12523	Hs.184411	albumin	49.94
	409041	AB033025	Hs.50081	KIAA1199 protein	49.18
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	42.22
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	34.64
50	429201	X03178	Hs.198246	group-specific component (vitamin D bind	33.38
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	33.10
	447033	AI357412	Hs.157601	ESTs	31.24
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	26.84
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	25.40
55	413841	M34276	Hs.75576	plasminogen	24.68
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	23.18
	452862	AW378065	Hs.8687	ESTs	21.34
	415989	AI267700	Hs.317584	ESTs	20.92
60	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.22
	421470	R27496	Hs.1378	annexin A3	17.92
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	17.36
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.28
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.08
65	421462	AF016495	Hs.104624	aquaporin 9	17.02
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	16.98
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	16.70
	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	16.64
	433447	U29195	Hs.3281	neuronal pentraxin II	16.59
70	414386	X00442	Hs.75990	haptoglobin	16.19
	425260	L47726	Hs.1870	phenylalanine hydroxylase	16.08
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	15.82
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	15.80
	443211	AI128388	Hs.143655	ESTs	15.78
75	439608	AW864696	Hs.301732	hypothetical protein MGC5306	15.52
	414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	15.42
	412719	AW016610	Hs.129911	ESTs	15.24
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	15.18
	448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	15.03

	416402	NM_000715	Hs.1012	complement component 4-binding protein,	14.60
	453863	X02544	Hs.572	orosomucoid 1	14.35
	441243	AI767056	Hs.193002	ESTs	14.30
5	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	14.30
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	13.91
	433213	AW665130	Hs.137190	ESTs	13.80
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	13.52
	438578	AA811244	Hs.164168	ESTs	13.40
10	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	13.36
	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	13.00
	449199	AI990122	Hs.196988	ESTs	12.98
	436393	AW022213	Hs.143617	ESTs	12.90
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	12.83
15	451561	N52812	Hs.177403	ESTs	12.72
	420734	AW972872	Hs.293736	ESTs	12.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfami	12.50
	441377	BE218239	Hs.202656	ESTs	12.45
	435981	H74319	Hs.188620	ESTs	12.38
20	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	12.38
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.38
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypotheti	12.34
	430290	AI734110	Hs.136355	ESTs	12.30
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.26
25	450628	AW382884	Hs.204715	ESTs	12.24
	446232	AI281848	Hs.194691	retinoic acid induced 3	12.16
	428223	AA424313	Hs.98402	ESTs	12.08
	432582	AI623817	Hs.168457	ESTs	12.08
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	12.02
30	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	12.01
	407202	N58172	Hs.109370	ESTs	11.84
	422109	S73265	Hs.1473	gastrin-releasing peptide	11.68
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	11.68
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	11.67
35	443162	T49951	Hs.9029	DKFZP434G032 protein	11.67
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.62
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	11.46
	453909	AW004045	Hs.203365	ESTs	11.42
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	11.34
40	452903	AI953425	Hs.246911	ESTs, Weakly similar to I38022 hypotheti	11.32
	433011	H07960	Hs.306044	CGI-05 protein	11.30
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	11.22
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	11.20
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	11.08
45	407168	R45175	Hs.117183	ESTs	10.91
	407633	NM_007069	Hs.37189	similar to rat HREV107	10.90
	400534				10.88
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	10.76
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	10.68
50	440526	AI832243	Hs.211471	ESTs	10.63
	427544	AI767152	Hs.181400	ESTs, Weakly similar to I78885 serine/th	10.62
	447974	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	10.52
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	10.52
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
55	457065	AI476318	Hs.192480	ESTs	10.40
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.38
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	10.34
	414718	H95348	Hs.107987	ESTs	10.29
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	10.28
60	404567				10.14
	428536	AI143139	Hs.2288	visinin-like 1	10.06
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.05
	437267	AW511443	Hs.258110	ESTs	10.00
	420583	H77859	Hs.65450	reticulon 4	10.00
65	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	9.99
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	9.97
	449655	AI021987	Hs.59970	ESTs	9.91
	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.90
	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	9.90
70	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	9.88
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.84
	448106	AI800470	Hs.171941	ESTs	9.64
	439192	AW970536	Hs.105413	ESTs	9.64
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	9.61
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	9.50
75	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	9.44
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	9.40
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	9.36
	401742	NA		NA	9.30
80	416393	N54037	Hs.262869	plasminogen-like	9.28
	413339	AI818080	Hs.194290	ESTs	9.28
	437641	AA811452	Hs.291911	ESTs	9.28
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	9.22
	431319	AA873350	Hs.302232	ESTs	9.21

	434008	AA740878	Hs.112982	ESTs	9.20
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.16
	419968	X04430	Hs.93913	interleukin 6 (Interferon, beta 2)	9.16
5	413597	AW302885	Hs.117183	ESTs	9.15
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	9.14
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	9.14
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	9.05
	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	8.98
10	450164	AI239923	Hs.30098	ESTs	8.95
	432867	AW016936	Hs.233364	ESTs	8.93
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	8.92
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	8.92
	452712	AW838616		gb:RC5-LT0054-140200-013-D01 LT0054 Homo	8.90
15	419131	AA406293	Hs.41167	ESTs	8.86
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	8.82
	418895	AA894638	Hs.14600	ESTs	8.82
	422665	AJ011812	Hs.119018	transcription factor NRF	8.82
	409757	NM_001898	Hs.123114	cystatin SN	8.78
20	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	8.74
	412446	AI768015	Hs.92127	ESTs	8.71
	433285	AW975944	Hs.237396	ESTs	8.68
	414538	AW612228	Hs.107987	ESTs	8.64
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	8.62
25	430835	AI240006	Hs.192326	ESTs	8.60
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	8.59
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	8.52
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	8.52
	428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	8.50
30	444478	W07318	Hs.240	M-phase phosphoprotein 1	8.47
	439398	AA284267	Hs.221504	ESTs	8.44
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	8.43
	403776				8.42
	418973	AA233056	Hs.191518	ESTs	8.42
35	445436	AI224105	Hs.151408	ESTs	8.38
	417958	AA767382	Hs.193417	ESTs	8.34
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	8.34
	425761	AW664214	Hs.196729	ESTs	8.33
	449419	R34910	Hs.119172	ESTs	8.29
40	407007	U22961		gb:Human mRNA clone with similarity to L	8.28
	420900	AL045633	Hs.44269	ESTs	8.25
	452503	AB000509	Hs.29736	TNF receptor-associated factor 5	8.23
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.18
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.16
45	432363	AA534489		gb:nf76g11.s1 NCL_CGAP_Co3 Homo sapiens	8.16
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	8.12
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	418379	AA218940	Hs.137516	fidgeline-like 1	8.07
	424560	AA158727	Hs.150555	protein predicted by clone 23733	8.06
50	453116	AI276680	Hs.146086	ESTs	8.04
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.04
	409687	T51125	Hs.8493	ESTs	8.00
	407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	8.00
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
55	418036	Z37976	Hs.83337	latent transforming growth factor beta b	7.99
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	7.96
	421633	AF121860	Hs.106260	sorting nexin 10	7.92
	432542	AW083920	Hs.16098	claudin 2	7.86
	414869	AA157291	Hs.21479	ubiquitin 1	7.84
60	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	7.80
	406666	V00495	Hs.184411	albumin	7.78
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.78
	439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT	7.77
	406360	NA		NA	7.76
65	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	7.76
	431510	AA580082	Hs.112264	ESTs	7.76
	414312	AA155694	Hs.191060	ESTs	7.71
	443450	N66045	Hs.133529	ESTs	7.70
	449870	AI672487	Hs.15423	hypothetical protein HDCMC04P	7.64
70	425681	AB018297	Hs.159183	KIAA0754 protein	7.63
	408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	7.62
	443285	AI301918	Hs.334264	ESTs	7.60
	420807	AA280627	Hs.57846	ESTs	7.60
	424650	AW576156	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	7.60
75	410718	AI920783	Hs.191435	ESTs	7.60
	430848	AW021726		gb:zf7e02.y1 Morton Fetal Cochlea Homo	7.60
	434294	AJ271379	Hs.76194	ribosomal protein S5	7.60
	445808	AV655234	Hs.298083	ESTs, Moderately similar to PC4259 ferri	7.56
	438604	AA811896	Hs.44604	ESTs	7.54
	458997	AW937420	Hs.69662	ESTs	7.54
80	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.54
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	7.52
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	7.49
	404996				7.48

	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.48
	433859	AW896758	Hs.273789	ESTs	7.44
	423952	AW877787	Hs.136102	KIAA0853 protein	7.44
5	431193	AW749505	Hs.296770	KIAA1719 protein	7.43
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	7.40
	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	7.40
	424613	AL079850	Hs.151236	highly charged protein	7.37
	417720	AA205625	Hs.208067	ESTs	7.35
10	449347	AV649748	Hs.295901	KIAA0493 protein	7.34
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	7.34
	447499	AW262580	Hs.147674	protocadherin beta 16	7.32
	426890	AA393167	Hs.41294	ESTs	7.31
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	7.28
	445019	AI205540	Hs.281295	ESTs	7.28
15	419474	AW968619	Hs.155849	ESTs	7.24
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	7.24
	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	7.24
	448816	AB033052	Hs.22151	KIAA1226 protein	7.18
20	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	7.18
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	7.18
	420777	AA280223	Hs.130865	ESTs	7.16
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	7.14
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.14
25	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.14
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	7.13
	441124	T97717	Hs.119563	ESTs	7.12
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	7.10
	446432	AI377320	Hs.150058	ESTs	7.10
30	439295	AW206091	Hs.253536	ESTs	7.08
	436902	AW247145	Hs.192729	ESTs	7.08
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	7.08
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	7.08
	421373	AA808229	Hs.167771	ESTs	7.06
35	432435	BE218886	Hs.282070	ESTs	7.05
	427933	AW974643	Hs.190571	ESTs	7.04
	436330	NM_004413	Hs.109	dipeptidase 1 (renal)	7.04
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	7.01
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	6.98
40	446322	N23033	Hs.155814	ESTs	6.98
	442577	AA292998	Hs.163900	ESTs	6.96
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.94
	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	6.92
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	6.90
45	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	6.90
	453204	R10799	Hs.191990	ESTs	6.90
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.88
	427878	C05766	Hs.181022	CGI-07 protein	6.88
	454438	AA224053	Hs.172405	cell division cycle 27	6.86
50	424402	M63108	Hs.1769	lutinizing hormone/choriogonadotropin r	6.86
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.84
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	419629	AB020695	Hs.91662	KIAA0888 protein	6.80
55	451686	AA059246	Hs.110293	ESTs	6.80
	430829	AW451999	Hs.194024	ESTs	6.78
	446501	AI302616	Hs.150819	ESTs	6.78
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.78
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.76
60	437773	U24186	Hs.283018	replication protein A complex 34 kd subu	6.73
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	6.72
	425478	AB007953	Hs.268840	ESTs	6.70
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	6.70
	418555	AI17215	Hs.87159	hypothetical protein FLJ12577	6.67
65	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	6.62
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.62
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.60
	450480	X82125	Hs.25040	zinc finger protein 239	6.58
	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.56
70	414575	H11257	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	6.54
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	6.54
	410116	AW630671	Hs.58636	squamous cell carcinoma antigen recogniz	6.54
	449894	AK001578	Hs.24129	CLLL7 protein	6.53
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	6.53
75	424745	AA214618	Hs.152759	activator of S phase kinase	6.52
	441801	AW242799	Hs.86366	ESTs	6.52
	435542	AA687376	Hs.269533	ESTs	6.51
	427072	H38046	Hs.303193	ESTs	6.50
	418051	AW192535	Hs.19479	ESTs	6.46
80	436217	T53925	Hs.107	fibrinogen-like 1	6.46
	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.46
	430704	AW813091	Hs.335799	ESTs	6.44
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.43
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	6.41

	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	438202	AW169287	Hs.22588	ESTs	6.38
5	458311	AF069478		gb:AF069478 Homo sapiens astrocytoma lib	6.36
	451389	N73222	Hs.279009	matrix Glia protein	6.36
	427899	AA829286	Hs.332053	serum amyloid A1	6.35
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.34
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.34
10	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	6.32
	433908	AW298141	Hs.157975	ESTs	6.32
	430114	AA847744	Hs.99640	ESTs	6.32
	434032	AW009951	Hs.206892	ESTs	6.31
	444656	AI277924	Hs.145199	ESTs	6.30
	433607	AA602004	Hs.23260	ESTs	6.26
15	440659	AF134160	Hs.7327	claudin 1	6.25
	435663	AI023707	Hs.134273	ESTs	6.24
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.24
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	6.24
	447500	AI381900	Hs.159212	ESTs	6.24
20	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.22
	417715	AW969587	Hs.86366	ESTs	6.22
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	6.20
	438138	R98299	Hs.177502	ESTs	6.20
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	6.20
25	416857	AA188775	Hs.292453	ESTs	6.20
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.18
	429598	AA811257	Hs.269710	ESTs	6.18
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.18
30	438940	AF075045	Hs.271609	ESTs	6.18
	400195	NA		NA	6.15
	430473	AW130690	Hs.59962	ESTs	6.12
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.10
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.10
35	427513	AI476318	Hs.192480	ESTs	6.10
	448934	AI598134	Hs.225592	ESTs, Highly similar to T51146 ring-box	6.10
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	6.08
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	6.08
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	6.08
40	409048	H59990	Hs.37699	ESTs	6.08
	427674	NM_003528	Hs.2178	H2B histone family, member Q	6.08
	452689	F33868	Hs.284176	transferrin	6.06
	453804	AA300204	Hs.35276	KIAA0852 protein	6.06
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	6.05
45	408243	Y00787	Hs.624	interleukin 8	6.04
	420721	AA927802	Hs.159471	ZAP3 protein	6.04
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	6.04
	435420	AI928513	Hs.59203	ESTs	6.04
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	6.04
50	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.02
	442116	AI884570	Hs.128813	ESTs	6.00
	423568	NM_005256	Hs.129818	growth arrest-specific 2	6.00
	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	5.99
	441794	AW197794	Hs.253338	ESTs	5.99
55	434739	AA804487	Hs.144130	ESTs	5.98
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.96
	420218	AW958037	Hs.286	ribosomal protein L4	5.96
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	5.94
	445546	AW468821	Hs.156054	ESTs	5.94
60	439095	AA830185	Hs.269680	ESTs	5.94
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.94
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.94
	417246	AI760098	Hs.21411	ESTs	5.94
	433190	M26901	Hs.3210	renin	5.92
65	418744	AI887288	Hs.196379	ESTs, Weakly similar to putative p150 [H	5.92
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.92
	434342	AI791138	Hs.116768	ESTs	5.92
	406668	T62745	Hs.184411	albumin	5.92
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.90
70	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	5.90
	408867	AA437199	Hs.656	cell division cycle 25C	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.88
	450380	AI863675	Hs.114017	ESTs	5.88
	413026	AA809485	Hs.124219	hypothetical protein FLJ12934	5.88
75	454653	AW812227		gb:RC2-ST0173-201099-011-g09 ST0173 Homo	5.87
	457876	AI821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	5.86
	437222	AL117588	Hs.12778	ESTs	5.86
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	5.86
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	5.84
80	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	5.84
	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.84
	401352				5.84
	419088	AI538323	Hs.52620	integrin, beta 8	5.84
	431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	5.83

	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	5.82
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.82
	419220	AA811938	Hs.291759	ESTs	5.82
5	439303	W00605	Hs.102784	ESTs	5.80
	415954	AA171850	Hs.42251	ESTs	5.80
	418849	AW474547	Hs.53555	Homo sapiens PIG-M mRNA for mannosyltran	5.80
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	439527	AW298119	Hs.202536	ESTs	5.78
10	435380	AA679001	Hs.192221	ESTs	5.78
	424086	AI351010	Hs.102267	lysyl oxidase	5.76
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	5.76
	428460	AA428865	Hs.98563	ESTs	5.74
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	5.74
	413982	BE503035	Hs.279193	ESTs	5.74
15	453240	AI969564	Hs.166254	hypothetical protein DKFZp566i133	5.74
	410505	AW752139	Hs.314323	ESTs	5.72
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.72
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	5.72
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	5.71
20	433384	AI021992	Hs.124244	ESTs	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	5.68
25	448666	NM_014953	Hs.323346	KIAA1008 protein	5.68
	412246	AI160873	Hs.69233	zinc finger protein	5.68
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.66
	418269	AA806113	Hs.189025	ESTs	5.64
	443316	AI478463	Hs.18443	aldehyde dehydrogenase 8 family, member	5.64
	422805	AA436989	Hs.121017	H2A histone family, member A	5.62
30	442252	AI733395	Hs.129124	ESTs	5.60
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.60
	435040	AI932350	Hs.152825	ESTs	5.59
	438777	AA825487	Hs.142179	ESTs	5.58
	433849	BE465884	Hs.280728	ESTs	5.58
35	438639	AI278360	Hs.31409	ESTs	5.58
	411274	NM_002776	Hs.69423	kallikrein 10	5.55
	436008	AF150262	Hs.162898	ESTs	5.55
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	5.54
40	452881	AW135220	Hs.241921	ESTs	5.54
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.54
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.54
	418971	AA360392	Hs.87113	ESTs	5.52
	453716	AA037675	Hs.152675	ESTs	5.52
45	406972	M32053		gb:Human H19 RNA gene, complete cds.	5.51
	417543	AA203620	Hs.110153	ESTs	5.51
	419423	D26488	Hs.90315	KIAA0007 protein	5.51
	434674	AA831879	Hs.136985	ESTs	5.50
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
50	404227	NA		NA	5.49
	412766	BE544475	Hs.54347	ESTs	5.49
	441708	AI469911	Hs.26498	hypothetical protein FLJ21657	5.49
	408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	5.48
55	437440	AA846804	Hs.123694	ESTs	5.48
	410486	AW235094	Hs.69233	zinc finger protein	5.46
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.44
	437378	AI198823	Hs.160473	ESTs	5.44
	436907	AA737171	Hs.131809	ESTs	5.44
60	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.44
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.42
	441795	N58115	Hs.21137	AD024 protein	5.42
	452449	AW068658	Hs.20943	ESTs	5.42
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.40
65	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	5.40
	441217	AI922183	Hs.213246	ESTs	5.40
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone CO	5.40
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	5.40
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	5.40
70	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	5.39
	446142	AI754693	Hs.145968	ESTs	5.38
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	5.36
	433929	AI375499	Hs.27379	ESTs	5.36
	421155	H87879	Hs.102267	lysyl oxidase	5.34
75	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.34
	453931	AL121278	Hs.25144	ESTs	5.34
	409091	AW970386	Hs.269423	ESTs	5.33
	416057	AI927382	Hs.29857	ESTs	5.33
	438647	AA813118	Hs.163230	ESTs	5.32
80	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.32
	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.30
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.30
	403432				5.29
	435820	AA700580	Hs.189000	ESTs	5.28

	401714	NA	NA	5.28
	449508	AK001566	Hs.23618 hypothetical protein FLJ10704	5.28
	413151	H47969	Hs.141971 ESTs, Weakly similar to ALU1_HUMAN ALU S	5.28
	414853	U31116	Hs.77501 sarcoglycan, beta (43kD dystrophin-assoc	5.28
5	417372	T99755	Hs.334728 ESTs	5.28
	443613	AI079356	gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	5.28
	412610	X90908	Hs.74126 fatty acid binding protein 6, ileal (gas	5.27
	408943	NM_007070	Hs.49105 FKBP-associated protein	5.26
10	415139	AW975942	Hs.48524 ESTs	5.26
	447982	H22953	Hs.137551 ESTs	5.26
	430789	AA632577	Hs.310235 ESTs, Weakly similar to I78885 serine/th	5.24
	453921	AI824009	Hs.44577 ESTs	5.24
	409582	R27430	Hs.271565 ESTs	5.24
	420911	U77413	Hs.100293 O-linked N-acetylglucosamine (GlcNAc) tr	5.23
15	422956	BE545072	Hs.122579 hypothetical protein FLJ10461	5.23
	418661	NM_001949	Hs.1189 E2F transcription factor 3	5.22
	446271	D82484	Hs.330994 ESTs	5.22
	435905	AW997484	Hs.5003 KIAA0456 protein	5.21
20	434551	BE387162	Hs.280858 ESTs, Highly similar to A35661 DNA excis	5.21
	415245	N59650	Hs.27252 ESTs	5.20
	436016	AA806465	Hs.121536 Human DNA sequence from clone RP11-472E5	5.20
	431242	AA987742	Hs.251278 KIAA1201 protein	5.20
	439818	AL360137	Hs.19934 Homo sapiens mRNA full length insert cDN	5.20
25	424281	AA766243	gb:oa13b11.s1 NCL_CGAP_GCB1 Homo sapiens	5.20
	449138	AW294215	Hs.195631 ESTs	5.20
	449416	AI651016	Hs.246311 ESTs	5.20
	430092	AI821399	Hs.16514 ESTs	5.20
	436574	AW293527	Hs.126465 ESTs	5.18
30	433377	AI752713	Hs.43845 ESTs	5.18
	440987	AA911705	Hs.130229 ESTs	5.18
	426116	AA868729	Hs.144694 ESTs	5.18
	441928	AI370188	Hs.211454 ESTs	5.17
	432657	AA831815	Hs.270940 ESTs, Weakly similar to I78885 serine/th	5.17
35	438011	BE466173	Hs.145696 splicing factor (CC1.3)	5.16
	437257	AI283085	Hs.290931 ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.16
	423926	X03833	Hs.1722 interleukin 1, alpha	5.16
	433393	AF038564	Hs.98074 itchy (mouse homolog) E3 ubiquitin prote	5.15
	415757	AA830854	Hs.187810 ESTs	5.14
40	420170	U43374	Hs.95631 Human normal keratinocyte mRNA	5.14
	420493	AI635113	Hs.270366 ESTs, Weakly similar to I78885 serine/th	5.12
	425739	T19016	Hs.159410 molybdopterin synthase sulfurylase	5.12
	440652	AI216751	Hs.143977 ESTs	5.12
	419706	C04649	Hs.77899 tropomyosin 1 (alpha)	5.12
45	427728	AJ245600	Hs.180545 Homo sapiens mRNA for hypothetical prote	5.12
	416113	AA173525	Hs.118758 ESTs, Weakly similar to RLF [H.sapiens]	5.12
	446223	BE300091	Hs.119699 hypothetical protein FLJ12969	5.11
	407624	AW157431	Hs.248941 ESTs	5.11
	447197	R36075	gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.11
50	452465	AA610211	Hs.34244 ESTs	5.10
	442833	AA328153	Hs.88201 ESTs, Weakly similar to A Chain A, Cryst	5.10
	448952	AI609595	Hs.208038 ESTs	5.10
	408170	AW204516	Hs.31835 ESTs	5.08
	424238	AA337401	Hs.137635 ESTs	5.07
55	421072	AI215069	Hs.89113 ESTs	5.06
	424717	H03754	Hs.152213 wingless-type MMTV integration site fami	5.06
	423654	AI674253	Hs.35828 ESTs	5.06
	436862	AI821940	Hs.264622 ESTs, Moderately similar to ALU8_HUMAN A	5.06
	436554	AI985810	Hs.301173 ESTs	5.05
60	433264	D85782	Hs.3229 cysteine dioxygenase, type I	5.04
	452387	AI680772	Hs.306094 trinucleotide repeat containing 12	5.04
	412666	AL080116	Hs.74420 origin recognition complex, subunit 3 (y	5.03
	430287	AW182459	Hs.125759 ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.03
	413293	AL047483	Hs.302498 GTP-binding protein homologous to Saccha	5.00
65	418217	AI910647	Hs.13442 ESTs	5.00
	401480	NA	NA	5.00
	456179	H75490	Hs.271930 ESTs	5.00

TABLE 7B

70	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
<hr/>			
75	Pkey	CAT number	Accession
	408432	1058667_1	AW195262 R27868 AW811262
	408690	107490_1	AW864542 AA056567 AW882724
	411765	125700_1	H43346 AA248302 AA095182
	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
80	424281	237742_1	AA766243 AA338252 AA338213

5	424492	240008_1	AI133482 AI207619 AA341626
	428679	294049_1	AA431765 AA432015
	430848	324621_1	AW021726 AA487752 AA488085
	432340	345248_1	AA534222 AA632632 T81234
	432363	345469_1	AA534489 AW970240 AW970323
	432639	351744_1	AW973785 H60163 AA557608
	434609	38950_1	R76593 AF147390 R76594
	439518	47334_1	W76326 AF086341 W72300
10	443613	575391_1	AI079356 W23287
	447197	711623_1	R36075 AI366546 R36167
	447974	745643_1	R76886 AI453674 R77049
	452712	928309_1	AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784
	454653	1228081_1	AW812227 AW812294 AW812092
15	458311	543550_1	AF069478 AF069479 AF069480

TABLE 7C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

25	Pkey	Ref	Strand	Nt_position
	400534	6981826	Minus	278637-279292
	401352	9931258	Minus	26064-26208
30	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401714	6715702	Plus	96484-96681
	401742	2911728	Plus	64003-64147
	403432	9719611	Minus	68204-68392
	403776	7770611	Minus	1414-1513,1624-1756
	404227	7838233	Minus	93110-93259
35	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	406360	9256107	Minus	7513-7673

40 Table 8A shows 538 genes significantly down-regulated in colon cancer compared to normal colon. These were selected as for Table 7A and the ratio was equal to or less than than 0.33.

TABLE 8A: 538 GENES SIGNIFICANTLY DOWN-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

45	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title
50	R1:	Ratio of tumor to normal colon

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
55	421996	AW583807	Hs.1460	glucagon	0.0233
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	0.0307
	457407	AA505035	Hs.195651	ESTs	0.0416
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	0.0564
	426651	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.0567
60	425920	AL049977	Hs.162209	claudin 8	0.0601
	431436	AA505035	Hs.195651	ESTs	0.0607
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.0629
	442009	AI733281	Hs.128320	ESTs	0.0634
	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	0.0707
65	429050	X81333	Hs.194777	meprin A, beta	0.0714
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.0735
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	0.0739
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	0.0769
	443506	H10661	Hs.192124	ESTs, Weakly similar to I38022 hypotheti	0.0838
70	415314	N88802	Hs.5422	glycoprotein M6B	0.0853
	451181	AI796330	Hs.207461	ESTs	0.0873
	429001	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	0.0888
	426635	BE395109	Hs.129327	hypothetical protein MGC13057	0.0900
	429350	AI754634	Hs.131987	ESTs	0.0927
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	0.0931

5	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	0.0951
	441066	AW205427	Hs.190726	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.0957
	431252	NM_005478	Hs.251380	insulin-like 5	0.0985
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	0.0987
	433546	AI075877	Hs.125461	hypothetical protein FLJ11539	0.1007
10	415154	D63175		gb:HUM501B09B Clontech human placenta po	0.1032
	409921	AW600239		gb:EST00009 pGEM-T library Homo sapiens	0.1067
	432440	X63597	Hs.2996	sucrase-isomaltase	0.1107
	430468	NM_004673	Hs.241519	angiopoietin-like 1	0.1114
	427167	AI239607	Hs.99196	hypothetical protein MGC11324	0.1147
15	441212	AW242447	Hs.146182	cytosolic beta-glucosidase	0.1167
	423605	AF047826	Hs.129887	cadherin 19, type 2	0.1190
	411381	AW841862	Hs.306831	Homo sapiens cDNA: FLJ22549 fis, clone H	0.1211
	412639	AW961284	Hs.296235	ESTs	0.1239
	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.1240
20	403548				0.1248
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	0.1274
	457982	AW856093	Hs.183617	ESTs	0.1277
	448835	BE277929	Hs.11081	UBX domain-containing 2	0.1277
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	0.1291
25	441805	AA285136	Hs.301914	neuronal specific transcription factor D	0.1309
	407639	AW205369	Hs.312830	ESTs	0.1315
	421741	AK001879	Hs.107527	hypothetical protein FLJ11017	0.1325
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	0.1328
	451742	T77609	Hs.117970	ankyrin 2, neuronal	0.1335
30	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	0.1379
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	0.1393
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	0.1395
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	0.1456
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	0.1459
35	404767				0.1460
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	0.1462
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	0.1463
	452768	AW069459	Hs.61539	ESTs	0.1466
	418692	AK000268	Hs.87383	hypothetical protein	0.1471
40	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	0.1471
	407551	Y10516		gb:H.sapiens mRNA for CD58 T3 protein.	0.1486
	402076				0.1487
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	0.1500
	442080	AW444761	Hs.44565	ESTs	0.1500
45	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	0.1513
	429545	AI824164	Hs.77667	lymphocyte antigen 6 complex, locus E	0.1523
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	0.1529
	435056	AW023337	Hs.5422	glycoprotein M6B	0.1532
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	0.1538
50	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	0.1542
	408221	AA912183	Hs.47447	ESTs	0.1552
	425220	AW975317	Hs.162987	ESTs	0.1558
	445200	AA084460	Hs.12409	somatostatin	0.1558
	443238	T78886	Hs.284450	ESTs	0.1563
55	456064	AA256213	Hs.72010	ESTs	0.1582
	428133	AW167727	Hs.11873	ESTs	0.1605
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.1615
	437734	AA693951	Hs.180284	ESTs	0.1637
	414290	AI568801	Hs.71721	ESTs	0.1638
60	418935	T28499	Hs.89485	carbonic anhydrase IV	0.1656
	411939	AI365585	Hs.146246	ESTs	0.1660
	442496	R55073	Hs.124130	ESTs	0.1676
	450693	AW450461	Hs.203965	ESTs	0.1698
	420736	AI263022	Hs.82204	ESTs	0.1718
65	405385				0.1745
	404638				0.1751
	427333	AF067797	Hs.176658	aquaporin 8	0.1757
	404246				0.1763
	433785	BE044593	Hs.112704	ESTs	0.1767
70	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	0.1769
	406980	S69265		(NONE)	0.1781
	421666	AL035250	Hs.1408	endothelin 3	0.1784
	452854	AA437061	Hs.14060	prokineticin 1 precursor	0.1795
	400514				0.1805
75	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	0.1808
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	0.1812
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	0.1812
	412474	AI791451		gb:ni50c09.y5 NCI_CGAP_Ov2 Homo sapiens	0.1812
	436008	AI078428	Hs.58785	ESTs	0.1820
80	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	0.1828
	431728	NM_007351	Hs.268107	multimerin	0.1832
	419746	AW867943	Hs.127216	hypothetical protein FLJ13465	0.1835
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	0.1838
	415672	N53097	Hs.193579	ESTs	0.1838
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	0.1838
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	0.1842
	413714	AI560944	Hs.71428	ESTs	0.1845

	427061	AB032971	Hs.173392	KIAA1145 protein	0.1847
	405282				0.1848
	400163				0.1855
5	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.1863
	447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	0.1876
	407891	AA486620	Hs.41135	endomucin-2	0.1895
	437140	AA312799	Hs.283689	activator of CREM in testis	0.1901
	431544	AK000770	Hs.299329	Homo sapiens cDNA FLJ20763 fis, clone CO	0.1904
10	436659	AI217900	Hs.144464	ESTs	0.1905
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	0.1926
	453698	AA037615	Hs.42746	ESTs	0.1928
	423743	AB023148	Hs.173373	KIAA0931 protein	0.1941
	428412	AA428240	Hs.126083	ESTs	0.1942
15	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	0.1944
	434683	AW298724	Hs.202639	ESTs	0.1957
	421865	AA609911	Hs.109012	MAX dimerization protein	0.1957
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	0.1969
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	0.1981
20	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	0.2004
	437740	AA810265	Hs.122915	ESTs	0.2016
	405610				0.2017
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	0.2025
	416961	BE391476	Hs.80617	ribosomal protein S16	0.2041
25	401465				0.2045
	437425	AW183714	Hs.20981	hypothetical protein DKFZp547M236	0.2049
	416231	H30333	Hs.165062	ESTs	0.2049
	401753				0.2050
	433430	AI863735	Hs.186755	ESTs	0.2051
30	432150	AK000224	Hs.272789	hypothetical protein FLJ20217	0.2052
	411644	H92064	Hs.278626	Arg/Abi-interacting protein ArgBP2	0.2059
	403957				0.2063
	435900	AI243036	Hs.16094	ESTs	0.2070
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.2075
35	445500	AW451938	Hs.257512	ESTs	0.2075
	419956	AL137939	Hs.40096	ESTs	0.2090
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	0.2093
	423655	AA722425	Hs.182785	ESTs, Moderately similar to 1207289A rev	0.2118
	401381				0.2120
40	426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014 8 simil	0.2122
	433476	AA594394	Hs.152616	ESTs	0.2125
	423405	NM_014151	Hs.128155	HSPC053 protein	0.2130
	442826	AI018777	Hs.131241	ESTs	0.2132
	427060	AW378993	Hs.90286	ESTs	0.2137
45	437354	AA749215	Hs.291886	ESTs	0.2137
	447734	AI421412	Hs.163659	ESTs	0.2144
	424585	AA464840	Hs.131987	ESTs	0.2146
	458016	AW188099	Hs.131813	ESTs	0.2151
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	0.2151
	401521				0.2157
50	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (0.2165
	401024				0.2171
	414802	AI793107	Hs.27018	Ris	0.2179
	441083	BE562611		gb:601336446F1 NIH_MGC_44 Homo sapiens c	0.2185
55	417355	D13168	Hs.82002	endothelin receptor type B	0.2186
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	0.2188
	442930	AW881975	Hs.213923	ESTs	0.2193
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	0.2209
	444567	AV654020	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	0.2212
60	405654				0.2217
	415471	F09747	Hs.268707	ESTs	0.2222
	449243	AW295031	Hs.198671	ESTs	0.2229
	436088	AA704687	Hs.191294	ESTs	0.2232
	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapi	0.2242
65	427552	NM_005771	Hs.179608	retinol dehydrogenase homolog	0.2243
	416439	AA180363	Hs.118769	ESTs	0.2244
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	0.2254
	459395	Z30300	Hs.281935	ESTs	0.2257
	439039	AI656707	Hs.48713	ESTs	0.2268
70	433575	AA600175	Hs.39720	ESTs	0.2268
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	0.2273
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	0.2283
	441899	AI372588	Hs.8022	TU3A protein	0.2283
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	0.2290
75	434839	AI743069	Hs.134736	ESTs	0.2294
	435731	AA699581	Hs.186811	ESTs	0.2299
	400865				0.2304
	446294	AI284935		gb:qk55g09.x1 NCI_CGAP_Co8 Homo sapiens	0.2305
	414193	BE260069		gb:601150964F1 NIH_MGC_19 Homo sapiens c	0.2309
80	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	0.2315
	453098	Z25935	Hs.86379	ESTs	0.2315
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	0.2319
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	0.2320
	443482	AW188093	Hs.250385	ESTs	0.2326

5	432134	AI816782	Hs.122583	hypothetical protein FLJ21934	0.2329
	421539	AA292747	Hs.97296	ESTs	0.2330
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	0.2344
	408001	AA046458	Hs.95296	ESTs	0.2347
	409331	M36634	Hs.53973	vasoactive intestinal peptide	0.2351
10	431094	AW972276	Hs.116195	ESTs	0.2354
	429575	AA706003	Hs.99387	ESTs	0.2358
	404958				0.2361
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	0.2364
	452742	AW589945	Hs.97876	hypothetical protein DKFZp564K0322	0.2380
15	417511	AL049176	Hs.82223	chordin-like	0.2381
	404927				0.2387
	430297	AW243166	Hs.129806	ESTs	0.2412
	447482	AB033059	Hs.18705	KIAA1233 protein	0.2415
	418332	R34976	Hs.78293	ESTs	0.2416
20	454145	AA046872	Hs.62798	ESTs	0.2421
	422472	R59096	Hs.279939	mitochondrial carrier homolog 1	0.2424
	404070				0.2427
	421232	AA989220	Hs.292100	ESTs	0.2427
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	0.2432
25	412622	AW664708	Hs.171959	ESTs	0.2433
	454430	AI082777	Hs.61384	sema domain, seven thrombospondin repeat	0.2437
	416694	AW161284	Hs.79564	neuronal PAS domain protein 1	0.2443
	426724	AA383623	Hs.293616	ESTs	0.2444
	405073				0.2445
30	401236	H24185	Hs.92918	hypothetical protein	0.2445
	414203	BE262170	Hs.78629	ATPase, Na ⁺ /K ⁺ transporting, beta 1 poly	0.2451
	401776				0.2452
	404696				0.2462
	426666	AW500131	Hs.171763	CD22 antigen	0.2471
35	427078	AI676062	Hs.111902	ESTs	0.2474
	424682	AW604804	Hs.151717	KIAA0437 protein	0.2478
	440383	AA884208	Hs.30484	ESTs	0.2481
	419118	AA234223	Hs.139204	ESTs	0.2494
	443515	AV657547	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	0.2495
40	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	0.2499
	404605				0.2500
	446066	AI343931	Hs.149383	ESTs	0.2505
	408345	R93851	Hs.63063	ESTs	0.2506
	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-re	0.2508
45	416950	AL049798	Hs.80552	dermatopontin	0.2510
	423555	AW958201	Hs.178589	hepatocellular carcinoma antigen gene 52	0.2513
	449833	R82252	Hs.106106	protein kinase (cAMP-dependent, catalytic)	0.2515
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	0.2519
	408897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	0.2523
50	422743	BE304678	Hs.119598	ribosomal protein L3	0.2526
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telen	0.2532
	450880	AK002183	Hs.285885	Homo sapiens cDNA FLJ11321 fis, clone PL	0.2536
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	0.2536
	451979	F06972	Hs.27372	BMX non-receptor tyrosine kinase	0.2549
55	440274	R24595	Hs.7122	scrapie responsive protein 1	0.2553
	430097	AI523245	Hs.127638	ESTs	0.2558
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	0.2564
	402695				0.2565
	453992	AW014995	Hs.281080	ESTs	0.2569
60	453888	AW450670	Hs.252819	ESTs	0.2569
	401371				0.2574
	456145	BE299427	Hs.21446	KIAA1716 protein	0.2579
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiesterase	0.2580
	422591	L07648	Hs.118630	MAX-interacting protein 1	0.2582
65	452359	BE167229	Hs.29206	hypothetical protein MGC14376	0.2584
	447569	AI393202	Hs.147554	hypothetical protein FLJ23392	0.2586
	405880				0.2588
	420321	D78761	Hs.96657	hypothetical protein	0.2595
	454415	AK000846	Hs.58679	solute carrier family 7, (cationic amino	0.2602
70	437032	AW867372	Hs.302063	immunoglobulin heavy constant mu	0.2604
	448025	BE502965	Hs.170426	ESTs	0.2605
	444304	AW628433	Hs.271296	ESTs, Weakly similar to I54374 gene NF2	0.2605
	424885	AI333771	Hs.82204	ESTs	0.2608
	425381	D84371	Hs.1898	paraoxonase 1	0.2611
75	457413	AA743462	Hs.165337	ESTs	0.2618
	452078	AA022620	Hs.52170	ESTs	0.2624
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	0.2628
	401974				0.2639
	411319	BE537094		gb:601063333F1 NIH_MGC_10 Homo sapiens c	0.2646
80	417761	R13727	Hs.21435	ESTs	0.2648
	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	0.2653
	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	0.2653
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	0.2660
	402182				0.2660
	402610				0.2661
	444814	BE010749	Hs.255097	ESTs	0.2663
	450017	W56434	Hs.201608	ESTs	0.2663

5	408684	R61377	Hs.12727	hypothetical protein FLJ21610	0.2667
	444209	AI753134	Hs.146494	ESTs	0.2668
	415022	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid	0.2677
	416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	0.2681
	422909	AA533356		gb:nj67f10.s1 NCL_CGAP_Pr10 Homo sapiens	0.2681
10	412047	AA934589	Hs.49696	ESTs	0.2693
	426356	BE536836	Hs.98682	hypothetical protein FKSG32	0.2703
	442238	AW135374	Hs.270949	ESTs, Moderately similar to F41925 hypot	0.2709
	402425				0.2710
	450545	AW135582	Hs.201767	ESTs	0.2710
15	417118	U38654	Hs.50477	RAB27A, member RAS oncogene family	0.2725
	419850	F06844		gb:HSC1ME091 normalized infant brain cDN	0.2727
	428020	L19058	Hs.181581	glutamate receptor, ionotropic, kainate	0.2730
	441493	AW070446	Hs.127037	ESTs	0.2733
	413541	BE147036		gb:QV4-HT0222-091199-024-e10 HT0222 Homo	0.2733
20	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.2734
	455597	BE008545	Hs.156110	immunoglobulin kappa constant	0.2740
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	0.2740
	444195	AB002351	Hs.10587	KIAA0353 protein	0.2743
	415160	T82802		gb:yd38a04.r1 Soares fetal liver spleen	0.2747
25	421823	N40850	Hs.28625	ESTs	0.2755
	434464	BE063921	Hs.295971	ESTs	0.2755
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [0.2756
	430073	U86136	Hs.232070	telomerase-associated protein 1	0.2762
	432018	AA524447	Hs.152377	ESTs	0.2763
30	422954	AW998605		gb:PM0-BN0065-100300-001-b10 BN0065 Homo	0.2768
	416397	H53035	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	0.2775
	442420	AI024834	Hs.131729	ESTs	0.2775
	410950	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	0.2778
	427114	AI219896	Hs.97592	ESTs	0.2778
35	448466	AI522109	Hs.171066	ESTs	0.2778
	434445	AI349306	Hs.11782	ESTs	0.2784
	457115	AA420712		gb:nc63c07.s1 NCL_CGAP_Pr1 Homo sapiens	0.2785
	459511	AI142379		gb:qg64c01.r1 Soares_testis_NHT Homo sap	0.2786
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase (alanine	0.2794
40	433633	AI880516	Hs.84630	ESTs, Weakly similar to 2004399A chromos	0.2799
	440236	AW996722	Hs.125297	ESTs	0.2799
	405691				0.2804
	405334				0.2804
	403047				0.2809
45	412506	AW957159		gb:EST369229 MAGE resequences, MAGD Homo	0.2809
	441042	AA077736		gb:7B48A07 Chromosome 7 Fetal Brain cDNA	0.2815
	434660	AA764768	Hs.121158	hypothetical protein DKFZp434J0113	0.2816
	444453	AW379394	Hs.145126	ESTs	0.2817
	457736	AK000390	Hs.4205	hypothetical protein FLJ20124	0.2820
50	454012	M76424	Hs.37014	carbonic anhydrase VII	0.2821
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombo	0.2822
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	0.2827
	435021	AA922192	Hs.54709	ESTs	0.2828
	413344	U46024	Hs.75302	myotubular myopathy 1	0.2837
55	447787	BE620108		gb:601483015F1 NIH_MGC_69 Homo sapiens c	0.2840
	457290	AA465293	Hs.105069	ESTs	0.2841
	458244	AI929453	Hs.122489	Homo sapiens cDNA FLJ13289 fis, clone OV	0.2841
	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	0.2842
	407938	AA905097	Hs.85050	phospholamban	0.2845
60	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	0.2846
	428212	AW444451	Hs.134812	ESTs	0.2853
	424433	H04607	Hs.9218	ESTs	0.2857
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	0.2857
	404769				0.2863
65	411620	AW854536		gb:RC3-CT0255-200100-024-a08 CT0255 Homo	0.2868
	428746	AW503820	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	0.2870
	431822	AA516049		gb:ng65d01.s1 NCL_CGAP_Lip2 Homo sapiens	0.2872
	441290	W27501	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.2874
	422033	AW245905	Hs.110903	claudin 5 (transmembrane protein deleted	0.2877
70	421935	AA131632	Hs.109672	CMP-NeuAC;(beta)-N-acetylgalactosaminide	0.2878
	447955	BE544271	Hs.288390	hypothetical protein FLJ22795	0.2880
	405364				0.2881
	422165	AL041199	Hs.1481	histidine decarboxylase	0.2882
	431087	H12723	Hs.290791	ESTs	0.2882
75	450610	AA010370	Hs.60386	nuclear RNA export factor 3	0.2882
	445627	AW818475	Hs.7363	ESTs	0.2883
	436144	AW881250	Hs.148367	ESTs	0.2886
	445152	AI214667	Hs.283597	ESTs	0.2891
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.2891
80	455614	AI693369	Hs.202274	ESTs	0.2899
	419683	AA248897	Hs.48784	ESTs	0.2900
	411886	AL046810	Hs.20021	vesicle-associated membrane protein 1 (s	0.2904
	430770	AA765694	Hs.123296	ESTs	0.2913
	444459	AI680624	Hs.148676	ESTs	0.2913
	444918	AI202262	Hs.283362	ESTs	0.2915
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	0.2915
	435598	AA689470	Hs.163026	ESTs	0.2921

	413056	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	0.2922
	443998	AI620661	Hs.296276	ESTs	0.2924
	424412	H15512	Hs.10043	hypothetical protein FLJ13074	0.2925
5	421204	AW081587	Hs.165051	ESTs	0.2928
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	0.2938
	440507	H06994		gb:yl81b07.r1 Soares infant brain 1NIB H	0.2943
	445555	AW974013	Hs.260809	ESTs	0.2945
	438570	AW888554	Hs.84298	CD74 antigen (invariant polypeptide of m	0.2948
10	447195	T73745	Hs.279870	ESTs, Weakly similar to A46010 X-linked	0.2950
	423267	AL137416	Hs.126177	Homo sapiens mRNA; cDNA DKFZp434O192 (fr	0.2956
	421920	BE551245	Hs.1438	gamma-aminobutyric acid (GABA) receptor,	0.2956
	412177	Z23091	Hs.73734	glycoprotein V (platelet)	0.2959
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	0.2959
15	433745	AF075320	Hs.28980	hypothetical protein FLJ14540	0.2969
	417935	R53697	Hs.170044	ESTs	0.2970
	420674	NM_000055	Hs.1327	butyrylcholinesterase	0.2973
	413537	BE146866		gb:QV4-HT0222-211099-014-f06 HT0222 Homo	0.2973
	445194	AI215667	Hs.175044	ESTs	0.2974
20	454135	AW135965	Hs.246783	ESTs	0.2976
	403418				0.2986
	457605	AV657778	Hs.3314	selenoprotein P, plasma, 1	0.2989
	408896	AI610447	Hs.48778	niban protein	0.2993
	448542	BE256176	Hs.278712	eukaryotic translation initiation factor	0.2994
25	417945	R29072		gb:F1-101D 22 week old human fetal liver	0.2994
	412518	BE047637	Hs.173739	hypothetical protein FLJ10297	0.2996
	424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	0.2997
	430778	D90337	Hs.247916	natriuretic peptide precursor C	0.3000
	451531	AA018311	Hs.114762	ESTs	0.3003
30	444926	AI202492	Hs.212933	ESTs, Weakly similar to CLD4_HUMAN CLAUD	0.3003
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	0.3012
	459456	AA486036	Hs.190124	ESTs	0.3012
	417111	AW016321	Hs.82306	destrin (actin depolymerizing factor)	0.3012
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	0.3012
35	451959	AA056203	Hs.27337	hypothetical protein FLJ20623	0.3012
	410482	AW772187	Hs.191859	ESTs	0.3013
	417700	M36542	Hs.1101	POU domain, class 2, transcription facto	0.3018
	404414				0.3019
	432247	AA531287	Hs.105805	ESTs	0.3023
40	453471	AL037887	Hs.208179	ESTs	0.3028
	417481	AA203281	Hs.21798	ESTs	0.3029
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	0.3032
	448744	AL135424	Hs.9469	pleckstrin homology domain-containing, f	0.3033
	429223	BE264152	Hs.221994	ESTs	0.3034
45	404501	AW247252	Hs.75514	nucleoside phosphorylase	0.3037
	406829	AW419128	Hs.84298	CD74 antigen (invariant polypeptide of m	0.3039
	438839	AW297945	Hs.128490	ESTs	0.3039
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.3042
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	0.3045
50	458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	0.3048
	443294	AI733625	Hs.133053	ESTs	0.3050
	447023	AA356764	Hs.17109	integral membrane protein 2A	0.3052
	458583	AI479646	Hs.157081	hypothetical protein MGC4170	0.3056
	414567	BE281057	Hs.184519	hypothetical protein FLJ12949	0.3057
55	445123	AI762911	Hs.145369	ESTs	0.3064
	412682	AW983772		gb:RC3-HN0002-060400-012-h09 HN0002 Homo	0.3065
	434361	AF129755	Hs.117772	ESTs	0.3071
	414026	BE241713		gb:TCAAP1E0472 Pediatric acute myelogeno	0.3072
	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	0.3073
60	408350	AW183350	Hs.250127	ESTs	0.3074
	401042				0.3077
	422586	AA312704	Hs.59457	hypothetical protein FLJ22127	0.3077
	438692	AB007950	Hs.6360	KIAA0481 gene product	0.3077
	447452	BE618258	Hs.102480	Homo sapiens, clone IMAGE:3869590, mRNA,	0.3083
65	444414	AW293214	Hs.8752	transmembrane protein 4	0.3085
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	0.3088
	430410	AF099144	Hs.250700	trypsin beta 1	0.3090
	419299	AI311085	Hs.62406	hypothetical protein FLJ22573	0.3091
	400672				0.3094
70	444010	AW976457	Hs.282887	ESTs	0.3096
	451699	AL118571	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPO	0.3096
	432471	BE244667	Hs.296155	CGI-100 protein	0.3105
	405277				0.3106
	456765	AI497900	Hs.33067	ESTs	0.3106
75	452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	0.3106
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	0.3106
	406592				0.3106
	423621	BE002904		gb:QV4-BN0090-070400-163-c07 BN0090 Homo	0.3107
	417919	AI928203	Hs.86379	ESTs	0.3110
80	414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	0.3110
	457439	AW410408	Hs.271167	L-pipecolic acid oxidase	0.3116
	426449	AL134009	Hs.169936	Homo sapiens mRNA; cDNA DKFZp586N1918 (f	0.3116
	419942	U25138	Hs.93841	potassium large conductance calcium-acti	0.3119
	458544	AI631036	Hs.196843	ESTs	0.3119

	447778	BE620592	Hs.71190	ESTs, Weakly similar to S16506 hypotheti	0.3121
	449097	BE271708	Hs.95110	ESTs, Weakly similar to A55943 1-phospha	0.3125
	429338	AW170591	Hs.13967	ESTs, Weakly similar to PSM_HUMAN PROSTA	0.3125
5	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	0.3125
	446404	AA019961	Hs.26216	LOC50627	0.3130
	446616	R65964	Hs.241569	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.3132
	409404	BE220053	Hs.129056	ESTs	0.3135
	417318	AW953937	Hs.12891	ESTs	0.3139
10	443980	AI459140	Hs.299087	ESTs	0.3140
	459138	AI903291		gb:RC-BT029-080199-047 BT029 Homo sapien	0.3142
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.3143
	434704	AW135276	Hs.192311	ESTs	0.3143
	414214	D49958	Hs.75819	glycoprotein M6A	0.3145
15	446378	AI905699	Hs.239760	citrate synthase	0.3145
	459233	AI939966		gb:MR0-CT0015-160799-002-b06 CT0015 Homo	0.3146
	428193	NM_004235	Hs.7934	Kruppel-like factor 4 (gut)	0.3148
	426515	BE394222	Hs.231444	Homo sapiens, Similar to hypothetical pr	0.3150
	426597	AA382250	Hs.145601	ESTs	0.3153
20	459729	AL037285	Hs.289848	EST, Weakly similar to ALU4_HUMAN ALU SU	0.3157
	405071				0.3160
	407457	AJ242724		gb:Homo sapiens mRNA for partial putativ	0.3162
	409922	AW505582	Hs.130732	KIAA1575 protein	0.3172
	438219	AI916151	Hs.257194	ESTs	0.3173
25	412944	AA384110	Hs.197143	ESTs	0.3175
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	0.3178
	426662	AA879474	Hs.122710	ESTs	0.3178
	444391	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	0.3179
	432168	AK000563	Hs.272805	hypothetical protein FLJ20556	0.3181
30	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	0.3183
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	0.3185
	448812	H30775	Hs.22140	BM88 antigen	0.3188
	411288	AW835511		gb:QV0-LT0015-180200-127-d02 LT0015 Homo	0.3189
	422884	AW860975	Hs.13256	ESTs	0.3190
35	405535				0.3195
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	0.3195
	455353	W26786		gb:15d7 Human retina cDNA randomly prime	0.3195
	414540	BE379050	Hs.306969	Homo sapiens, clone MGC:10782, mRNA, com	0.3195
	428568	AC004755	Hs.184922	Homo sapiens chromosome 19, fosmid 37502	0.3195
40	428106	BE620016	Hs.182470	PTD010 protein	0.3198
	411856	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	0.3202
	445682	AW378397		gb:RC3-HT0220-031299-012-g06 HT0220 Homo	0.3205
	437568	AI954795	Hs.156135	ESTs	0.3205
	448943	AI608810	Hs.193288	ESTs	0.3205
45	431999	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	0.3207
	419279	AA235900	Hs.87500	ESTs	0.3208
	405913				0.3209
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	0.3212
	424729	AF063012	Hs.152531	heart and neural crest derivatives expre	0.3212
50	440020	AI480204	Hs.177131	ESTs	0.3213
	429082	AL135682	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	0.3215
	433663	AF083131	Hs.229535	CATX-15 protein	0.3215
	400641				0.3216
	406140				0.3216
55	415280	R56473	Hs.268715	ESTs	0.3217
	447635	AI669669	Hs.195362	ESTs	0.3217
	401887				0.3217
	400767				0.3221
	457713	H47495	Hs.13810	hypothetical protein MGC15504	0.3221
60	448758	AB018311	Hs.21917	KIAA0768 protein	0.3222
	444750	AW242684	Hs.243623	ESTs	0.3223
	411466	AW847669		gb:IL3-CT0213-280100-056-G10 CT0213 Homo	0.3226
	432749	NM_014438	Hs.278909	interleukin 1, eta	0.3231
	408112	AW451982	Hs.248613	ESTs	0.3231
65	433234	AB040928	Hs.65366	KIAA1495 protein	0.3231
	422831	R02504	Hs.332943	ESTs	0.3234
	403215				0.3236
	451868	R85962	Hs.221926	ESTs, Weakly similar to I38022 hypotheti	0.3236
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	0.3242
70	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	0.3254
	445848	AA774824	Hs.13377	Homo sapiens clone 23649 and 23755 unkno	0.3257
	441143	AI027604	Hs.159650	ESTs	0.3257
	405138				0.3262
	412888	M86151		gb:EST02679 Hippocampus, Stratagene (cat	0.3262
75	409662	AW452320	Hs.279726	ESTs	0.3262
	425438	T62216	Hs.270840	ESTs	0.3263
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	0.3263
	423512	AW844694	Hs.306752	Homo sapiens cDNA: FLJ21391 fis, clone C	0.3264
	436777	AA731199	Hs.293130	ESTs	0.3267
	431651	BE250915	Hs.266914	hypothetical protein FLJ10355	0.3267
80	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	0.3268
	426048	AI768853	Hs.134478	ESTs	0.3269
	451096	BE383234	Hs.25925	Homo sapiens, clone MGC:15393, mRNA, com	0.3270
	426942	AA393551	Hs.97450	ESTs	0.3271

	454947	AW846590	gb:QV0-CT0180-011099-025-d07 CT0180 Homo	0.3275
	413814	BE169692	gb:PM1-HT0527-290200-006-a05 HT0527 Homo	0.3275
	422818	AA404290	Hs.97848 ESTs	0.3277
5	423634	AW959908	Hs.1690 heparin-binding growth factor binding pr	0.3278
	414002	NM_006732	Hs.75578 FBj murine osteosarcoma viral oncogene h	0.3278
	452164	AI863171	gb:tz44b02.x1 NCL_CGAP_Brn52 Homo sapien	0.3279
	458477	NM_000314	Hs.10712 phosphatase and tensin homolog (mutated	0.3279
	433197	AB040889	Hs.281022 KIAA1456 protein	0.3280
	405701			0.3282
10	437782	AI370876	Hs.79090 exportin 1 (CRM1, yeast, homolog)	0.3284
	459001	AI761313	Hs.204605 ESTs	0.3286
	422783	AA598956	Hs.120439 ethanolamine kinase	0.3289
	417036	AF039918	Hs.80975 ectonucleoside triphosphate diphosphohyd	0.3290
15	456041	BE270795	Hs.268864 ESTs	0.3295
	423310	AA325225	Hs.124023 Homo sapiens cDNA FLJ14218 fis, clone NT	0.3296
	427530	AA405093	Hs.126519 ESTs	0.3296
	420172	AA601122	Hs.95655 secreted and transmembrane 1	0.3297
	445610	AI831648	Hs.143993 ESTs	0.3297
20	411328	AW837063	gb:QV1-LT0037-150200-069-g08 LT0037 Homo	0.3300

Table 8B

	Pkey:	Unique Eos probeset identifier number
25	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
Pkey	CAT number	Accession
30	409921	1159516_1 AW600239 AW600255 AW505332
	410626	1212621_1 BE407727
	410845	1223881_1 AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280 AW807283
	410950	1227728_1 AW811633 AW811652 AW811898
	411288	1237709_1 AW835511 AW835517 AW835513
35	411319	1238595_1 BE537094 AW836542
	411328	1238987_1 AW837063 AW935882 AW935957
	411466	1246771_1 AW847669 AW847667 BE145799
	411514	1248638_1 AW850178 AW850233 AW850445 AW850446
	411620	1252014_1 AW854536 AW854417 AW854495 AW854355
40	411880	1263110_1 AW872477 BE088101 T05990
	412474	129869_1 AI791451 AI791288 BE019234 BE296601 AA111939
	412506	1301336_1 AW957159 H09937 T75143
	412682	1321572_1 AW983772 AW983730 AW983769 AW983836 AW983835 AW983837
45	412888	1334784_1 M86151 BE061884 BE061883 BE061898 BE061882 BE061887 BE061891 BE061890 BE061896 BE061893 BE061895 BE061894 BE061885 BE007474
		BE007481 BE007553
	413056	1347545_1 BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072
	413537	1375441_1 BE146866 BE146865 BE146867
	413541	1375499_1 BE147036 BE146951 BE146958 BE146966 BE146976 BE146955
50	413814	1391574_1 BE169692 BE169421
	414026	1411109_1 BE241713 BE241912
	414193	1424706_2 BE260069
	414349	1437515_1 BE512968
	414484	1452830_1 BE314385
55	414539	1460320_1 BE379046 BE395459
	415154	1525577_1 D63175 D78984 D63269
	415160	1525766_1 T82802 D78670 R08505
	416035	1567254_1 H42314 H43080 H45217 H15384
	417945	1711126_1 R29072 R29717 R29699 R29709 R29751 R29609 R29060 R29718 R29057 R29591 R29683 R29575 R28913 R28910
60	419850	188485_1 F06844 F06845 Z45488 AW748501 AW748591 AW752021 AW748545 AW853362 AW853363 AW853427 AA251253
	422909	222858_1 AA533356 AW468427 R67736 AA779031 AA614088 AI823404 AA318991 AA720986
	422954	223239_1 AW998605 AW993131 BE514709 AA319445
	423621	230314_1 BE002904 H64880 AA328679
	424648	241947_1 AA344576 AA732430 AA344601
65	426132	261431_1 AA370501 AW962784 AA370727
	426497	268121_1 AA379913 AA379981 AW963523
	430553	319868_1 AW392821 AW392809 AW843258 AW843049 AW603156 BE165656 AW821728
	431822	338082_1 AA516049 AW004922
	434098	380006_1 AA625499 AA625269 AA625184
	437483	43756_1 AL390174 AW898817
70	440507	495677_1 H06994 BE147898
	441042	50823_1 AA077736 AA078505 BE562497 Z17859
	441083	50904_1 BE562611 AA436054
	445682	647580_1 AW378397 AW378390 AW378358 AI247957
75	446294	670076_1 AI284935 AW409822 BE408182
	446901	697809_1 AI347274 AW844024
	447787	73719_1 BE620108 BE312062 AW896316 BE262546
	451385	86787_1 AA017656 AA017374 AA019761
	452164	902091_1 AI863171 BE047919
80	454186	1049791_1 BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581
		BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460
		BE141749 AW177598

454790 1234752_1 AW820852 AW820773 AW821088
 454947 1245953_1 AW846590 AW846615 AW846584 AW846592 AW846621 AW846610
 455353 1284289_1 W26786 AW998612 AW902272
 457115 286601_1 AA420712 AA469165 AA420737
 459138 918860_1 AI903291 AI903455 AI903367 AI903403 AI903447 AI903405 AI903364 AI903229 AI903240 AI903346
 459233 944881_1 AI939966 AI939988 AI939951 AI939981 AI939976 AI939959

Table 8C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
400641	8117693	Plus	4786-4992
400672	8118724	Minus	148067-148503
400767	8131627	Minus	80531-80629,82169-82278
400865	1945037	Minus	44482-45526
401024	8117489	Plus	60551-60802
401042	8117611	Plus	151364-151606
401371	9650602	Plus	80901-81283
401381	8570226	Minus	118629-119146,119392-119657
401465	6682292	Plus	25676-25800
401521	7705251	Plus	9127-9234
401753	9838183	Minus	155287-155529,159719-159997
401776	9966323	Plus	115535-115743,117746-117839,120290-120455
401887	7229981	Plus	93973-94120
401974	3126777	Plus	85330-85683
402076	8117410	Plus	128316-128627
402182	8575917	Minus	98298-98439
402425	9796347	Minus	50224-50395
402610	9926549	Minus	22955-23124
402695	8569871	Minus	159927-160055
403047	3540153	Minus	59793-59968
403215	7630945	Minus	177270-177971
403418	6862692	Minus	176202-176395
403548	8081591	Minus	38760-39352
403957	8076835	Minus	81649-81754
404070	2996642	Plus	7210-7414,10043-10195
404246	7406725	Plus	82477-82628,82721-82817,82910-83071,83149-83387
404414	7382165	Plus	143127-143398
404605	9212566	Plus	125032-125291
404638	9796751	Minus	99433-99528,100035-100161
404696	9800109	Minus	60037-60144,62675-63081
404767	7882827	Minus	23244-23759
404769	8099713	Minus	175801-176823
404927	7342002	Plus	68690-69563
404958	7407941	Minus	2731-4531
405071	7708797	Minus	11115-11552
405073	7769921	Plus	31419-31774
405138	8576241	Plus	90303-90516
405277	3980473	Plus	23471-23572
405282	3810573	Minus	10482-10689
405334	3135285	Plus	139386-139856
405364	2281075	Minus	48325-48491,49136-49252
405385	6552772	Plus	48332-48454
405535	9795658	Plus	63384-63545
405610	5757553	Minus	71907-72080
405654	4895155	Minus	53624-53759
405691	4508112	Plus	171350-171739
405701	4263751	Plus	93243-93364
405880	6758747	Minus	55673-56287
405913	7712139	Minus	7484-7678
406140	9168231	Minus	49887-50219
406592	4567182	Plus	352560-352963

Table 9A lists about 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). In order to remove gene-specific

background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of tumor samples divided by the 70th percentile of normal body tissue samples, where the 15th percentile of normal body tissues was subtracted from the numerator and denominator

Pkey	ExAccn	UnigeneID	Unigene Title	R1
436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	29.34
406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	25.56
406667	M12523			20.28
414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	18.84
428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	17.38
416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	16.99
446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	16.61
431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S384_H	16.42
437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	15.92
407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	15.84
423541	AA236922	Hs.129778	NM_014471:Homo sapiens serine protease i	15.59
441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	14.54
422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	13.68
432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.23
421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	13.21
453863	X02544	Hs.572	Hs.572:orosomucoid 1	13.06
421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	12.35
436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.11
422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	11.99
418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, LI c	11.87
407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	11.81
424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	11.27
414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	10.82
413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	10.73
450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	10.57
418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.10
423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	9.68
447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	9.44
421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	9.38
406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	9.34
427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (9.18
422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	9.06
406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.02
409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	8.89
424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.53
422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	8.23
452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	8.10
430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	8.05
413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	7.96
406399				7.73
422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	7.71
428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	7.43
417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 1	7.40
435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	7.29
430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.25
451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	7.19
452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	7.18
452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	7.03
424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	7.00
443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	6.92
452194	AI694413	Hs.373599	Hs.373599:EST	6.88
411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.59
422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	6.55
431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	6.49
422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	6.33
412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	6.31
451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I isof	6.30
428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.29
430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	6.28
422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	6.27
444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	6.26
409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	6.23

5	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.23
	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	6.23
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	6.17
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	6.17
	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.17
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.16
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	6.14
10	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	6.13
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis,	6.09
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	6.02
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	5.95
	403220				5.90
15	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	5.88
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	5.87
	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	5.79
	414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	5.79
	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis I	5.77
20	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	5.77
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
	431301	AA502384	Hs.151529	Hs.151529:ESTs	5.71
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	5.71
	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	5.68
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	5.66
25	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	5.61
	431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine deficie	5.57
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	5.55
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.54
30	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.50
	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	5.38
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	5.33
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	5.32
35	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	5.32
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	5.28
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.28
	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	5.27
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.26
40	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	5.25
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	5.25
	436251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	5.25
	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.23
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	5.22
45	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	5.20
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	5.18
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.13
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	5.12
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	5.11
50	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	5.08
	426174	AA547959	Hs.115838	Hs.115838:ESTs	5.07
	403218				5.07
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	5.00
55	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	4.98
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	4.96
	431779	AW971178	Hs.268571	(locuslink)NM_001645:Homo sapiens apolip	4.92
	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif	4.91
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	4.91
	422667	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix prot	4.90
60	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
	424010	AI080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	4.86
	428953	AA306610	Hs.348183	NM_003923:Homo sapiens tumor necrosis fa	4.86
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	4.83
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	4.81
65	428289	M26301	Hs.2253	Hs.2253:complement component 2	4.79
	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	4.78
	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.77
	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	4.72
70	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	4.72
	430680	AW138724	Hs.168974	Hs.168974:ESTs	4.69
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.69
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	4.67
	403221				4.65
75	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	4.65
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	4.64
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	4.64
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.64
	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	4.60
80	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene po	4.60
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	4.60
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	4.59
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	4.57
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.56

	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	4.56
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	4.55
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.55
5	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	4.55
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	4.54
	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.53
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.53
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	4.53
10	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.49
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	4.48
	432378	AI493046	Hs.146133	Hs.146133:ESTs	4.48
	431958	X63629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	4.47
15	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.47
	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.47
	422511	AI076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	4.46
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.46
20	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	4.44
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.44
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.43
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ2182 fi	4.43
	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	4.40
25	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	4.38
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.37
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	4.36
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	4.36
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.35
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	4.33
30	432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	4.33
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	4.33
	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.32
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.32
35	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.30
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.30
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.30
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
40	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.29
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	4.28
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	4.28
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.27
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.27
45	414361	AI086138	Hs.204044	Hs.204044:ESTs	4.26
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.26
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	4.24
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.22
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
50	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	4.19
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.18
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.18
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	4.18
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	4.18
55	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	4.17
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	4.17
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.16
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.15
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.15
60	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3-)glycoprote	4.14
	403219				4.14
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.14
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.14
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
65	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (4.12
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.12
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	4.12
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (4.11
	428698	AA852773	Hs.334838	Hs.334838:KIAA1866 protein	4.10
70	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	4.09
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.07
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.07
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.06
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
75	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.05
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (4.04
	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	4.03
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.03
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.03
	452721	AI269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.02
80	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.01
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.01
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.01
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.01

	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	3.99
	403739				3.99
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.98
	405484				3.98
5	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.98
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	3.97
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.97
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.97
	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.96
10	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.96
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.96
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.95
	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	3.95
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	3.93
15	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.93
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	3.93
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	3.92
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.92
20	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.91
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	3.90
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	3.89
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutas	3.89
	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	3.88
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.88
25	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis,	3.88
	409453	AI885516	Hs.95612	Hs.95612:ESTs	3.87
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.86
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	3.86
	434263	N34895	Hs.79187	Hs.79187:coxsaackie virus and adenovirus	3.85
30	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	3.85
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	3.84
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	3.84
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	3.84
35	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.83
	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.83
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.83
	426514	BE616633	Hs.170195	Hs.170195:bone morphogenetic protein 7 (3.82
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	3.82
40	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	3.81
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	3.81
	409636	AA305729	Hs.18272	(locuslink)NM_030574:Homo sapiens solute	3.81
	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	3.80
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	3.79
45	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	3.79
	405556				3.79
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.79
	400529				3.79
50	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.78
	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	3.78
	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	3.77
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	3.77
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.77
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	3.76
55	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.76
	431350	AI192528	Hs.164537	Hs.164537:ESTs	3.76
	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.75
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	3.75
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	3.74
60	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.74
	413063	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.72
	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	3.72
65	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.72
	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypoth	3.72
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.71
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	3.71
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	3.71
70	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.70
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.70
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.70
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	3.69
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.69
	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	3.69
75	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	3.69
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	3.69
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.68
	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.68
80	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	3.67
	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	3.67
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	3.67
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	3.67
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	3.67

5	452679	Z42387	Hs.83883	(locuslink)NM_020182:Homo sapiens transmembrane protein 7 (CLDN7)	3.66
	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	3.66
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical protein	3.66
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap)	3.66
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.66
10	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.65
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	3.64
	404826				3.63
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	3.63
	409964	AW368226	Hs.67928	Hs.67928:ESTs	3.63
15	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.63
	452098	AI858183		BF755039:QV0-CT0583-181000-428-f07 CT058	3.62
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protein	3.61
	439223	AW238299	Hs.250618	NM_025217:Homo sapiens UL16 binding protein	3.60
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	3.59
20	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	3.59
	436856	AI469355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	3.59
	449667	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.59
	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcino	3.58
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	3.58
25	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cisplatin	3.58
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.57
	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolinic acid phospho	3.57
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	3.57
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility complex	3.56
30	413880	AI680842	Hs.110915	NM_021258:Homo sapiens interleukin 22 receptor	3.55
	421357	AK000609	Hs.103808	NM_017896:Homo sapiens chromosome 20 open reading	3.55
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guaranine	3.55
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	3.55
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.55
35	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.55
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	3.55
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	3.54
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.54
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphatase	3.54
40	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	3.54
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger protein	3.53
	414812	X72755	Hs.77367	NM_002416:Homo sapiens monokine induced	3.53
	423058	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, renal	3.53
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	3.53
45	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation factor	3.53
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	3.52
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.52
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.51
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.51
50	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyrosine	3.51
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell death	3.51
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373	3.51
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF receptor	3.51
	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulated	3.51
55	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisiae	3.51
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	3.51
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976	3.51
	419693	AA133749	Hs.301350	Hs.301350:FXD domain-containing ion transport	3.51
	407971	AI469117	Hs.62918	Hs.62918:CDCC91 cell division cycle 91-like	3.50
60	424865	AF011333	Hs.153563	NM_002349:Homo sapiens lymphocyte antigen	3.50
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.50
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.50
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	3.50
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger protein	3.50
65	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lymphoma	3.50
	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell death	3.50
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyridoxal	3.49
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptide	3.49
	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical protein	3.48
70	407137	T97307			3.48
	454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypothetical	3.48
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433	3.48
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.47
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DNA	3.47
75	413380	AI904232	Hs.75323	Hs.75323:prohibitin	3.46
	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.46
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 open	3.45
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	3.45
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.44
80	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.44
	420319	AW406289	Hs.96593	NM_019034:Homo sapiens ras homolog gene	3.44
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	3.44
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.43
	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inactive)	3.43
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically defined	3.43
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens melanoma transforming	3.43
	428093	AW594506	Hs.104830	Hs.104830:ESTs	3.43

	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	3.43
	400750				3.42
5	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	3.41
	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	3.40
	453857	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.40
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	3.39
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.39
	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	3.39
10	450506	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.39
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	3.38
	440676	NM_004987	Hs.112378	(locuslink)NM_004987:Homo sapiens LIM an	3.38
	400847				3.37
	431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	3.37
15	410199	AW377424	Hs.205126	Hs.205126:Homo sapiens cDNA: FLJ22667 fi	3.37
	432633	AI796390	Hs.210667	Hs.210667:ESTs	3.36
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (3.36
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.36
	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	3.35
20	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	3.35
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.35
	400448				3.35
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.35
25	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	3.35
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.35
	429824	AA296363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.35
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.34
	451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.34
30	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.34
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	3.34
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	3.34
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	3.34
35	421190	U95031	Hs.102482	Hs.102482:mucin 5, subtype B, tracheobro	3.34
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.33
	435975	AL118990	Hs.373554	(locuslink)NM_130786:Homo sapiens alpha-	3.33
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	3.33
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	3.33
40	441128	AA570256	Hs.348504	Hs.348504:hypothetical protein BC014072	3.33
	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	3.33
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens interf	3.32
	410219	T98226	Hs.171952	Hs.171952:occludin	3.32
45	410663	AA194952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.32
	402829				3.32
	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	3.32
	414198	AW050308	Hs.75812	NM_004563:Homo sapiens phosphoenolpyruva	3.32
	443425	AI056776	Hs.133397	Hs.133397:ESTs	3.32
50	436485	X59135	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.31
	410268	AA316181	Hs.61635	NM_012449:Homo sapiens six transmembrane	3.30
	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	3.30
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.30
	421814	L12350	Hs.108623	NM_003247:Homo sapiens thrombospondin 2	3.30
55	432215	AU076609	Hs.2934	NM_001033:Homo sapiens ribonucleotide re	3.30
	409402	AF208234	Hs.695	Hs.695:cystatin B (stefin B)	3.30
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.29
	424408	AI754813	Hs.146428	Hs.146428:collagen, type V, alpha 1	3.29
	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	3.29
60	442821	BE391929	Hs.8752	Hs.8752:transmembrane protein 4	3.29
	459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	3.28
	400846				3.28
	422256	M64673	Hs.1499	NM_005526:Homo sapiens heat shock transc	3.28
65	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	3.28
	432078	BE314877	Hs.24553	(locuslink)NM_022369:Homo sapiens hypoth	3.27
	435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.27
	456534	X91195	Hs.100623	NM_138689:Homo sapiens protein phosphata	3.27
	447335	BE617695	Hs.286192	NM_032192:Homo sapiens protein phosphata	3.27
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	3.27
70	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	3.26
	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	3.26
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	3.26
	457635	AV660976	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.26
	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.25
75	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	3.25
	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-rat simian leuk	3.25
	401179				3.25
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	3.25
80	453323	AF034102	Hs.32951	NM_001532:Homo sapiens solute carrier fa	3.25
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.25
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	3.25
	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.24
	428390	AI640377	Hs.350077	NM_000982:Homo sapiens ribosomal protein	3.24
	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.24

5	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.24
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.24
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.23
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.23
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.23
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.23
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	3.23
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-li	3.23
10	409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multid	3.23
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.23
	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.22
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.22
	413835	AI272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	3.22
15	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.22
	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	3.21
	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.21
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.21
	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.21
20	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.21
	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.21
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.21
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diffe	3.20
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.20
25	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.20
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.20
	413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjuga	3.19
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.19
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.19
30	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfet 4 (SURF4)	3.19
	430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripar	3.19
	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutat	3.18
	434224	AA380731	Hs.84	NM_000206:Homo sapiens interleukin 2 rec	3.18
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associat	3.18
35	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.18
	420531	AI652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.18
	417389	BE260964	Hs.82045	Hs.82045:midkine (neurite growth-promoti	3.18
	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.18
	452700	AI859390	Hs.268940	NM_021259:Homo sapiens transmembrane pro	3.18
40	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.18
	414883	AA926960	Hs.348669	Hs.348669:CDK28 protein kinase 1	3.18
	421743	T35958	Hs.107614	Hs.107614:DKFZP56411171 protein	3.18
	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.17
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
45	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2-I	3.17
	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.17
	449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.17
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
50	428484	AF104032	Hs.184601	(locuslink)NM_003486:Homo sapiens solute	3.16
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.16
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.15
	447151	AI022813	Hs.92679	(locuslink)NM_145754:Homo sapiens kinesi	3.15
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.15
55	410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.15
	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.15
	435886	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.15
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (3.14
	420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.14
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.14
60	450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXD d	3.14
	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
	406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.13
65	426841	AI052358	Hs.131741	Hs.131741:ESTs	3.13
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.12
	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.12
	438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
70	439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.12
	412326	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.12
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.11
	421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.11
	400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.11
75	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.11
	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.11
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.11
	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.11
	433179	AW362945	Hs.162459	Hs.162459:ESTs	3.11
80	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.11
	418641	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.10
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	3.10
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.10
	457670	AF119666	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.10

5	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.10
	428293	BE250944	Hs.183556	Hs.183556:solute carrier family 1 (neur	3.10
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.10
10	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.09
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.09
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.08
	404240				3.08
	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	3.08
15	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.08
	446506	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.08
	402260				3.08
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.08
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.08
20	445937	AI452943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.07
	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.07
	422611	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosy	3.07
	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31350 fis	3.07
	449644	AW980707	Hs.148324	Hs.148324:ESTs	3.07
25	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.07
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.07
	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.07
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.07
30	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.06
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.06
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.06
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.06
	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.06
35	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	3.06
	430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.06
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.06
	412525	AA581439	Hs.152328	Hs.152328:ESTs	3.06
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.05
40	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.05
	408806	AW847814	Hs.75608	Hs.75608:tight junction protein 2 (zona	3.05
	435730	AB020635	Hs.4984	Hs.4984:KIAA0828 protein	3.05
	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.05
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.05
45	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.05
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.05
	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.05
	406363				3.05
	439841	AF038961	Hs.6710	NM_004870:Homo sapiens mannose-P-dolicho	3.05
50	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-fl	3.04
	447966	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	3.04
	439246	AI498072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.04
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.04
	427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.04
55	430281	AI878842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.04
	446620	AA128808	Hs.179902	(locuslink)NM_022109:Homo sapiens CDw92	3.04
	452865	AI924046	Hs.119567	Hs.119567:ESTs, Weakly similar to ALU1_H	3.04
	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.04
	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.04
60	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antimicr	3.03
	417777	AI823763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis	3.03
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.03
	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
65	409430	R21945	Hs.346735	Hs.346735:Homo sapiens, clone IMAGE:3881	3.03
	440659	AF134160	Hs.7327	NM_021101:Homo sapiens claudin 1 (CLDN1)	3.03
	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.03
	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.02
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.02
70	426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.02
	425966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.02
	448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.02
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	3.02
	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.02
75	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	3.02
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.01
	442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.01
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.01
	410293	AK000047	Hs.61960	NM_018992:Homo sapiens hypothetical prot	3.01
80	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.01
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.00
	447032	AK000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.00
	414249	AI797994	Hs.279929	(locuslink)NM_017510:Homo sapiens gp25L2	3.00
	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.00
	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.00
	419452	U33635	Hs.90572	Hs.90572:PTK7 protein tyrosine kinase 7	3.00
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.00

5	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.00
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.00
	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.00
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	2.99
	437763	AA469369	Hs.5831	Hs.5831:tissue inhibitor of metalloprote	2.99
	406865	AI025931	Hs.181357	Hs.181357: laminin receptor 1 (67kD, ribo	2.99
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.99
	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca	2.98
10	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	2.98
	432396	AW295956	Hs.11900	(locuslink)NM_032527:Homo sapiens hypoth	2.98
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	2.98
	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	2.98
	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.98
15	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	2.98
	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	2.98
	452124	AA454220	Hs.61170	Hs.61170:ESTs	2.98
	416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	2.98
	419092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transmem	2.97
20	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	2.97
	437296	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	2.97
	407736	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	2.97
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.97
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	2.97
25	430354	AA954810	Hs.239784	Hs.239784:scribble	2.97
	417079	U65590	Hs.81134	(locuslink)NM_000577:Homo sapiens interl	2.97
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.97
	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prostasin)	2.97
	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	2.96
30	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kinesi	2.96
	412429	AV650262	Hs.75765	NM_002089:Homo sapiens GRO2 oncogene (GR	2.96
	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	2.96
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	2.96
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.96
35	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.96
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	2.96
	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	2.96
	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	2.96
	429597	NM_003816	Hs.2442	Hs.2442:a disintegrin and metalloprotein	2.95
40	421179	U72664	Hs.148495	NM_002810:Homo sapiens proteasome (proso	2.95
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.95
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	2.95
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alpha	2.95
	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	2.95
45	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	2.95
	445720	AL040482	Hs.286173	Hs.286173:KIAA1595 protein	2.95
	429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	2.95
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif	2.94
50	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.94
	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	2.94
	444824	AA843575	Hs.12056	NM_001671:Homo sapiens asialoglycoprotei	2.94
	431629	AU077025	Hs.265827	NM_022873:Homo sapiens interferon, alpha	2.94
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	2.94
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.93
55	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.93
	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	2.93
	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	2.93
	412088	AI689496	Hs.108932	Hs.108932:ESTs	2.93
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.92
60	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	2.92
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.92
	417944	AU077196	Hs.82985	NM_000393:Homo sapiens collagen, type V,	2.92
	428343	AL043021	Hs.12705	(locuslink)NM_145294:Homo sapiens simila	2.92
	435640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	2.92
65	451608	AA384525	Hs.26745	NM_016499:Homo sapiens HSPC244 (MGC:1337	2.92
	434608	AA805443	Hs.179909	NM_024831:Homo sapiens nuclear receptor	2.92
	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	2.91
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	2.91
	438549	BE386801	Hs.21858	Hs.21858:serine (or cysteine) proteinase	2.91
70	440246	W52010	Hs.191379	Hs.191379:ESTs	2.91
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	2.91
	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	2.91
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	2.91
	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	2.91
75	450167	AA446404	Hs.24563	NM_013248:Homo sapiens NTF2-like export	2.91
	408815	AW957974	Hs.25485	(locuslink)NM_024599:Homo sapiens hypoth	2.91
	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	2.91
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	2.91
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	2.91
80	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	2.90
	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	2.90
	405203				2.90
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	2.90
	412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	2.90

	455967	L12535	Hs.75551	(locuslink)NM_012425:Homo sapiens Ras su	2.90
	402104				2.90
	414814	D14697	Hs.77393	(locuslink)NM_002004:Homo sapiens farnes	2.90
5	442739	NM_007274	Hs.8679	(locuslink)NM_007274:Homo sapiens cyto	2.90
	456157	AW979153	Hs.336881	Hs.336881:ESTs	2.90
	429505	AW820035	Hs.278679	NM_033274:Homo sapiens a disintegrin and	2.89
	430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	2.89
	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	2.89
10	438543	AA810141	Hs.192182	Hs.192182:ESTs	2.89
	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	2.89
	441455	AJ271671	Hs.7854	NM_014437:Homo sapiens solute carrier fa	2.89
	420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	2.89
	415674	BE394784	Hs.78596	NM_002797:Homo sapiens proteasome (proso	2.89
15	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.89
	418062	AW630656	Hs.83383	NM_006406:Homo sapiens peroxiredoxin 4 (2.89
	436540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	2.89
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	2.89
	417018	M16038	Hs.80887	Hs.80887:v-yes-1 Yamaguchi sarcoma viral	2.89
20	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	2.88
	429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylation	2.88
	411030	BE387193	Hs.67896	(locuslink)NM_007346:Homo sapiens opioid	2.88
	413822	R08950	Hs.272044	Hs.272044:ESTs, Weakly similar to hypoth	2.88
	438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	2.88
25	409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	2.88
	440490	AW513684	Hs.7218	Hs.7218:acetyl-Coenzyme A synthetase 2 (2.87
	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	2.87
	423570	AW838306	Hs.129819	NM_018344:Homo sapiens hypothetical prot	2.87
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	2.87
30	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	2.87
	442643	U82756	Hs.374973	(locuslink)NM_004697:Homo sapiens PRP4 p	2.87
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	2.87
	421178	BE267994	Hs.102419	Hs.102419:zinc finger protein	2.87
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	2.87
35	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	2.87
	453145	R63438	Hs.183454	Hs.183454:Homo sapiens cDNA FLJ14883 fis	2.86
	427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	2.86
	424732	D80001	Hs.152629	Hs.152629:KIAA0179 protein	2.86
	426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	2.86
40	450273	AW296454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	2.86
	407082	Z47055			2.86
	450038	AA005159	Hs.188489	Hs.188489:ESTs	2.86
	457274	AW674193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.85
	417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rh-related antige	2.85
45	417824	AA084798	Hs.82646	NM_006145:Homo sapiens DnaJ (Hsp40) homo	2.85
	426989	A1815206	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (2.85
	434916	AF161383	Hs.284207	Hs.284207:hypothetical protein BC003515	2.85
	412664	AA421404	Hs.346868	NM_006824:Homo sapiens EBNA1 binding pro	2.85
	414172	AW954324	Hs.75790	(locuslink)NM_002642:Homo sapiens phosph	2.85
50	409504	AA304961	Hs.699	Hs.699:peptidylprolyl isomerase B (cyclo	2.84
	439920	H05430	Hs.288433	NM_016522:Homo sapiens neurotrimin (HNT)	2.84
	418462	BE001596	Hs.85266	Hs.85266:integrin, beta 4	2.84
	442199	BE277633	Hs.372542	NM_004879:Homo sapiens etoposide-induced	2.84
	406710	A1708347	Hs.184014	Hs.184014:ribosomal protein L31	2.84
55	433435	BE545277	Hs.340959	NM_005726:Homo sapiens Ts translation el	2.84
	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3)-glycopro	2.84
	448730	AB032983	Hs.21894	Hs.21894:KIAA1157 protein	2.84
	433027	AF191018	Hs.279923	(locuslink)NM_014366:Homo sapiens putati	2.84
	449090	AK001735	Hs.22983	NM_020121:Homo sapiens UDP-glucose enam	2.84
60	439737	A1751438	Hs.41271	Hs.41271:Homo sapiens mRNA full length i	2.84
	403912				2.84
	423225	AA852604	Hs.125359	NM_006288:Homo sapiens Thy-1 cell surfac	2.84
	458376	AB023179	Hs.9059	Hs.9059:KIAA0962 protein	2.84
	429211	AF052693	Hs.198249	NM_005268:Homo sapiens gap junction prot	2.84
65	452518	AA280722	Hs.24758	Hs.24758:Homo sapiens cDNA FLJ32068 fis	2.84
	418127	BE243982	Hs.83532	(locuslink)NM_002389:Homo sapiens membra	2.83
	448489	A1523875		R45782:Ha616-f Adult heart, Clontech Hom	2.83
	426194	T50872	Hs.2001	NM_001061:Homo sapiens thromboxane A syn	2.83
	422129	AU076635	Hs.1478	NM_000185:Homo sapiens serine (or cystei	2.83
70	437651	BE560672	Hs.13543	(locuslink)NM_145214:Homo sapiens tripar	2.83
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	2.83
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	2.83
	444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methy	2.83
	423323	A1951628	Hs.127007	NM_003740:Homo sapiens potassium channel	2.83
75	439720	A1935202	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.83
	435550	A1224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	2.83
	425907	AA365752	Hs.155965	Hs.155965:ESTs	2.83
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	2.82
	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	2.82
80	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	2.82
	415697	A1365603	Hs.279696	Hs.279696:DKFZP5661024 protein	2.82
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	2.82
	430040	AW503115	Hs.227823	NM_014287:Homo sapiens pM5 protein (PM5)	2.82
	449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	2.82

	427022	AW245839	Hs.173255	NM_004596:Homo sapiens small nuclear rib	2.82
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	2.82
	400845				2.81
5	419501	AW843822	Hs.199961	Hs.199961:ESTs, Weakly similar to hypoth	2.81
	418140	BE613836	Hs.83551	(locuslink)NM_002403:Homo sapiens microf	2.81
	422032	AA476966	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	2.81
	419768	T72104	Hs.93194	Hs.93194:apolipoprotein A-I	2.81
	436673	AF201931	Hs.5268	Hs.5268:zinc finger, DHHC domain contain	2.81
10	421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	2.81
	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	2.81
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	2.81
	433061	AW068033	Hs.296422	(locuslink)NM_025233:Homo sapiens nucleo	2.81
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.81
15	407338	AA773213	Hs.91202	Hs.91202:Homo sapiens cDNA FLJ25946 fis,	2.81
	410240	AL157424	Hs.61289	Hs.61289:synaptojanin 2	2.80
	423880	BE278111	Hs.134200	Hs.134200:DKFZP564C186 protein	2.80
	422098	H03117	Hs.111497	Hs.111497:neuronal protein 17.3	2.80
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	2.80
20	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	2.80
	456602	AA411607	Hs.118964	NM_017660:Homo sapiens hypothetical prot	2.80
	457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	2.80
	426437	BE076537	Hs.169895	Hs.169895:ubiquitin-conjugating enzyme E	2.79
	412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	2.79
25	452695	AW780199	Hs.30327	NM_003668:Homo sapiens mitogen-activated	2.79
	409531	BE384319	Hs.54702	(locuslink)NM_007255:Homo sapiens xylosy	2.79
	448988	Y09763	Hs.22785	NM_021987:Homo sapiens gamma-aminobutyri	2.79
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	2.79
	419846	NM_015977	Hs.285681	NM_032951:Homo sapiens Williams Beuren s	2.79
30	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	2.79
	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Not56 (D. melanog	2.79
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	2.79
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	2.79
	407844	AW073716	Hs.8037	(locuslink)NM_005723:Homo sapiens tetras	2.79
35	448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	2.79
	419235	AW470411	Hs.288433	NM_016522:Homo sapiens neurotrimin (HNT)	2.78
	407754	AA527348	Hs.288967	Hs.288967:Homo sapiens, similar to RIKEN	2.78
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	2.78
	414181	AK000476	Hs.75798	NM_016470:Homo sapiens chromosome 20 ope	2.78
40	418869	AW516555		AA229762:nc49f01.r1 NCLCGAP_Pr3 Homo sa	2.78
	419444	NM_002496	Hs.90443	NM_002496:Homo sapiens NADH dehydrogenas	2.78
	430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	2.78
	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.78
	423013	AW875443	Hs.22209	Hs.22209:secreted modular calcium-bindin	2.78
45	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.78
	447402	H54520	Hs.351327	(locuslink)NM_017828:Homo sapiens hypoth	2.78
	417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	2.78
	422051	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	2.78
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	2.78
50	419757	AA773820	Hs.63970	Hs.63970:ESTs	2.77
	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	2.77
	408044	BE206939	Hs.42287	NM_001952:Homo sapiens E2F transcription	2.77
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	2.77
	451690	AW451469	Hs.209990	Hs.209990:ESTs	2.77
55	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	2.77
	444207	AI565004	Hs.374415	Hs.374415:ESTs	2.77
	417089	H52280	Hs.18612	Hs.18612:Homo sapiens cDNA: FLJ21909 fis	2.77
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	2.77
	425978	BE253927	Hs.24983	Hs.24983:hypothetical protein from EUROI	2.77
60	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	2.77
	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	2.77
	450701	H39960	Hs.288467	Hs.288467:Homo sapiens cDNA FLJ12280 fis	2.77
	412890	T85247	Hs.351875	NM_004374:Homo sapiens cytochrome c oxid	2.77
	415752	BE314524	Hs.78776	NM_012342:Homo sapiens putative transmem	2.76
65	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	2.76
	450770	AA019924	Hs.28803	Hs.28803:ESTs	2.76
	419594	AA013051	Hs.91417	(locuslink)NM_007027:Homo sapiens topois	2.76
	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 I	2.76
	417767	BE242241	Hs.82542	NM_001637:Homo sapiens acyloxyacyl hydro	2.76
70	439968	AA224760	Hs.153	NM_000971:Homo sapiens ribosomal protein	2.76
	426520	BE545684	Hs.343566	Hs.343566:KIAA0251 protein	2.75
	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.75
	445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	2.75
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.75
75	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	2.75
	416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	2.75
	435025	T08990	Hs.4742	Hs.4742:GPAA1P anchor attachment protein	2.75
	421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.75
	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	2.75
80	408196	AL034548	Hs.43627	NM_006943:Homo sapiens SRY (sex determin	2.75
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	2.75
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.75
	451356	AA748418	Hs.33368	Hs.33368:hypothetical protein FLJ11175	2.75
	421643	BE281170	Hs.106357	NM_007126:Homo sapiens valosin-containin	2.74

	423527	AI206965	Hs.105861	(locustlink)NM_024712:Homo sapiens engulf	2.74
	428000	R35145	Hs.291904	Hs.291904:accessory protein BAP31	2.74
	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	2.74
5	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	2.74
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	2.74
	440457	BE387593	Hs.21321	(locuslink)NM_145808:Homo sapiens granul	2.74
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	2.74
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	2.73
10	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	2.73
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	2.73
	421921	H83363	Hs.355993	NM_012456:Homo sapiens translocase of in	2.73
	403217				2.73
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to choli	2.73
15	418733	AA227714	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.73
	400275		Hs.4888	NM_006513:Homo sapiens seryl-tRNA synthe	2.73
	445084	H38914	Hs.250848	Hs.250848:Homo sapiens cDNA FLJ14761 fis	2.73
	411872	AW327356	Hs.90918	Hs.90918:chromosome 11 open reading fram	2.73
	403483				2.73
20	438119	AW963217	Hs.203961	Hs.203961:ESTs, Weakly similar to hypoth	2.73
	422009	AI742845	Hs.110713	NM_003472:Homo sapiens DEK oncogene (DNA	2.73
	436995	AI160015	Hs.125489	Hs.125489:KIAA1961 protein	2.73
	400509				2.73
	429305	AF095727	Hs.287832	Hs.287832:myelin protein zero-like 1	2.73
25	445899	AI263736	Hs.145626	Hs.145626:Homo sapiens, Similar to hypot	2.72
	453557	AA522464	Hs.285996	NM_024956:Homo sapiens hypothetical prot	2.72
	446859	AI494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.72
	424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	2.72
	437809	AL137723	Hs.5855	Hs.5855:Homo sapiens mRNA; cDNA DKFZp434	2.72
30	428466	AF151063	Hs.184456	NM_016486:Homo sapiens hypothetical prot	2.71
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic I	2.71
	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protei	2.71
	429359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metallopro	2.71
	427782	AI956052	Hs.115960	NM_024036:Homo sapiens hypothetical prot	2.71
35	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.71
	400277		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.71
	426263	AI908774	Hs.259785	Hs.259785:carnitine palmitoyltransferase	2.71
	445515	BE388665	Hs.179999	Hs.179999:Homo sapiens, clone IMAGE:3457	2.71
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	2.71
40	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	2.71
	420511	AF052692	Hs.98485	NM_024009:Homo sapiens gap junction prot	2.71
	424965	AW956282	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.71
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	2.71
	412973	L37368	Hs.75104	Hs.75104:RNA binding protein S1, serine-	2.70
45	410113	AW996564	Hs.250824	Hs.250824:Homo sapiens cDNA: FLJ23435 fi	2.70
	413092	AA126856	Hs.118665	Hs.118665:ESTs	2.70
	447096	BE539199	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	2.70
	450493	M93718	Hs.166373	Hs.166373:nitric oxide synthase 3 (endot	2.70
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	2.70
50	450747	AI064821	Hs.129953	Hs.129953:Ewing sarcoma breakpoint regio	2.70
	436042	AF284422	Hs.119178	(locuslink)NM_020246:Homo sapiens cation	2.70
	432981	NM_002733	Hs.3136	Hs.3136:protein kinase, AMP-activated, g	2.70
	431341	AA307211	Hs.251531	NM_002789:Homo sapiens proteasome (proso	2.70
	408204	AA454501	Hs.43666	NM_007079:Homo sapiens protein tyrosine	2.70
55	416770	AW163570	Hs.79768	NM_014740:Homo sapiens KIAA0111 gene pro	2.70
	447507	H59696	Hs.18747	NM_005837:Homo sapiens POP7 (processing	2.70
	424500	AF040704	Hs.149443	(locuslink)NM_007022:Homo sapiens putati	2.69
	414237	BE536554	Hs.278270	Hs.278270:inactive progesterone receptor	2.69
	400231		Hs.169476	NM_002046:Homo sapiens glyceraldehyde-3-	2.69
60	431209	NM_001533	Hs.2730	Hs.2730:heterogeneous nuclear ribonucleo	2.69
	444118	AA458542	Hs.10326	NM_007263:Homo sapiens coatomer protein	2.69
	424608	X80695	Hs.151134	Hs.151134:oxidase (cytochrome c) assembl	2.69
	418546	AA224827		AA224827:nc32g04.s1 NCL CGAP_Pr2 Homo sa	2.69
	440002	AW769844	Hs.111222	Hs.111222:hypothetical protein FLJ22875	2.69
65	449957	D31365	Hs.24220	(locuslink)NM_016479:Homo sapiens scotin	2.69
	432920	U37689	Hs.3128	NM_006232:Homo sapiens polymerase (RNA)	2.69
	450306	AL080080	Hs.24766	NM_030755:Homo sapiens thioredoxin domai	2.69
	429544	BE299343	Hs.2430	NM_005997:Homo sapiens transcription fac	2.68
	428582	BE336699	Hs.185055	Hs.185055:BENE protein	2.68
70	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XIII	2.68
	453905	NM_002314	Hs.36566	NM_016735:Homo sapiens LIM domain kinase	2.68
	418883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	2.68
	420957	X98743	Hs.100555	Hs.100555:DEAD/H (Asp-Glu-Ala-Asp/His) b	2.68
	418187	NM_004604	Hs.83734	NM_004604:Homo sapiens syntaxin 4A (plac	2.68
75	409533	AW969543	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.68
	433184	AA147979	Hs.285005	NM_020243:Homo sapiens translocase of ou	2.68
	455303	AW892049		BE066891:PM3-BT0338-211299-002-e12 BT033	2.68
	452600	AI910842	Hs.103381	Hs.103381:ESTs, Weakly similar to hypoth	2.68
80	415410	AF037332	Hs.278569	NM_014748:Homo sapiens KIAA0064 gene pro	2.67
	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paraoxonase 2 (PO	2.67
	435049	AL122067	Hs.4746	NM_021941:Homo sapiens hypothetical prot	2.67
	450528	NM_014072	Hs.25063	NM_031268:Homo sapiens PRO0461 protein (2.67
	433339	AF019226	Hs.8036	NM_004283:Homo sapiens RAB3D, member RAS	2.67
	408783	AF192522	Hs.47701	NM_013389:Homo sapiens NPC1 (Niemann-Pic	2.67

	451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	2.67
	427716	L38951	Hs.180446	Hs.180446:karyopherin (importin) beta 1	2.67
	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	2.67
5	415116	AA160363	Hs.269956	Hs.269956:ESTs	2.67
	425838	NM_014071	Hs.159613	NM_014071:Homo sapiens nuclear receptor	2.66
	418706	U73524	Hs.87465	NM_006831:Homo sapiens ATP/GTP-binding p	2.66
	410165	BE560228	Hs.71869	NM_013258:Homo sapiens apoptosis-associa	2.66
	410134	U68140	Hs.58927	(locuslink)NM_002533:Homo sapiens nuclea	2.66
10	430066	AI929659	Hs.237825	Hs.237825:signal recognition particle 72	2.66
	425910	AA830797	Hs.184760	NM_005760:Homo sapiens CCAAT-box-binding	2.66
	427954	J03060	Hs.247551	NM_002455:Homo sapiens metaxin 1 (MTX1),	2.66
	439971	W32474	Hs.301746	Hs.301746:Homo sapiens cDNA FLJ37267 fis	2.66
	438449	AK001333	Hs.6216	Hs.6216:DnaJ (Hsp40) homolog, subfamily	2.66
15	435906	AI686379	Hs.110796	(locuslink)NM_020150:Homo sapiens SAR1 p	2.66
	433387	L76528	Hs.3260	NM_000021:Homo sapiens presenilin 1 (Alz	2.66
	447191	NM_014521	Hs.17667	(locuslink)NM_014521:Homo sapiens SH3-do	2.66
	444099	D87432	Hs.10315	NM_003983:Homo sapiens solute carrier fa	2.66
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	2.66
20	418529	AW005695	Hs.250897	Hs.250897:TRK-fused gene	2.65
	426025	AW138330	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.65
	420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	2.65
	408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	2.65
	444395	N66148	Hs.11125	(locuslink)NM_014041:Homo sapiens signal	2.65
25	431222	X56777	Hs.273790	NM_007155:Homo sapiens zona pellucida gl	2.65
	406790	AA293303	Hs.356342	Hs.356342:ESTs, Highly similar to 211320	2.65
	440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	2.65
	416526	H61082	Hs.14743	Hs.14743:ESTs	2.65
	413995	BE048146	Hs.75671	NM_004603:Homo sapiens syntaxin 1A (brai	2.65
30	424908	AW513963	Hs.39143	Hs.39143:hypothetical protein MGC13125	2.65
	442110	AF113008	Hs.8102	NM_001023:Homo sapiens ribosomal protein	2.65
	452882	AW972990	Hs.196270	NM_030780:Homo sapiens folate transporte	2.65
	406862	AW150807	Hs.356262	Hs.356262:ESTs, Highly similar to A31233	2.64
	451295	AI557212	Hs.17132	Hs.17132:ESTs	2.64
35	448428	AF282874	Hs.21201	NM_015480:Homo sapiens necln 3 (DKFZP56	2.64
	426611	BE176050	Hs.171271	NM_001904:Homo sapiens catenin (cadherin	2.64
	426216	N77630	Hs.13895	Hs.13895:Homo sapiens cDNA FLJ11654 fis,	2.64
	407223	H96850		H96850:yo03b12.s1 Soares melanocyte 2NbH	2.64
	427725	U66839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	2.64
40	420157	AA857991	Hs.123106	Hs.123106:ESTs	2.64
	428471	X57348	Hs.184510	Hs.184510:stratifin	2.64
	451544	AK000429	Hs.26570	NM_017814:Homo sapiens hypothetical prot	2.64
	413245	BE244334	Hs.75249	Hs.75249:ADP-ribosylation factor-like 6	2.64
	415020	BE249915	Hs.293533	Hs.293533:Homo sapiens cDNA FLJ37093 fis	2.64
45	437193	BE259190	Hs.289721	Hs.289721:growth arrest-specific 5	2.64
	418684	U82987	Hs.87246	NM_014417:Homo sapiens BCL2 binding comp	2.64
	410668	BE379794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	2.64
	436183	AI146327	Hs.334802	(locuslink)NM_024718:Homo sapiens hypoth	2.64
	441226	BE563042	Hs.118620	Hs.118620:hypothetical protein BC007882	2.64
50	432788	AA521091	Hs.178499	Hs.178499:HSPC063 protein	2.64
	432746	AA564512	Hs.372775	Hs.372775:Homo sapiens, clone IMAGE:3946	2.64
	450377	AB033091	Hs.355925	Hs.355925:KIAA1265 protein	2.64
	434633	AI189587	Hs.120915	Hs.120915:ESTs	2.64
	424707	BE061914	Hs.10844	Hs.10844:leucine-rich alpha-2-glycoprote	2.64
55	427600	AW630918	Hs.179774	Hs.179774:proteasome (prosome, macropain	2.63
	446522	NM_003876	Hs.15196	NM_003876:Homo sapiens putative receptor	2.63
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	2.63
	410701	AF198620	Hs.10283	NM_005105:Homo sapiens RNA binding motif	2.63
	410182	NM_001983	Hs.59544	NM_001983:Homo sapiens excision repair c	2.63
60	406716	AW148546	Hs.169476	Hs.169476:glyceraldehyde-3-phosphate deh	2.63
	430308	BE540865	Hs.238990	NM_004064:Homo sapiens cyclin-dependent	2.63
	431074	BE072772	Hs.8997	Hs.8997:Sad1 unc-84 domain protein 1	2.63
	412867	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	2.63
	440524	R71264	Hs.16798	Hs.16798:Homo sapiens mRNA; cDNA DKFZp56	2.63
65	435968	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens integr	2.63
	422672	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	2.63
	447528	AI612027	Hs.76277	NM_138393:Homo sapiens hypothetical prot	2.63
	406774	AW518383	Hs.177592	Hs.177592:ribosomal protein, large, P1	2.63
	439755	AW748482	Hs.77873	Hs.77873:B7 homolog 3	2.63
70	435311	W86610	Hs.185736	Hs.185736:ESTs	2.63
	428699	AW578252	Hs.190161	Hs.190161:LR8 protein	2.62
	410678	BE540516	Hs.378825	Hs.378825:Homo sapiens cDNA FLJ37850 fis	2.62
	414839	X63692	Hs.77462	(locuslink)NM_001379:Homo sapiens DNA (c	2.62
	443217	NM_001545	Hs.9078	Hs.9078:immature colon carcinoma transcr	2.62
75	448749	AW859679	Hs.21902	Hs.21902:Homo sapiens clone 25237 mRNA s	2.62
	450009	AI399947	Hs.166486	Hs.166486:Homo sapiens cDNA FLJ11432 fis	2.62
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	2.62
	442232	AI357813	Hs.337460	Hs.337460:ESTs, Highly similar to HYEP_H	2.62
	419625	U91616	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.62
80	416114	AI695549	Hs.183868	Hs.183868:glucuronidase, beta	2.62
	439437	AI207788	Hs.343628	Hs.343628:sialyltransferase 4B (beta-gal	2.61
	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	2.61
	443142	AI696513	Hs.108705	Hs.108705:protein phosphatase 2 (formerl	2.61
	426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.61

	419667	AJ077005	Hs.92208	NM_003815:Homo sapiens a disintegrin and	2.61
	415072	BE253687	Hs.77876	Hs.77876:hypothetical gene MGC19595	2.61
	406670	W79632	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.61
	403399				2.61
5	419579	W49529	Hs.296200	NM_023948:Homo sapiens hypothetical prot	2.61
	437202	AA326110	Hs.374481	Hs.374481:ESTs, Weakly similar to T34549	2.61
	414020	NM_002984	Hs.75703	NM_002984:Homo sapiens small inducible c	2.61
	421295	AW081061	Hs.103180	Hs.103180:DC2 protein	2.61
	446488	AB037782	Hs.15119	Hs.15119:KIAA1361 protein	2.61
10	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	2.60
	448204	AI475124	Hs.170561	Hs.170561:ESTs	2.60
	449175	AJ005892	Hs.23170	(locuslink)NM_012280:Homo sapiens FlsJ h	2.60
	411201	T74588	Hs.8509	Hs.8509:ESTs, Weakly similar to C3HU com	2.60
15	424805	AF230904	Hs.153260	NM_031892:Homo sapiens SH3-domain kinase	2.60
	425421	L11669	Hs.157145	Hs.157145:tetracycline transporter-like	2.60
	422739	H20106	Hs.119591	(locuslink)NM_004069:Homo sapiens adapt	2.60
	450858	C18458	Hs.25597	Hs.25597:elongation of very long chain f	2.59
	443195	BE148235	Hs.193063	Hs.193063:Homo sapiens cDNA FLJ14201 fis	2.59
	430504	H52761	Hs.44095	Hs.44095:cyclin M3	2.59
20	439578	AW263124	Hs.350547	NM_024665:Homo sapiens nuclear receptor	2.59
	416041	AA345547	Hs.53263	(locuslink)NM_024647:Homo sapiens nucleo	2.59
	451920	AA224483	Hs.27239	Hs.27239:zinc finger, DHHC domain contai	2.59
	414163	BE262310	Hs.75782	NM_001521:Homo sapiens general transcrip	2.59
25	422140	BE295918	Hs.112193	(locuslink)NM_025259:Homo sapiens chromo	2.59
	452817	AA322859	Hs.284275	Hs.284275:p21 (CDKN1A)-activated kinase	2.59
	413353	AW293542	Hs.75309	Hs.75309:eukaryotic translation elongati	2.59
	421700	BE515018	Hs.107014	NM_016641:Homo sapiens membrane interact	2.59
	410801	BE275469	Hs.66493	NM_016430:Homo sapiens Down syndrome cri	2.59
30	440511	AF132959	Hs.7236	NM_015953:Homo sapiens eNOS interacting	2.59
	407887	AA579668	Hs.41072	(locuslink)NM_004568:Homo sapiens serine	2.59
	425356	BE244879	Hs.155939	NM_005541:Homo sapiens inositol polyphos	2.59
	408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	2.59
	417952	AI192838	Hs.173135	Hs.173135:dual-specificity tyrosine-(Y)-	2.59
35	433053	BE301909	Hs.279952	NM_015917:Homo sapiens glutathione S-tra	2.59
	450935	BE514743	Hs.379039	NM_005851:Homo sapiens tumor suppressor	2.59
	417891	W79410	Hs.82887	(locuslink)NM_021959:Homo sapiens protei	2.59
	438364	AK000860	Hs.6191	NM_020441:Homo sapiens coronin, actin-bi	2.59
	430976	AA505112	Hs.282990	NM_033550:Homo sapiens chromosome 20 ope	2.58
40	444838	AV651680	Hs.208558	Hs.208558:ESTs	2.58
	416435	AI431301	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.58
	415444	BE247295	Hs.78452	Hs.78452:solute carrier family 20 (phosp	2.58
	452222	AW806287	Hs.21432	Hs.21432:SEX gene	2.58
	400541				2.58
45	444309	U83236	Hs.10803	Hs.10803:calcium and integrin binding 1	2.58
	416116	H51847	Hs.99858	Hs.99858:ribosomal protein L7a	2.58
	418629	BE247550	Hs.86859	(locuslink)NM_005310:Homo sapiens growth	2.58
	432996	AF105025	Hs.279901	Hs.279901:PTD009 protein	2.57
	426781	AL048967	Hs.172207	(locuslink)NM_007363:Homo sapiens non-PO	2.57
50	452636	BE615074	Hs.145279	Hs.145279:SET translocation (myeloid leu	2.57
	406851	AA609784	Hs.352392	Hs.352392:major histocompatibility compl	2.57
	447674	BE270640	Hs.19192	NM_001798:Homo sapiens cyclin-dependent	2.57
	445647	AV654627	Hs.271808	Hs.271808:Homo sapiens cDNA FLJ38018 fis	2.57
	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	2.57
	402861				2.57
55	450069	AI698139	Hs.202093	Hs.202093:ESTs	2.57
	414029	BE297731	Hs.75709	NM_002355:Homo sapiens mannose-6-phospha	2.57
	427700	AA262294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.57
	449961	AW265634	Hs.133100	Hs.133100:ESTs	2.56
60	449378	AW664026	Hs.59892	Hs.59892:ESTs, Weakly similar to alpha 5	2.56
	442599	AF078037	Hs.324051	(locuslink)NM_006663:Homo sapiens RelA-a	2.56
	448633	AA311426	Hs.21635	NM_001070:Homo sapiens tubulin, gamma 1	2.56
	416078	AL034349	Hs.79005	NM_002844:Homo sapiens protein tyrosine	2.56
	428044	AA093322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	2.56
65	451564	AU076698	Hs.132760	(locuslink)NM_001467:Homo sapiens glucos	2.56
	457601	AF041429	Hs.284265	(locuslink)NM_145169:Homo sapiens simila	2.56
	439630	AA313607	Hs.58633	Hs.58633:Homo sapiens cDNA: FLJ22145 fis	2.55
	419587	S62907	Hs.91343	NM_000807:Homo sapiens gamma-aminobutyri	2.55
	448279	BE250564	Hs.283655	Hs.283655:lysophospholipase II	2.55
	453350	AI917771	Hs.61790	(locuslink)NM_024658:Homo sapiens import	2.55
70	423720	AL044191	Hs.23388	NM_030817:Homo sapiens hypothetical prot	2.55
	400237		Hs.83347	NM_001087:Homo sapiens angio-associated,	2.55
	420856	BE513294	Hs.205736	Hs.205736:KIAA1978 protein	2.55
	421541	NM_003942	Hs.105584	Hs.105584:ribosomal protein S6 kinase, 9	2.55
75	434848	BE256304	Hs.32148	NM_018445:Homo sapiens AD-015 protein (L	2.55
	424488	AK000413	Hs.149227	(locuslink)NM_017806:Homo sapiens hypoth	2.55
	449089	D78850	Hs.250465	Hs.250465:Homo sapiens mRNA; cDNA DKFZp4	2.55
	430053	AF052155	Hs.227949	NM_030673:Homo sapiens SEC13-like 1 (S.	2.55
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	2.55
	407755	AI151353	Hs.29742	Hs.29742:Homo sapiens cDNA FLJ32147 fis,	2.55
80	446673	NM_016361	Hs.15871	NM_016361:Homo sapiens LPAP for lysophos	2.55
	411766	AA399871	Hs.71969	Hs.71969:Homo sapiens mRNA; cDNA DKFZp66	2.55
	415198	AW009480	Hs.943	Hs.943:natural killer cell transcript 4	2.55
	436495	BE258948	Hs.290874	Hs.290874:Homo sapiens, clone MGC:31984	2.55

5	417785	X59812	Hs.82568	NM_000784:Homo sapiens cytochrome P450,	2.55
	443358	H65417	Hs.17757	(locuslink)NM_021622:Homo sapiens plecks	2.55
	452349	AB028944	Hs.29189	Hs.29189:ATPase, Class VI, type 11A	2.55
	427721	AI582843	Hs.180455	NM_005053:Homo sapiens RAD23 homolog A (2.54
	407559	AA313352	Hs.280858	Hs.280858:Homo sapiens cDNA FLJ32370 fis	2.54
10	413426	U88837	Hs.75354	Hs.75354:GCN1 general control of amino-a	2.54
	425465	L18964	Hs.1904	Hs.1904:protein kinase C, iota	2.54
	444152	AI125694	Hs.149305	Hs.149305:hypothetical protein MGC2603	2.54
	451820	AW058357	Hs.199248	NM_000958:Homo sapiens prostaglandin E r	2.54
	441356	BE384361	Hs.182885	(locuslink)NM_004556:Homo sapiens nuclea	2.54
15	444410	BE387360	Hs.33719	Hs.33719:Homo sapiens, similar to data s	2.54
	415200	AL040328	Hs.78202	NM_003072:Homo sapiens SWI/SNF related,	2.54
	403955				2.54
	430361	AI033965	Hs.239926	Hs.239926:sterol-C4-methyl oxidase-like	2.54
	432401	NM_013330	Hs.274479	NM_013330:Homo sapiens NME7 (NME7), mRNA	2.54
20	446719	W39500	Hs.301872	Hs.301872:hypothetical protein MGC4840	2.54
	439941	AI392640	Hs.18272	NM_030674:Homo sapiens solute carrier fa	2.54
	436685	W28661	Hs.5288	Hs.5288:Homo sapiens mRNA; cDNA DKFZp434	2.54
	424522	AL134847	Hs.149957	Hs.149957:ribosomal protein S6 kinase, 9	2.54
	442904	AW575008	Hs.11355	Hs.11355:thymopoietin	2.54
25	422605	H16646	Hs.118666	Hs.118666:hypothetical protein PP591	2.54
	442069	AW664144	Hs.297007	Hs.297007:Homo sapiens cDNA FLJ32174 fis	2.54
	447362	AW176120	Hs.9061	NM_024099:Homo sapiens hypothetical prot	2.53
	416305	AU076628	Hs.79187	NM_001338:Homo sapiens coxsackie virus a	2.53
	422624	BE616678	Hs.76152	NM_006854:Homo sapiens KDEL (Lys-Asp-Glu	2.53
30	447298	BE617527	Hs.239818	NM_006219:Homo sapiens phosphoinositide-	2.53
	412833	AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.53
	404854				2.53
	415761	AA132666	Hs.78802	(locuslink)NM_002093:Homo sapiens glycog	2.53
	431104	AW970859	Hs.313503	Hs.313503:ESTs	2.53
35	439180	AI393742	Hs.199067	Hs.199067:v-erb-b2 erythroblastic leukem	2.53
	424250	AF073310	Hs.143648	NM_003749:Homo sapiens insulin receptor	2.53
	452878	AW081128	Hs.246374	Hs.246374:Homo sapiens cDNA FLJ31250 fis	2.53
	415742	BE410243	Hs.78769	NM_003249:Homo sapiens thimet oligopepti	2.53
	404140				2.53
40	407255	AA012992	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.53
	422509	AA258513	Hs.117865	Hs.117865:solute carrier family 17 (anio	2.53
	434866	AW002565	Hs.355460	Hs.355460:Homo sapiens cDNA: FLJ21763 fi	2.53
	429743	AA804398	Hs.288995	(locuslink)NM_017961:Homo sapiens hypoth	2.53
	433047	M86135	Hs.279946	NM_004990:Homo sapiens methionine-tRNA s	2.53
45	418945	BE246762	Hs.89499	Hs.89499:arachidonate 5-lipoxygenase	2.52
	445926	AF054284	Hs.334826	NM_012433:Homo sapiens splicing factor 3	2.52
	411353	BE383533	Hs.279784	Hs.279784:prolactin regulatory element b	2.52
	448252	BE622791	Hs.12199	NM_030577:Homo sapiens hypothetical prot	2.52
	447365	BE383676	Hs.334	(locuslink)NM_005435:Homo sapiens Rho gu	2.52
50	414844	AA296874	Hs.77494	NM_080916:Homo sapiens deoxyguanosine ki	2.52
	444025	AA578364	Hs.349093	NM_015945:Homo sapiens ovarian cancer ov	2.52
	416149	AA311965	Hs.79058	NM_003168:Homo sapiens suppressor of Ty	2.52
	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis,	2.52
	437952	D63209	Hs.5944	NM_014585:Homo sapiens solute carrier fa	2.52
55	445625	BE246743	Hs.353181	(locuslink)NM_025092:Homo sapiens hypoth	2.52
	431565	AF161470	Hs.260622	Hs.260622:butyrate-induced transcript 1	2.52
	410179	W27723	Hs.59498	(locuslink)NM_003718:Homo sapiens cell d	2.52
	431476	BE612705	Hs.256697	(locuslink)NM_005340:Homo sapiens histid	2.52
	406672	M26041	Hs.198253	(locuslink)NM_002122:Homo sapiens major	2.52
60	418180	BE618087	Hs.83724	Hs.83724:hypothetical protein MGC5466	2.52
	428248	AI126772	Hs.40479	Hs.40479:Homo sapiens cDNA FLJ25802 fis,	2.52
	419935	AB020980	Hs.93832	Hs.93832:putative membrane protein	2.52
	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.52
	426691	NM_006201	Hs.171834	(locuslink)NM_006201:Homo sapiens PCTAIR	2.51
65	408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	2.51
	456266	L29073	Hs.198726	NM_003651:Homo sapiens cold shock domain	2.51
	428921	Z43809	Hs.194638	Hs.194638:polymerase (RNA) II (DNA direc	2.51
	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxyribonuclease	2.51
	422607	Z45471	Hs.118684	NM_006923:Homo sapiens stromal cell-deri	2.51
70	421846	AA017707	Hs.1432	NM_002743:Homo sapiens protein kinase C	2.51
	414874	D26351	Hs.77515	NM_002224:Homo sapiens inositol 1,4,5-tr	2.51
	432956	AL037895	Hs.279861	NM_015959:Homo sapiens CGI-31 protein (L	2.51
	438393	AA351815	Hs.50740	Hs.50740:Homo sapiens mRNA; cDNA DKFZp76	2.51
	418360	AW296974	Hs.84264	NM_006401:Homo sapiens acidic (leucine-r	2.50
75	401061				2.50
	426559	AB001914	Hs.170414	Hs.170414:paired basic amino acid cleavi	2.50
	412204	AI125507	Hs.24937	Hs.24937:transformer-2 alpha (htra-2 alp	2.50
	448950	AF288687	Hs.9275	NM_020410:Homo sapiens CGI-152 protein (2.50
	409936	AK001691	Hs.57655	(locuslink)NM_018234:Homo sapiens duduli	2.50
80	414675	R79015	Hs.288968	Hs.288968:RAB22A, member RAS oncogene fa	2.50
	409983	D50922	Hs.57729	(locuslink)NM_012289:Homo sapiens Kelch-	2.50
	450914	AI743761	Hs.142528	Hs.142528:ESTs	2.50
	444630	AI753230	Hs.323562	(locuslink)NM_032121:Homo sapiens hypoth	2.50
	401353				2.50
80	441680	AW444598	Hs.7940	(locuslink)NM_021159:Homo sapiens RAP1,	2.50
	408680	AA876469		AA876469:oe48b04.s1 NCL_CGAP_Pr25 Homo s	2.50
	449163	AW161356	Hs.23119	NM_003492:Homo sapiens chromosome X open	2.50

432975	AA331517	Hs.286055	Hs.286055:chimerin (chimaerin) 2	2.50
430600	AW950967	Hs.274348	NM_004639:Homo sapiens HLA-B associated	2.50
407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	2.50

5 TABLE 9B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

10

Pkey	CAT Number	Accession
406685	0_0	M18728
452098	161393_1	BC028348 BF772844 H83066 AW817969 H90985 BF755039 AI858183
451129	1495511_1	BE072881 AI762181 BE072946
15 459306	223120_-4	AW578452
448489	2189115_1	R45782 R45781
418869	12789_14	AA229762 AA230035
418546	242836_1	T59708 AA224827 T59843 BE156903
20 455303	1152492_1	BE066891 BE066895 AW892049 BE066897 BE903884
406860	0_0	AA876469

TABLE 9C

25 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

30

Pkey	Ref	Strand	Nt_position
406399	9256288	Minus	63448-63554
403220	7630969	Plus	64338-64517
403218	7630969	Plus	58039-58149
35 403221	7630969	Plus	66294-66438,66936-67124
403219	7630969	Plus	61858-61995
403739	7630882	Plus	44563-44766,48209-48483,52255-52495
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
40 405556	1552511	Plus	163497-163623,164715-164968,165369-16550
400529	9796988	Plus	138232-138423
404826	6572184	Plus	47726-48046
400750	8119067	Plus	198991-199168,199316-199548
400847	9188605	Plus	44643-44835
45 400448	9887687	Minus	177372-177674
402829	8918414	Plus	101532-101852,102006-102263
400846	9188605	Plus	39310-39474
401179	9438647	Plus	113477-113893
404240	5002624	Minus	116132-116407,116653-116922
50 402260	3399665	Minus	113765-113910,115653-115765,116808-11694
406363	9256114	Plus	14403-14602,17000-17147,17241-17368
405203	7230116	Plus	125295-125463
402104	8119072	Plus	122409-122600
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
400845	9188605	Plus	34428-34612
55 403217	7630969	Plus	54089-54163,55427-55623
403483	9966188	Minus	144546-144854
400509	9796539	Minus	157909-158430
403399	6684178	Plus	61841-62145,62367-62756
400541	7574902	Plus	126235-126380,126478-126597
60 402861	2814366	Minus	14933-15231,15387-15627
403955	7770475	Minus	54527-54740
404854	7143420	Plus	14260-14537
404140	9843520	Plus	37761-38147
65 401061	3242744	Minus	99468-99549,100707-100848,100918-101107,
401353	9931296	Minus	50831-51352

70 Table 10A lists about 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium). These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 85th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

75

TABLE 10A: 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

80

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
5	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	15.54
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	14.52
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	14.04
	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	14.02
	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease i	13.72
10	406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	13.44
	418406	X73501	Hs.84905	Hs.84905:cytokeratin 20	12.70
	406667	M12523			12.42
	416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	11.98
	437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	11.58
15	422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	11.50
	418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, LI c	10.16
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.11
	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	10.01
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	9.77
20	441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	9.69
	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	9.48
	453863	X02544	Hs.572	Hs.572:orosomucoid 1	9.20
	407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	9.18
	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	9.04
25	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	8.69
	430178	AW449612	Hs.152475	Hs.152475:ESTs	8.51
	423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	8.43
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	8.17
	409583	U33317	Hs.711	NM_001926:Homo sapiens defensin, alpha 6	8.12
30	431777	AA570296	Hs.307047	NM_032579:Homo sapiens colon and small i	8.08
	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	8.06
	427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (7.95
	436624	T64297	Hs.351719	NM_001443:Homo sapiens fatty acid bindin	7.74
	410407	X66839	Hs.63287	NM_001216:Homo sapiens carbonic anhydras	7.46
35	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	7.41
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	7.40
	412374	X01388	Hs.73849	NM_000040:Homo sapiens apolipoprotein C-	7.34
	407244	M10014			7.31
	419741	NM_007019	Hs.93002	Hs.93002:ubiquitin-conjugating enzyme E2	7.31
40	406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	7.26
	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	7.21
	404519				7.18
	413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	7.13
	422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	7.10
45	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	7.02
	430828	AI763257	Hs.86327	Hs.86327:homeo box B9	6.83
	433927	AI557019	Hs.116467	NM_032391:Homo sapiens small nuclear pro	6.81
	406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	6.78
	423538	AW603823	Hs.146268	Hs.146268:ESTs, Weakly similar to C71400	6.53
50	434206	AW136973	Hs.362915	Hs.362915:Homo sapiens cDNA FLJ34876 fis	6.37
	409041	AB033025	Hs.50081	Hs.50081:KIAA1199 protein	6.33
	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	6.19
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.19
	436330	NM_004413	Hs.109	NM_004413:Homo sapiens dipeptidase 1 (re	6.01
55	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	6.00
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	5.97
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	5.94
	420923	AF097021	Hs.273321	NM_006418:Homo sapiens differentially ex	5.94
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	5.90
60	420802	U22376	Hs.1334	NM_005375:Homo sapiens v-myb myeloblasto	5.89
	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	5.89
	431727	AW293464	Hs.162031	Hs.162031:ESTs	5.85
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	5.84
	432023	AW273128	Hs.300268	Hs.300268:EST	5.75
65	447033	AI357412	Hs.157601	Hs.157601:ESTs	5.69
	411734	AW374954	Hs.71779	Hs.71779:ESTs, Weakly similar to S24C_AR	5.69
	406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	5.55
	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	5.48
	443247	BE614387	Hs.333893	Hs.333893:cell division cycle associated	5.45
70	409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	5.44
	449388	H53191	Hs.36723	Hs.36723:ESTs, Weakly similar to C05G5.5	5.38
	428046	AW812795	Hs.337534	Hs.337534:Homo sapiens cDNA FLJ25241 fis	5.38
	433013	AI697890	Hs.127337	(locuslink)NM_004655:Homo sapiens axin 2	5.38
	419079	AW014836	Hs.18844	Hs.18844:ESTs	5.37
75	428355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	5.35
	422956	BE545072	Hs.122579	(locuslink)NM_018098:Homo sapiens epithe	5.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	5.30
	450543	AI394037	Hs.170296	Hs.170296:Homo sapiens cDNA: FLJ22090 fi	5.30
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	5.30
80	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	5.28
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	5.28
	427722	AK000123	Hs.180479	NM_017671:Homo sapiens chromosome 20 ope	5.26
	430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	5.26
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	5.21
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	5.16

5	447208	BE315291	Hs.237971	NM_024096:Homo sapiens hypothetical prot	5.14
	430207	AW079559	Hs.152258	Hs.152258:ESTs	5.12
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	5.12
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.07
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	5.06
10	452194	AI694413	Hs.373599	Hs.373599:EST	5.01
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	4.99
	406399				4.98
	403220				4.94
	408380	AF123050	Hs.44532	NM_006398:Homo sapiens ubiquitin D (UBD)	4.92
15	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	4.92
	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	4.85
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	4.84
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	4.81
	441377	BE218239	Hs.202656	Hs.202656:ESTs	4.81
20	444666	BE293347	Hs.11638	(locuslink)NM_016234:Homo sapiens fatty-	4.80
	415701	NM_003878	Hs.78619	(locuslink)NM_003878:Homo sapiens gamma-	4.80
	419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	4.80
	455630	AV655701	Hs.75183	NM_000773:Homo sapiens cytochrome P450,	4.78
	422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	4.78
25	423337	NM_004655	Hs.127337	NM_004655:Homo sapiens axin 2 (conductin	4.75
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epi-regulin (EREG)	4.73
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	4.70
	423936	U77629	Hs.135639	NM_005170:Homo sapiens achaete-scute com	4.70
	404661				4.68
30	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	4.67
	420005	AW271106	Hs.133294	Hs.133294:ESTs	4.66
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I isofo	4.61
	427506	AK000134	Hs.179100	NM_017678:Homo sapiens hypothetical prot	4.60
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	4.59
35	453884	AA355925	Hs.36232	NM_021067:Homo sapiens KIAA0186 gene pro	4.55
	431301	AA502384	Hs.151529	Hs.151529:ESTs	4.54
	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	4.54
	449032	AA045573	Hs.22900	NM_004289:Homo sapiens nuclear factor (e	4.54
	434540	NM_016045	Hs.3945	NM_016045:Homo sapiens chromosome 20 ope	4.54
40	407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	4.53
	458748	AI381530	Hs.371132	Hs.371132:ESTs	4.53
	408298	AI745325	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.51
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	4.50
	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	4.49
45	425371	D49441	Hs.155591	NM_005823:Homo sapiens mesothelin (MSLN)	4.49
	451917	AW391351	Hs.50820	Hs.50820: hypothetical cardiac/skeletal m	4.46
	432867	AW016936	Hs.233364	Hs.233364:ESTs	4.44
	419559	Y07828	Hs.91096	NM_007028:Homo sapiens tripartite motif-	4.44
	430294	AI538226	Hs.32976	(locuslink)NM_004485:Homo sapiens guanin	4.42
50	411248	AA551538	Hs.69321	Hs.69321:KIAA1359 protein	4.39
	402496				4.38
	430937	X53463	Hs.2704	NM_002083:Homo sapiens glutathione perox	4.37
	434414	AI798376		AF134163:Homo sapiens Human endogenous r	4.36
	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	4.35
55	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.33
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	4.33
	450531	AW301032	Hs.203800	Hs.203800:ESTs	4.33
	403055				4.31
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	4.31
60	400965				4.30
	430204	AA618335	Hs.356664	Hs.356664: hypothetical protein FLJ32334	4.29
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	4.29
	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:225881	4.28
	430832	AI073913	Hs.100686	Hs.100686:anterior gradient protein 3	4.28
65	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	4.28
	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	4.27
	414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	4.27
	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	4.27
	439211	AI890347	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.27
70	459299	BE094291	Hs.155651	NM_021784:Homo sapiens hepatocyte nuclea	4.25
	449720	AA311152	Hs.288708	(locuslink)NM_025113:Homo sapiens hypoth	4.24
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	4.24
	421777	BE562088	Hs.108196	NM_016095:Homo sapiens HSPC037 protein (4.21
	419395	BE268326	Hs.90280	Hs.90280:5-aminimidazole-4-carboxamide	4.20
75	443211	AI128388	Hs.143655	Hs.143655:ESTs	4.20
	403218				4.20
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	4.19
	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	4.19
	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	4.19
80	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif-	4.18
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	4.18
	440869	NM_014297	Hs.7486	NM_014297:Homo sapiens protein expressed	4.17
	414075	U11862	Hs.75741	NM_001091:Homo sapiens amiloride binding	4.17
	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	4.16
	440409	AW294316	Hs.125608	Hs.125608:ESTs	4.16
	445564	AB028957	Hs.12896	Hs.12896:KIAA1034 protein	4.16
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	4.12

	401866				4.11
	431611	U58766	Hs.264428	Hs.264428:tissue specific transplantatio	4.10
	430187	AI799909	Hs.158989	Hs.158989:Homo sapiens cDNA FLJ37936 fis	4.10
5	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	4.08
	449281	AI808699	Hs.162717	NM_032756:Homo sapiens hypothetical prot	4.08
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	4.08
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	4.06
	435066	BE261750	Hs.4747	NM_001363:Homo sapiens dyskeratosis cong	4.05
10	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	4.04
	403221				4.04
	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.03
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	4.03
	431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine deficie	4.01
15	439759	AL359055	Hs.67709	Hs.67709:Homo sapiens mRNA full length i	4.00
	441362	BE614410	Hs.23044	NM_080668:Homo sapiens similar to RIKEN	3.99
	417900	BE250127	Hs.82906	Hs.82906:CD20 cell division cycle 20 ho	3.99
	428987	NM_004751	Hs.194710	NM_004751:Homo sapiens glucosaminyl (N-a	3.99
	456977	AK000252	Hs.169758	NM_017723:Homo sapiens hypothetical prot	3.99
20	445919	T53519	Hs.334692	Hs.334692:hypothetical protein MGC14141	3.98
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	3.98
	422827	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	3.97
	422363	T55979	Hs.115474	NM_002915:Homo sapiens replication facto	3.97
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	3.97
25	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	3.96
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	3.96
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	3.95
	432407	AA221036		AF134164:Homo sapiens Human endogenous r	3.95
	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	3.94
30	408494	AA554714	Hs.187578	Hs.187578:Homo sapiens cDNA FLJ11639 fis	3.94
	412610	X90908	Hs.74126	NM_001445:Homo sapiens fatty acid bindin	3.94
	433323	AA805132	Hs.159142	Hs.159142:lunatic fringe homolog (Drosop	3.94
	422515	AW500470	Hs.117950	Hs.117950:phosphoribosylaminoimidazole c	3.92
	436543	NM_002212	Hs.5215	Hs.5215:integrin beta 4 binding protein	3.91
35	418113	AI272141	Hs.83484	Hs.83484:SRY (sex determining region Y)-	3.91
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	3.90
	431939	AW008061	Hs.231994	Hs.231994:Homo sapiens, clone IMAGE:4341	3.90
	453439	AI572438	Hs.32976	NM_004485:Homo sapiens guanine nucleotid	3.89
	441888	AI733306	Hs.128071	NM_022901:Homo sapiens hypothetical prot	3.89
40	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	3.89
	425234	AW152225	Hs.165909	Hs.165909:ESTs, Weakly similar to hypoth	3.89
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	3.87
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	3.85
	436251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	3.85
45	422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	3.84
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	3.84
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	3.84
	416209	AA236776	Hs.79078	NM_002358:Homo sapiens MAD2 mitotic arre	3.83
	430680	AW138724	Hs.168974	Hs.168974:ESTs	3.83
50	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	3.82
	436481	AA379597	Hs.5199	NM_014176:Homo sapiens HSPC150 protein s	3.82
	453700	AB009426	Hs.560	NM_001644:Homo sapiens apolipoprotein B	3.81
	410619	BE512730	Hs.65114	Hs.65114:keratin 18	3.81
	409420	Z15008	Hs.54451	NM_005562:Homo sapiens laminin, gamma 2	3.79
55	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	3.79
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPH3), mR	3.78
	453967	AW009077	Hs.232947	Hs.232947:ESTs	3.78
	426106	AI678765	Hs.21812	Hs.21812:ESTs	3.78
	434170	AA626509	Hs.159642	(locuslink)NM_001490:Homo sapiens glucos	3.78
60	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	3.78
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	3.74
	419229	AI827237	Hs.362919	Hs.362919:ESTs	3.74
	437156	AI916600	Hs.121194	Hs.121194:Homo sapiens cDNA: FLJ21569 fi	3.74
	452833	BE559681	Hs.30736	(locuslink)NM_015201:Homo sapiens block	3.73
65	426831	BE296216	Hs.172673	NM_000687:Homo sapiens S-adenosylhomocys	3.73
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	3.72
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	3.71
	408832	AW085690	Hs.63428	Hs.63428:Homo sapiens cDNA FLJ34457 fis,	3.71
	440300	N39760	Hs.8859	NM_138793:Homo sapiens apyrase (SHAPY),	3.71
70	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	3.71
	432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	3.71
	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	3.71
	417001	AU076648	Hs.80741	NM_000282:Homo sapiens propionyl Coenzym	3.69
	421225	AA463798	Hs.102696	Hs.102696:MCT-1 protein	3.69
75	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	3.69
	428330	L22524	Hs.2256	NM_002423:Homo sapiens matrix metallopro	3.67
	447472	AW207347	Hs.211101	Hs.211101:ESTs	3.67
	423349	AF010258	Hs.127428	NM_002142:Homo sapiens homeo box A9 (HOX	3.67
	422026	U80736	Hs.110826	Hs.110826:trinucleotide repeat containin	3.66
	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	3.66
80	417720	AA205625	Hs.208067	Hs.208067:ESTs	3.66
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	3.66
	421515	Y11339	Hs.105352	(locuslink)NM_018414:Homo sapiens GalNAc	3.65
	433675	AW977653	Hs.75319	Hs.75319:ribonucleotide reductase M2 pol	3.65

	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	3.65
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis	3.64
	412140	AA219691	Hs.73625	NM_005733:Homo sapiens RAB6 interacting,	3.64
5	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	3.63
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	3.63
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	3.62
	428862	NM_000346	Hs.2316	Hs.2316:SRY (sex determining region Y)-b	3.62
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	3.62
10	412056	T28160	Hs.778	Hs.778:guanylate cyclase activator 2A (g	3.61
	401519				3.60
	428011	BE387514	Hs.181418	NM_014730:Homo sapiens KIAA0152 gene pro	3.60
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	3.60
	421903	AW079940	Hs.15951	(locuslink)NM_145202:Homo sapiens prolin	3.58
15	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	3.58
	424544	M88700	Hs.150403	NM_000790:Homo sapiens dopa decarboxylas	3.58
	431563	AI027643	Hs.120912	Hs.120912:ESTs	3.57
	435602	AF217515	Hs.283532	NM_018455:Homo sapiens uncharacterized b	3.57
	434369	AI650363	Hs.116462	Hs.116462:ESTs	3.57
20	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	3.56
	447334	AA515032	Hs.91109	Hs.91109:ESTs, Weakly similar to putativ	3.56
	422150	AI867118	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	3.56
	450663	H43540	Hs.25292	Hs.25292:ribonuclease H2, large subunit	3.56
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	3.56
25	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	3.55
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	3.55
	422532	AL008726	Hs.118126	(locuslink)NM_000308:Homo sapiens protec	3.55
	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	3.55
	442053	R35343	Hs.24968	Hs.24968:hypothetical protein BC016683	3.55
30	437386	W52452	Hs.356766	Hs.356766:Homo sapiens mRNA; cDNA DKFZp7	3.54
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	3.53
	446372	AB020644	Hs.14945	Hs.14945:fatty-acid-Coenzyme A ligase, I	3.53
	432378	AI493046	Hs.146133	Hs.146133:ESTs	3.53
	434171	BE247688	Hs.347349	(locuslink)NM_004749:Homo sapiens cell c	3.52
35	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	3.52
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	3.51
	414918	AI219207	Hs.72222	Hs.72222:fer-1-like 4 (C. elegans)	3.51
	440340	AW895503	Hs.125276	Hs.125276:Homo sapiens cDNA FLJ25833 fis	3.51
	418384	AW149266	Hs.25130	Hs.25130:Homo sapiens cDNA FLJ14923 fis	3.51
40	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	3.51
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	3.51
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	3.50
	431567	N51357	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (3.50
	453883	AI638516	Hs.347524	Hs.347524:Homo sapiens, clone MGC:24665	3.50
45	442700	AA377618	Hs.103834	NM_024056:Homo sapiens hypothetical prot	3.50
	410237	AI750589	Hs.61258	Hs.61258:argininosuccinate lyase	3.50
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	3.49
	436213	AA325512	Hs.71472	NM_024662:Homo sapiens hypothetical prot	3.49
	442923	AW248322	Hs.95835		3.49
50	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	3.48
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	3.48
	448993	AI471630	Hs.355952	Hs.355952:ESTs, Weakly similar to 090320	3.48
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	3.48
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	3.47
55	420996	AK001927	Hs.100895	(locuslink)NM_018099:Homo sapiens hypoth	3.47
	439580	AF086401	Hs.293847	Hs.293847:ESTs	3.46
	422158	L10343	Hs.112341	NM_002638:Homo sapiens protease inhibito	3.46
	418256	AW845318	Hs.12271	(locuslink)NM_012162:Homo sapiens F-box	3.46
	400157		Hs.356473	NM_006713:Homo sapiens activated RNA pol	3.46
60	406709	AI355761	Hs.242463	Hs.242463:keratin 8	3.46
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.46
	421526	AL080121	Hs.105460	NM_015393:Homo sapiens DKFZP564O0823 pro	3.45
	415164	AW084352	Hs.157123	Hs.157123:ESTs	3.45
	405451				3.44
65	414361	AI086138	Hs.204044	Hs.204044:ESTs	3.44
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	3.44
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.44
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	3.43
	450983	AA305384	Hs.25740	NM_014584:Homo sapiens ERO1-like (S. cer	3.43
70	421828	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.42
	418588	BE387040	Hs.182476	NM_031295:Homo sapiens Williams Beuren s	3.42
	417348	AI940507	Hs.318526	NM_025138:Homo sapiens hypothetical prot	3.42
	423554	M90516	Hs.1674	NM_002056:Homo sapiens glutamine-fructos	3.42
	451310	AW250651	Hs.26213	NM_052951:Homo sapiens chromosome 20 ope	3.41
75	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	3.41
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	3.40
	437575	AW954355	Hs.36529	NM_024320:Homo sapiens hypothetical prot	3.40
	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alph	3.40
	439955	AW203959	Hs.149532	Hs.149532:ESTs	3.40
80	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	3.40
	435745	AW967059	Hs.374342	Hs.374342:Homo sapiens clone 24711 mRNA	3.40
	403532				3.39
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	3.39
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	3.39

	424996	AF006005	Hs.154104	NM_002657:Homo sapiens pleiomorphic aden	3.38
	402944				3.37
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.37
5	427528	AU077143	Hs.179565	NM_002388:Homo sapiens MCM3 minichromoso	3.37
	426711	AA383471	Hs.343800	(locuslink)NM_033255:Homo sapiens epithe	3.37
	439186	AI697274	Hs.105435	Hs.105435:GDP-mannose 4,6-dehydratase	3.36
	444783	AK001468	Hs.62180	NM_018685:Homo sapiens anillin, actin bi	3.36
	426174	AA547959	Hs.115838	Hs.115838:ESTs	3.36
10	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	3.36
	421605	BE440108	Hs.106127	NM_015972:Homo sapiens RNA polymerase I	3.36
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	3.36
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	3.36
	403219				3.36
15	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	3.34
	456946	T29678	Hs.166068	Hs.166068:villin 1	3.33
	425580	L11144	Hs.1907	Hs.1907:galarin	3.33
	412605	AW410734	Hs.74111	Hs.74111:RNA binding protein (autoantige	3.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	3.33
20	416782	L35035	Hs.79886	(locuslink)NM_144563:Homo sapiens ribose	3.33
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	3.33
	441633	AW958544	Hs.112242	NM_032413:Homo sapiens normal mucosa of	3.32
	416975	NM_004131	Hs.1051	NM_004131:Homo sapiens granzyme B (granz	3.31
	428874	W32133	Hs.194366	Hs.194366:transferrin (prealbumin, amy	3.31
25	431192	AI670056	Hs.137274	Hs.137274:ESTs, Weakly similar to hypoth	3.30
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	3.30
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	3.29
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	3.29
30	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.29
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	3.29
	437810	BE246399	Hs.367646	NM_016617:Homo sapiens hypothetical prot	3.29
	403381				3.28
	434031	BE384165	Hs.23723	(locuslink)NM_025215:Homo sapiens pseudo	3.28
35	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.28
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.28
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	3.28
	412994	D32257	Hs.75113	Hs.75113:general transcription factor II	3.28
	443162	T49951	Hs.9029	(locuslink)NM_015515:Homo sapiens type I	3.28
40	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	3.28
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	3.28
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	3.27
	419359	AL043202	Hs.90073	Hs.90073:CSE1 chromosome segregation 1-I	3.27
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.27
45	444371	BE540274	Hs.239	Hs.239:forkhead box M1	3.27
	450221	AA328102	Hs.24641	NM_018204:Homo sapiens cytoskeleton asso	3.27
	449207	AL044222	Hs.23255	NM_004298:Homo sapiens nucleoporin 155kD	3.27
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	3.27
	403485				3.27
50	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	3.26
	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.26
	405484				3.26
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	3.26
	449139	BE268315	Hs.23111	NM_004461:Homo sapiens phenylalanine-tRN	3.26
	404684				3.25
55	447188	H65423	Hs.17631	NM_030804:Homo sapiens hypothetical prot	3.25
	423226	AA323414	Hs.146109	Hs.146109:ESTs, Weakly similar to T28937	3.24
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.24
	424243	AI949359	Hs.143600	Hs.143600:golgi phosphoprotein 4	3.24
60	435014	BE560898	Hs.10026	NM_022061:Homo sapiens ribosomal protein	3.24
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis	3.24
	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	3.23
	427333	AF067797	Hs.176558	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.23
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	3.23
65	432035	AA524725	Hs.162108	Hs.162108:ESTs	3.23
	408868	AW292286	Hs.255058	Hs.255058:ESTs	3.23
	429504	X99133	Hs.204238	Hs.204238:lipocalin 2 (oncogene 24p3)	3.22
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	3.22
	426991	AK001536	Hs.214410	Hs.214410:Homo sapiens cDNA FLJ31573 fis	3.22
70	408901	AK001330	Hs.48855	(locuslink)NM_018101:Homo sapiens hypoth	3.22
	439979	AW600291	Hs.6823	NM_018092:Homo sapiens neuropilin (NRP)	3.22
	453968	AA847843	Hs.62711	Hs.62711:Homo sapiens, clone IMAGE:33512	3.22
	457465	AW301344	Hs.122908	NM_030928:Homo sapiens DNA replication f	3.22
	426317	AA312350	Hs.169294	NM_003202:Homo sapiens transcription fac	3.21
75	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	3.21
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	3.20
	444261	AA298958	Hs.10724	Hs.10724:mitochondrial ribosomal protein	3.20
	454033	AF107457	Hs.37035	NM_005515:Homo sapiens homeo box HB9 (HL	3.20
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	3.20
80	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	3.20
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	3.19
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	3.19
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	3.19
	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.18

5	419239	AA468183	Hs.335798	(locuslink)NM_033103:Homo sapiens rhophi	3.18
	426215	AW963419	Hs.155223	NM_003714:Homo sapiens stanniocalcin 2 (3.18
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	3.17
	413313	NM_002047	Hs.293885	NM_002047:Homo sapiens glycyL-tRNA synth	3.17
	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	3.17
	408353	BE439838	Hs.44298	NM_015969:Homo sapiens mitochondrial rib	3.17
	400203		Hs.1390	NM_002794:Homo sapiens proteasome (proso	3.16
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.16
10	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	3.16
	416984	H38765	Hs.80706	NM_000903:Homo sapiens NAD(P)H dehydroge	3.16
	450635	AW403954	Hs.25237	NM_016647:Homo sapiens mesenchymal stem	3.16
	406708	AI282759		AI282759:qt84a01.x1 NCL CGAP_Co14 Homo s	3.16
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.16
15	430127	AA219498	Hs.233952	Hs.233952:proteasome (prosome, macropain	3.16
	417308	H60720	Hs.81892	NM_014736:Homo sapiens KIAA0101 gene pro	3.15
	408116	AA251393	Hs.289052	NM_052842:Homo sapiens BCL2-like 12 (pro	3.15
	402474				3.15
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	3.15
20	446595	T57448	Hs.15467	NM_017943:Homo sapiens hypothetical prot	3.15
	444954	AW247076	Hs.12163	NM_003908:Homo sapiens eukaryotic transl	3.15
	434263	N34895	Hs.79187	Hs.79187:cox sackie virus and adenovirus	3.15
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.15
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.15
	436391	AJ227892	Hs.146274	Hs.146274:ESTs	3.15
25	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	3.14
	445973	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.14
	432370	AA308334	Hs.274424	NM_018946:Homo sapiens N-acetylneuramini	3.14
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	3.14
30	417791	AW965339	Hs.44269	Hs.44269:Homo sapiens cDNA FLJ37972 fis,	3.14
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	3.13
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	3.13
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	3.13
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutas	3.13
35	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.13
	446386	AI032108	Hs.54424	Hs.54424:hepatocyte nuclear factor 4, al	3.12
	407804	AF228603	Hs.39957	NM_016445:Homo sapiens pleckstrin 2 (mou	3.12
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	3.12
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.11
40	407168	R45175	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	3.11
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	3.11
	426427	M86699	Hs.169840	Hs.169840:TTK protein kinase	3.11
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.10
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (3.10
45	434861	AA206153	Hs.4209	NM_016491:Homo sapiens mitochondrial rib	3.10
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	3.10
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.09
	454464	AW811606	Hs.271819	Hs.271819:mucin 17	3.09
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	3.09
50	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.09
	421470	R27496	Hs.1378	NM_005139:Homo sapiens annexin A3 (ANXA3	3.09
	419551	AW582256	Hs.91011	NM_006408:Homo sapiens anterior gradient	3.09
	418691	AW752389	Hs.87296	Hs.87296:Homo sapiens cDNA FLJ20269 fis,	3.08
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	3.08
55	447760	AI431328	Hs.348605	NM_052963:Homo sapiens mitochondrial top	3.08
	405506				3.08
	429957	AW204530	Hs.99500	Hs.99500:ESTs	3.08
	410166	AK001376	Hs.59346	NM_018122:Homo sapiens hypothetical prot	3.08
	422880	AF228704	Hs.193974	Hs.193974:glutathione reductase	3.08
60	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	3.08
	431722	AF161528	Hs.268049	(locuslink)NM_016101:Homo sapiens hypoth	3.08
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	3.08
	433659	AK001301	Hs.3487	NM_018093:Homo sapiens hypothetical prot	3.07
	439492	AF086310	Hs.103159	Hs.103159:ESTs, Weakly similar to TC6291	3.07
65	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	3.07
	412530	AA766268	Hs.266273	(locuslink)NM_024918:Homo sapiens chromo	3.07
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.06
	453132	AW951952	Hs.293724	Hs.293724:Homo sapiens cDNA FLJ12683 fis	3.06
	424971	AA479005	Hs.154036	NM_003311:Homo sapiens tumor suppressing	3.06
70	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	3.05
	439273	AW139099	Hs.367692	Hs.367692:Homo sapiens cDNA FLJ25668 fis	3.05
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	3.05
	435703	AW630133	Hs.83313	(locuslink)NM_020192:Homo sapiens GK003	3.05
	407289	AA135159	Hs.203349	Hs.203349:Homo sapiens cDNA FLJ12149 fis	3.04
	403739				3.04
75	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	3.04
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	3.04
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.04
	406545				3.03
80	450553	AW850613	Hs.8715	Hs.8715:hypothetical protein MGC3232	3.03
	418867	D31771	Hs.89404	NM_002449:Homo sapiens msh homeo box hom	3.03
	422976	AU076657	Hs.1600	Hs.1600:chaperonin containing TCP1, subu	3.03
	434523	AA703709	Hs.23410	(locuslink)NM_016539:Homo sapiens sirtui	3.03
	440088	BE559877	Hs.183232	NM_024839:Homo sapiens hypothetical prot	3.02

	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.02
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	3.02
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.02
5	422283	AW411307	Hs.114311	NM_003504:Homo sapiens CDC45 cell divisi	3.02
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.02
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.02
	417975	AA641836	Hs.30085	NM_024616:Homo sapiens hypothetical prot	3.02
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.01
10	436561	BE560135	Hs.5232	NM_014165:Homo sapiens HSPC125 protein (3.01
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cispla	3.01
	417678	X06560	Hs.82396	(locuslink)NM_002534:Homo sapiens 2',5'-	3.01
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.00
	429983	W92620	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (3.00
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.00
15	414732	AW410976	Hs.77152	Hs.77152:MCM7 minichromosome maintenance	3.00
	409614	BE297412	Hs.55189	NM_016489:Homo sapiens 5'-nucleotidase,	3.00
	439053	BE244588	Hs.6456	Hs.6456:chaperonin containing TCP1, subu	3.00
	411096	U80034	Hs.68583	NM_005932:Homo sapiens mitochondrial int	2.99
20	433312	AI241331	Hs.131765	Hs.131765:ESTs, Moderately similar to l3	2.99
	420767	AF072711	Hs.99918	Hs.99918:carboxyl ester lipase (bile sal	2.99
	429523	AK000788	Hs.205280	Hs.205280:Homo sapiens cDNA FLJ20781 fis	2.99
	423242	AL039402	Hs.125783	Hs.125783:chromosome 1 open reading fram	2.99
	420552	AK000492	Hs.98806	Hs.98806:hypothetical protein FLJ20485	2.99
25	413380	AI904232	Hs.75323	Hs.75323:prohibitin	2.99
	421533	N71826	Hs.105465	NM_003095:Homo sapiens small nuclear rib	2.99
	439352	BE614347	Hs.169615	NM_023080:Homo sapiens hypothetical prot	2.98
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	2.98
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.98
30	457211	AW972565	Hs.32399	(locuslink)NM_145240:Homo sapiens simila	2.98
	410467	AF102546	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.97
	422066	AW249275	Hs.343521	Hs.343521:malate dehydrogenase 2, NAD (m	2.97
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	2.97
	453012	T95804	Hs.31334	NM_012469:Homo sapiens chromosome 20 ope	2.97
35	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	2.97
	413813	M99566	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	2.97
	418362	AL031714	Hs.84285	NM_003345:Homo sapiens ubiquitin-conjuga	2.97
	431350	AI192528	Hs.164537	Hs.164537:ESTs	2.96
	417911	AA333337	Hs.82916	Hs.82916:chaperonin containing TCP1, sub	2.96
40	413597	AW302885	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	2.96
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (2.96
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	2.96
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	2.96
	408194	AA601038	Hs.191797	Hs.191797:ESTs	2.96
45	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	2.96
	459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	2.96
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	2.96
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	2.95
50	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	2.95
	432843	BE250865	Hs.279529	NM_013237:Homo sapiens px19-like protein	2.95
	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	2.95
	410006	AW732308	Hs.57783	NM_003751:Homo sapiens eukaryotic transt	2.94
	442577	AA292998	Hs.163900	Hs.163900:ESTs, Highly similar to winged	2.94
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	2.94
55	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	2.94
	427779	AA906997	Hs.180780	NM_021238:Homo sapiens TERA protein (TER	2.94
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	2.94
	414549	BE393069	Hs.183506	NM_024841:Homo sapiens hypothetical prot	2.93
	410817	AI262789	Hs.93659	(locuslink)NM_004911:Homo sapiens protei	2.93
60	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	2.93
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	2.93
	414416	AW409985	Hs.76084	(locuslink)NM_032737:Homo sapiens hypoth	2.93
	434094	AA305599	Hs.238205	Hs.238205:hypothetical protein PRO2013	2.93
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.93
65	429048	AI372949	Hs.44241	Hs.44241:Homo sapiens cDNA: FLJ21447 fis	2.93
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	2.92
	422397	AJ223366	Hs.116051	(locuslink)NM_138768:Homo sapiens myelom	2.92
	426715	AB037855	Hs.171917	Hs.171917:hypothetical protein FLJ11085	2.92
	429539	AK001839	Hs.206501	(locuslink)NM_020467:Homo sapiens hypoth	2.92
70	443715	AI583187	Hs.9700	NM_001238:Homo sapiens cyclin E1 (CCNE1)	2.92
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transt	2.92
	433888	BE176078	Hs.30819	Hs.30819:hypothetical protein C40	2.92
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	2.92
	422558	NM_006420	Hs.118249	Hs.118249:ADP-ribosylation factor guanin	2.92
75	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	2.92
	429626	U36787	Hs.211571	NM_005333:Homo sapiens holocytochrome c	2.92
	413374	NM_001034	Hs.75319	NM_001034:Homo sapiens ribonucleotide re	2.92
	442159	AW163390	Hs.278554	NM_007276:Homo sapiens chromobox homolog	2.92
	400133		Hs.184693	NM_005648:Homo sapiens transcription elo	2.91
80	419381	AB023420	Hs.90093	Hs.90093:heat shock 70kD protein 4	2.91
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	2.91
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	2.91
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	2.91
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	2.91

5	433487	U31814	Hs.3352	NM_001527:Homo sapiens histone deacetyla	2.91
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	2.90
	430287	AW182459	Hs.125759	Hs.125759:likely ortholog of mouse RING	2.90
	434026	R15486	Hs.285218	(locuslink)NM_021213:Homo sapiens phosph	2.90
	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	2.90
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	2.90
	432754	BE241691	Hs.3100	Hs.3100:lysyl-tRNA synthetase	2.90
	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	2.90
10	446228	NM_016046	Hs.14415	NM_016046:Homo sapiens exosomal core pro	2.90
	420421	AF281133	Hs.343589	Hs.343589:exosome component Rrp41	2.89
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	2.89
	414420	AA043424	Hs.76095	NM_052815:Homo sapiens immediate early r	2.89
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	2.89
	401405				2.89
15	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	2.89
	400247		Hs.356473	NM_006713:Homo sapiens activated RNA pol	2.89
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	2.89
	413610	AL117554	Hs.119908	NM_015934:Homo sapiens nucleolar protein	2.89
20	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	2.89
	418661	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription	2.88
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	2.88
	417634	W27202	Hs.82327	NM_000178:Homo sapiens glutathione synth	2.88
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	2.88
25	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	2.88
	446849	AU076617	Hs.16251	(locuslink)NM_016207:Homo sapiens cleava	2.88
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	2.88
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	2.88
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	2.88
30	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	2.87
	448250	NM_016034	Hs.20776	(locuslink)NM_016034:Homo sapiens mitoch	2.87
	428810	AF068236	Hs.193788	NM_000625:Homo sapiens nitric oxide synt	2.87
	427505	AA361562	Hs.178761	Hs.178761:26S proteasome-associated pad1	2.87
	418443	NM_005239	Hs.85146	Hs.85146:v-ets erythroblastosis virus E2	2.87
35	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	2.87
	409262	AK000631	Hs.52256	Hs.52256:hypothetical protein FLJ20624	2.87
	443323	BE560621	Hs.9222	Hs.9222:estrogen receptor binding site a	2.87
	450378	AW249181	Hs.154796	Hs.154796:Homo sapiens cDNA FLJ37976 fis	2.86
	411761	AI733848	Hs.71935	NM_021220:Homo sapiens zinc finger prote	2.86
40	415691	AW963979	Hs.24723	Hs.24723:ESTs	2.86
	417715	AW969587	Hs.86366	Hs.86366:ESTs	2.86
	452099	BE612992	Hs.27931	Hs.27931:hypothetical protein FLJ10607 s	2.86
	436138	H53323	Hs.25717	Hs.25717:Homo sapiens cDNA: FLJ23454 fis	2.86
45	432858	BE618609	Hs.279591	Hs.279591:Homo sapiens, Similar to RNA p	2.86
	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	2.86
	444237	AA336878	Hs.9842	Hs.9842:ESTs	2.85
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	2.85
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	2.85
50	424270	AK001818	Hs.144407	NM_018283:Homo sapiens hypothetical prot	2.85
	414396	BE548266	Hs.76057	(locuslink)NM_000403:Homo sapiens galact	2.85
	426120	AA325243	Hs.166887	Hs.166887:copine I	2.85
	448663	BE614599	Hs.356501	(locuslink)NM_032335:Homo sapiens hypoth	2.85
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	2.85
55	445863	R12234	Hs.13396	Hs.13396:Homo sapiens clone 25028 mRNA s	2.85
	434808	AF155108	Hs.256150	Hs.256150:NY-REN-41 antigen	2.85
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	2.85
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	2.85
	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens interf	2.84
60	446421	BE297434	Hs.15071	Hs.15071:chaperonin containing TCP1, sub	2.84
	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	2.84
	425549	U30930	Hs.158540	(locuslink)NM_003360:Homo sapiens UDP gl	2.84
	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	2.84
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	2.84
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	2.84
65	407833	AW955632	Hs.66666	Hs.66666:chromosome 7 open reading frame	2.84
	415083	AI632683	Hs.27179	Hs.27179:Homo sapiens cDNA FLJ12933 fis	2.83
	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	2.83
	443572	AA025610	Hs.9605	Hs.9605:cleavage and polyadenylation spe	2.83
70	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	2.83
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (2.83
	453028	AB006532	Hs.31442	NM_004260:Homo sapiens RecQ protein-like	2.83
	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	2.83
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	2.83
	410197	NM_005518	Hs.59889	(locuslink)NM_005518:Homo sapiens 3-hydr	2.83
75	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	2.83
	417677	NM_016055	Hs.82389	NM_016055:Homo sapiens mitochondrial rib	2.83
	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	2.82
	437430	W44671	Hs.124	NM_014628:Homo sapiens gene predicted fr	2.82
	428289	M26301	Hs.2253	Hs.2253:complement component 2	2.82
80	407137	T97307			2.82
	400750				2.82
	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	2.82
	432633	AI796390	Hs.210667	Hs.210667:ESTs	2.82
	432816	N38913	Hs.221575	Hs.221575:ESTs	2.82

	410045	AA806930	Hs.58189	Hs.58189:eukaryotic translation initiati	2.82
	454144	BE280478	Hs.182695	NM_024026:Homo sapiens mitochondrial rib	2.82
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	2.81
5	434583	AA095761	Hs.349092	Hs.349092:ESTs, Weakly similar to A42442	2.81
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	2.81
	428093	AW594506	Hs.104830	Hs.104830:ESTs	2.81
	416047	BE439894	Hs.78991	NM_012080:Homo sapiens DNA segment, nume	2.81
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	2.81
10	452199	BE255643	Hs.110695	Hs.110695:hypothetical protein MGC3133	2.81
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	2.80
	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	2.80
	422809	AK001379	Hs.121028	NM_018136:Homo sapiens hypothetical prot	2.80
	417869	BE076254	Hs.82793	Hs.82793:proteasome (prosome, macropain)	2.80
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	2.80
15	418731	AI264688	Hs.1197	NM_002157:Homo sapiens heat shock 10kD p	2.80
	432840	AK001403	Hs.279521	Hs.279521:hypothetical protein FLJ20530	2.80
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	2.80
	441181	AA416925	Hs.374811	Hs.374811:Homo sapiens, similar to 4-1BB	2.80
	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	2.79
20	450010	AW293801	Hs.255052	Hs.255052:ESTs	2.79
	418960	NM_004494	Hs.89525	(locuslink)NM_004494:Homo sapiens hepato	2.79
	401179				2.79
	419252	AW138434	Hs.129805	Hs.129805:ESTs	2.79
	434750	BE019254	Hs.4112	Hs.4112:t-complex 1	2.79
25	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	2.79
	400529				2.79
	436414	BE264633	Hs.143638	NM_033661:Homo sapiens WD repeat domain	2.79
	436291	BE568452	Hs.344037	(locuslink)NM_003981:Homo sapiens protei	2.79
30	427963	AI042582	Hs.181271	NM_016057:Homo sapiens CGI-120 protein (2.79
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	2.79
	413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	2.79
	442468	N77737	Hs.8349	NM_138933:Homo sapiens apobec-1 compleme	2.79
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	2.79
35	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	2.79
	430120	AW675298	Hs.233694	(locuslink)NM_018396:Homo sapiens putati	2.79
	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	2.79
	417164	AA338283	Hs.81361	Hs.81361:heterogeneous nuclear ribonucle	2.79
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	2.79
40	409636	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	2.78
	447619	AI174800	Hs.19054	(locuslink)NM_018530:Homo sapiens hypoth	2.78
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	2.78
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	2.78
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	2.78
45	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	2.78
	430512	AF182294	Hs.241578	NM_016200:Homo sapiens U6 snRNA-associa	2.78
	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	2.78
	414697	BE266134	Hs.76927	Hs.76927:translocase of outer mitochondr	2.78
	420665	AW469240	Hs.371581	Hs.371581:ESTs	2.78
50	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	2.78
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	2.77
	443343	BE409809	Hs.301005	Hs.301005:histone H2A.F/Z variant	2.77
	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	2.77
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	2.77
55	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	2.77
	432543	AA552690	Hs.152423	Hs.152423:Homo sapiens cDNA: FLJ21274 fi	2.77
	423271	W47225	Hs.126256	NM_000576:Homo sapiens interleukin 1, be	2.77
	410595	AW629223	Hs.64794	NM_006978:Homo sapiens zinc finger prote	2.77
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	2.77
60	457757	AA434109	Hs.12271	NM_012162:Homo sapiens F-box and leucine	2.77
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	2.77
	410094	BE147897	Hs.58593	NM_004128:Homo sapiens general transcrip	2.77
	403817				2.77
	459125	AA811363	Hs.29464	Hs.29464:Homo sapiens cDNA: FLJ23460 fis	2.77
65	432705	AI879473	Hs.157123	Hs.157123:ESTs	2.77
	446658	AI440137	Hs.164989	NM_138492:Homo sapiens hypothetical prot	2.76
	419485	AA489023	Hs.99807	Hs.99807:Homo sapiens mRNA; cDNA DKFZp31	2.76
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	2.76
	428438	NM_001955	Hs.2271	NM_001955:Homo sapiens endothelin 1 (EDN	2.76
70	414767	BE541381	Hs.178705	NM_033515:Homo sapiens MacGAP protein (M	2.76
	406830	AI829848	Hs.342389	Hs.342389:peptidylprolyl isomerase A (cy	2.76
	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	2.76
	430450	R23553	Hs.241489	(locuslink)NM_015913:Homo sapiens hypoth	2.76
	433808	NM_014062	Hs.3566	Hs.3566:ART-4 protein	2.75
75	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	2.75
	433369	Z49254	Hs.3254	NM_021134:Homo sapiens mitochondrial rib	2.75
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	2.75
	432204	AI916132	Hs.121593	Hs.121593:Homo sapiens cDNA FLJ13123 fis	2.75
	424438	AA340724	Hs.271912	Hs.271912:Homo sapiens cDNA FLJ38690 fis	2.75
80	433862	D86960	Hs.3610	NM_014873:Homo sapiens KIAA0205 gene pro	2.75
	417080	BE392846	Hs.1063	Hs.1063:small nuclear ribonucleoprotein	2.75
	428242	H55709	Hs.2250	Hs.2250:leukemia inhibitory factor (chol	2.75
	416188	BE157260	Hs.79070	NM_002467:Homo sapiens v-myc myelocytoma	2.75
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	2.75

5	419489	AW411280	Hs.90693	NM_013400:Homo sapiens replication initi	2.75
	407971	AI469117	Hs.62918	Hs.62918:CD91 cell division cycle 91-li	2.75
	432403	AA550815	Hs.124840	(locuslink)NM_138456:Homo sapiens hypoph	2.75
	410775	AB014460	Hs.66196	NM_002528:Homo sapiens nth endonuclease	2.75
	444197	BE266947	Hs.10590	NM_018683:Homo sapiens zinc finger prote	2.75
10	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	2.75
	406806	AW088535	Hs.350108	Hs.350108:ribosomal protein, large, P0	2.75
	411580	AL080088	Hs.70877	NM_015421:Homo sapiens DKFZP564K2062 pro	2.75
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	2.74
	426235	AI631964	Hs.34447	Hs.34447:Homo sapiens cDNA FLJ38512 fis,	2.74
15	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	2.74
	419713	AW968058	Hs.92381	NM_019094:Homo sapiens nudix (nucleoside	2.74
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	2.74
	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	2.74
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	2.74
20	452767	AW014195	Hs.61472	Hs.61472:Homo sapiens, clone IMAGE:51841	2.74
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	2.73
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	2.73
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	2.73
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	2.73
25	423908	AJ006422	Hs.135183	NM_006869:Homo sapiens centaurin, alpha	2.73
	433412	AV653729	Hs.8185	NM_021199:Homo sapiens sulfide dehydroge	2.73
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	2.73
	452461	N78223	Hs.108106	Hs.108106:ubiquitin-like, containing PHD	2.73
	407699	AA825974	Hs.32646	NM_024622:Homo sapiens hypothetical prot	2.73
30	412258	AA376768	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.73
	450256	AA286887	Hs.24724	Hs.24724:Homo sapiens cDNA FLJ39185 fis,	2.72
	443905	AI215948	Hs.143969	Hs.143969:ESTs	2.72
	413274	NM_004893	Hs.75258	NM_004893:Homo sapiens H2A histone famil	2.72
	408885	C02741	Hs.48712	NM_017948:Homo sapiens hypothetical prot	2.72
35	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	2.72
	424692	AA429834	Hs.151791	NM_014679:Homo sapiens KIAA0092 gene pro	2.72
	413762	AW411479	Hs.848	NM_002014:Homo sapiens FK506 binding pro	2.72
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	2.72
	450164	AI239923	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.71
40	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	2.71
	450897	W16741	Hs.351629	NM_014017:Homo sapiens HSPC003 protein (2.71
	447349	AI375546		BE743847:601577765F1 NIH_MGC_9 Homo sapi	2.71
	445413	AA151342	Hs.12677	(locuslink)NM_016077:Homo sapiens CGI-14	2.71
	448826	AI580252	Hs.255565	Hs.255565:Homo sapiens cDNA FLJ33892 fis	2.71
45	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	2.71
	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	2.71
	441020	W79283	Hs.35962	Hs.35962:Homo sapiens mRNA; cDNA DKFZp68	2.70
	458933	AI638429	Hs.24763	NM_002882:Homo sapiens RAN binding prote	2.70
	423787	AJ295745	Hs.236204	Hs.236204:nuclear pore complex protein	2.70
50	430462	AI584156	Hs.105640	Hs.105640:hypothetical protein BC007772	2.70
	439656	AW138241	Hs.160602	Hs.160602:Homo sapiens cDNA FLJ36008 fis	2.70
	425236	AW067800	Hs.155223	NM_003714:Homo sapiens stannocalcin 2 (2.70
	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	2.70
	448296	BE622756	Hs.10949	Hs.10949:Homo sapiens cDNA FLJ14162 fis,	2.70
55	430200	BE613337	Hs.234896	Hs.234896:geminin	2.70
	424308	AW975531	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.70
	423453	AW450737	Hs.128791	NM_015939:Homo sapiens CGI-09 protein (L	2.70
	421344	AW631030	Hs.103665	(locuslink)NM_015873:Homo sapiens villin	2.70
	446607	AI691065	Hs.155780	Hs.155780:ESTs	2.70
60	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	2.70
	443835	AF016371	Hs.9880	NM_006347:Homo sapiens peptidyl prolyl i	2.70
	413794	AF234532	Hs.61638	NM_012334:Homo sapiens myosin X (MYO10),	2.70
	451481	AA300228	Hs.295866	(locuslink)NM_030974:Homo sapiens hypoth	2.70
	458820	BE552151	Hs.108118	Hs.108118:hypothetical protein FLJ22474	2.70
65	425905	AB032959	Hs.318584	NM_032173:Homo sapiens hypothetical prot	2.69
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	2.69
	431201	AA678405	Hs.8854	Hs.8854:Pvt1 oncogene homolog, MYC activ	2.69
	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	2.69
	441703	AW390054	Hs.192843	NM_022145:Homo sapiens leucine zipper pr	2.69
70	433916	AW732839	Hs.3631	NM_001551:Homo sapiens immunoglobulin (C	2.69
	422516	BE258862	Hs.117950	NM_006452:Homo sapiens phosphoribosylami	2.69
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	2.69
	427464	BE262956	Hs.178292	Hs.178292:protein O-fucosyltransferase 1	2.69
	453876	AW021748	Hs.110406	Hs.110406:ESTs	2.69
75	424373	AJ133798	Hs.146219	NM_014427:Homo sapiens copine VII (CPNE7	2.69
	411619	AI418609	Hs.71040	NM_017816:Homo sapiens hypothetical prot	2.69
	413004	T35901	Hs.75117	Hs.75117:interleukin enhancer binding fa	2.69
	420062	AW411096	Hs.94785	(locuslink)NM_021809:Homo sapiens TGF-beta	2.69
	446077	BE251048	Hs.22579	Hs.22579:Homo sapiens clone CDABP0036 mR	2.68
80	446269	AW263155	Hs.14559	NM_018131:Homo sapiens hypothetical prot	2.68
	428728	NM_016625	Hs.191381	Hs.191381:hypothetical protein LOC51319	2.68
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	2.68
	421933	R98881	Hs.109655	NM_006746:Homo sapiens sex comb on midle	2.68
	417750	AI267720	Hs.260523	Hs.260523:neuroblastoma RAS viral (v-ras	2.68
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	2.68
	421720	AF155096	Hs.107213	Hs.107213:formin binding protein 3	2.68
	425601	AW629485	Hs.140720	NM_012083:Homo sapiens frequently rearra	2.68

5	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	2.68
	433159	AB035898	Hs.150587	NM_020242:Homo sapiens kinesin-like 7 (K	2.68
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	2.68
	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	2.68
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (2.68
10	427719	AI393122	Hs.134726	(locuslink)NM_145060:Homo sapiens hypoth	2.68
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	2.68
	457313	AF047002	Hs.241520	NM_005782:Homo sapiens transcriptional c	2.67
	413142	M81740	Hs.75212	(locuslink)NM_002539:Homo sapiens ornith	2.67
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	2.67
15	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	2.67
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	2.67
	447913	AW438602	Hs.191179	Hs.191179:ESTs	2.67
	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	2.67
	439586	AA922936	Hs.110039	Hs.110039:ESTs	2.67
20	427477	AW973119	Hs.178391	NM_021029:Homo sapiens ribosomal protein	2.67
	421839	BE258778	Hs.108809	NM_006429:Homo sapiens chaperonin contai	2.67
	400448				2.67
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	2.67
	445304	BE613206	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	2.67
25	417601	NM_014735	Hs.82292	NM_014735:Homo sapiens KIAA0215 gene pro	2.66
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	2.66
	431021	AI869664	Hs.351863	(locuslink)NM_003312:Homo sapiens thiosu	2.66
	453157	AF077036	Hs.31989	NM_015449:Homo sapiens NICE-3 protein (N	2.66
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	2.66
30	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	2.66
	456248	AL035786	Hs.82425	NM_005717:Homo sapiens actin related pro	2.66
	427691	AW194426	Hs.20726	Hs.20726:ESTs, Moderately similar to hyp	2.66
	419705	AW368634	Hs.154331	Hs.154331:ESTs	2.66
	421254	AK001724	Hs.102950	NM_016128:Homo sapiens coat protein gamm	2.66
35	422719	BE017985	Hs.102558	Hs.102558:Homo sapiens cDNA FLJ40369 fis	2.66
	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	2.66
	432435	BE218886	Hs.282070	Hs.282070:ESTs	2.66
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.65
	436106	AI050715	Hs.2331	Hs.2331:E2F transcription factor 5, p130	2.65
40	431127	U66618	Hs.250581	Hs.250581:SVN/SNF related, matrix associ	2.65
	425568	AW963118	Hs.161784	Hs.161784:ESTs	2.65
	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	2.65
	414761	AU077228	Hs.77256	NM_004456:Homo sapiens enhancer of zeste	2.65
	412738	N34731	Hs.74562	NM_078480:Homo sapiens fuse-binding prot	2.65
45	408893	AW247090	Hs.57101	Hs.57101:MCM2 minichromosome maintenanc	2.65
	421743	T35958	Hs.107614	Hs.107614:DKFZP56411171 protein	2.64
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protei	2.64
	417957	H53497	Hs.83006	NM_016071:Homo sapiens mitochondrial rib	2.64
	409119	AA531133	Hs.4253	Hs.4253:hypothetical protein MGC2574	2.64
50	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	2.64
	409214	AW405967	Hs.333388	Hs.333388:similar to CG3714 gene product	2.64
	414883	AA926960	Hs.348669	Hs.348669:CDC28 protein kinase 1	2.64
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	2.64
	408633	AW963372	Hs.222088	NM_014109:Homo sapiens PRO2000 protein (2.64
55	447769	AW873704	Hs.320831	Hs.320831:chromosome 20 open reading fra	2.64
	432964	AF118395	Hs.279865	NM_014317:Homo sapiens trans-prenyltrans	2.63
	444855	BE409261	Hs.12084	Hs.12084:Tu translation elongation facto	2.63
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	2.63
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	2.63
60	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	2.63
	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	2.63
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	2.63
	406122				2.63
	420988	AW006352	Hs.159643	Hs.159643:ESTs, Weakly similar to putati	2.63
65	436433	AW631437	Hs.5184	(locuslink)NM_016397:Homo sapiens TH1-li	2.63
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	2.63
	410397	AF217517	Hs.63042	NM_018457:Homo sapiens DKFZp564J157 prot	2.63
	419420	AA355435	Hs.30724	(locuslink)NM_001516:Homo sapiens genera	2.63
	400298	AA032279	Hs.61635	Hs.61635:six transmembrane epithellal an	2.63
70	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	2.63
	436199	R38946	Hs.127951	Hs.127951:Homo sapiens cDNA FLJ14503 fis	2.63
	425081	X74794	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.63
	442025	AW887434	Hs.11810	NM_032026:Homo sapiens CDA11 protein (CD	2.62
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	2.62
75	409703	NM_006187	Hs.56009	Hs.56009:2'-5'-oligoadenylate synthetase	2.62
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	2.62
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	2.62
	451926	AW134519	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.62
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	2.62
80	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	2.62
	421405	AA251944	Hs.104058	NM_015957:Homo sapiens CGI-29 protein (L	2.62
	429491	NM_012111	Hs.204041	NM_012111:Homo sapiens chromosome 14 ope	2.62
	453335	AW857376	Hs.169238	NM_000149:Homo sapiens fucosyltransferas	2.62
	441126	NM_000429	Hs.323715	(locuslink)NM_000429:Homo sapiens methio	2.62
	417404	NM_007350	Hs.82101	(locuslink)NM_007350:Homo sapiens plecks	2.62
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	2.62
	446766	AF083208	Hs.16178	NM_012138:Homo sapiens apoptosis antagon	2.62

	437033	AW248364	Hs.5409	(locuslink)NM_004875:Homo sapiens RNA po	2.62
	412123	BE251328	Hs.73291	NM_018256:Homo sapiens WD repeat domain	2.62
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	2.61
5	433037	NM_014158	Hs.279938	NM_014158:Homo sapiens HSPC067 protein (2.61
	414438	AI879277	Hs.76136	(locuslink)NM_003329:Homo sapiens thiore	2.61
	416221	BE513171	Hs.79086	(locuslink)NM_007208:Homo sapiens mitoch	2.61
	443898	AW804296	Hs.9950	NM_014302:Homo sapiens Sec61 gamma (SEC6	2.61
	410007	AW950887	Hs.57813	NM_014596:Homo sapiens zinc ribbon domai	2.61
10	412715	NM_000947	Hs.74519	NM_000947:Homo sapiens primase, polypept	2.61
	449864	BE276386	Hs.111429	NM_032486:Homo sapiens dynactin 4 (MGC32	2.61
	448625	AW970786	Hs.178470	NM_024829:Homo sapiens hypothetical prot	2.61
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	2.61
	410686	AI733735	Hs.114905	NM_033266:Homo sapiens ER to nucleus sig	2.60
	411400	AA311919	Hs.69851	NM_018983:Homo sapiens nucleolar protein	2.60
15	429770	AI766047	Hs.99736	Hs.99736:hypothetical protein MGC39350	2.60
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	2.60
	420237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	2.60
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	2.60
20	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	2.60
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	2.60
	457234	AW968360	Hs.14355	Hs.14355:Homo sapiens cDNA FLJ13207 fis,	2.60
	420911	U77413	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (2.60
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.60
25	438533	AI440266	Hs.170673	NM_138969:Homo sapiens retinal short cha	2.60
	421699	AL161994	Hs.107003	NM_021178:Homo sapiens enhancer of invas	2.60
	452220	BE158006	Hs.212296	Hs.212296:ESTs	2.60
	439148	AA372280	Hs.178576	(locuslink)NM_030877:Homo sapiens cateni	2.60
	453949	AU077146	Hs.36927	(locuslink)NM_006644:Homo sapiens heat s	2.59
	451110	AI955040	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.59
30	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	2.59
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	2.59
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	2.59
	424290	AA197226	Hs.19347	NM_032351:Homo sapiens mitochondrial rib	2.59
35	424197	AF096834	Hs.142989	NM_015982:Homo sapiens germ cell specifi	2.59
	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	2.59
	410219	T98226	Hs.171952	Hs.171952:occludin	2.59
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	2.59
	441153	BE562826		BE562826:601336534F1 NIH_MGC_44 Homo sap	2.59
40	410570	AI133096	Hs.64593	NM_006356:Homo sapiens ATP synthase, H+	2.58
	430594	AK000790	Hs.246885	NM_017958:Homo sapiens hypothetical prot	2.58
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	2.58
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.58
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.58
45	449019	AI949095	Hs.67776	Hs.67776:Homo sapiens, clone IMAGE:54556	2.58
	410442	X73424	Hs.63788	Hs.63788:propionyl Coenzyme A carboxylas	2.58
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	2.58
	454417	AI244459	Hs.110826	Hs.110826:trinucleotide repeat containin	2.58
	416330	AU077101	Hs.79222	Hs.79222:galactosidase, beta 1	2.58
50	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	2.58
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	2.58
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	2.58
	406180				2.58
	416297	AA157634	Hs.79172	Hs.79172:solute carrier family 25 (mitoc	2.58
55	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	2.58
	447532	AK000614	Hs.18791	NM_017899:Homo sapiens hypothetical prot	2.57
	420309	AW043637	Hs.21766	Hs.21766:ESTs, Weakly similar to hypothe	2.57
	447418	AA063074	Hs.18552	Hs.18552:E2f2 protein	2.57
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	2.57
60	428342	AI739168	Hs.349283	Hs.349283:Homo sapiens cDNA FLJ31753 fis	2.57
	427254	AL121523	Hs.97774	Hs.97774:ESTs	2.57
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (2.57
	425689	W16480	Hs.24283	Hs.24283:Homo sapiens cDNA FLJ25952 fis,	2.57
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	2.57
65	427678	BE267756	Hs.180312	NM_016065:Homo sapiens mitochondrial rib	2.57
	444656	AI277924	Hs.145199	Hs.145199:ESTs, Weakly similar to hypoth	2.57
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	2.57
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	2.56
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	2.56
70	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.56
	409964	AW368226	Hs.67928	Hs.67928:ESTs	2.56
	431910	AK000142	Hs.101774	Hs.101774:hypothetical protein FLJ23045	2.56
	413010	AA393273	Hs.75133	NM_003201:Homo sapiens transcription fac	2.56
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	2.56
75	419423	D26488	Hs.90315	Hs.90315:KIAA0007 protein	2.56
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.56
	437623	D63880	Hs.5719	NM_014865:Homo sapiens chromosome conden	2.56
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	2.56
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	2.56
80	425368	AB014595	Hs.155976	(locuslink)NM_003588:Homo sapiens cullin	2.56
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	2.56
	427876	AI494291	Hs.369171	Hs.369171:ESTs	2.56
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	2.56
	416432	BE391767	Hs.79322	(locuslink)NM_005051:Homo sapiens glutam	2.55

5	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	2.55
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	2.55
	454003	AA058944	Hs.116602	Hs.116602:hypothetical protein BC009115	2.55
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	2.55
	457400	AF032906	Hs.252549	NM_001336:Homo sapiens cathepsin Z (CTSZ	2.55
10	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	2.55
	402829				2.55
	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	2.55
	400995				2.55
	452945	AW978187	Hs.79103	NM_030579:Homo sapiens cytochrome b5 out	2.55
15	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	2.55
	422192	AA305159	Hs.113019	NM_015931:Homo sapiens fis485 (LOC51066)	2.55
	424755	AB033094	Hs.152925	Hs.152925:KIAA1268 protein	2.55
	410012	AW015832	Hs.57898	(locuslink)NM_017819:Homo sapiens hypoth	2.55
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	2.55
20	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	2.55
	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	2.55
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	2.55
	406629	AW277078	Hs.181165	Hs.181165:eukaryotic translation elongat	2.55
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	2.54
25	446715	AI337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	2.54
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	2.54
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	2.54
	427368	BE041451	Hs.177507	Hs.177507:hypothetical protein HSPC155	2.54
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	2.54
30	409532	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	2.54
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCCTA00142	2.54
	456031	AA335996	Hs.355907	Hs.355907:ESTs, Weakly similar to protei	2.54
	442432	BE093589	Hs.38178	NM_024629:Homo sapiens hypothetical prot	2.54
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	2.54
35	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	2.54
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	2.54
	432876	AW248272	Hs.279652	NM_015956:Homo sapiens mitochondrial rib	2.53
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	2.53
	425994	AK000207	Hs.165803	NM_017708:Homo sapiens hypothetical prot	2.53
40	445982	BE410233	Hs.13501	(locuslink)NM_014303:Homo sapiens pescad	2.53
	444232	W56010	Hs.347297	(locuslink)NM_013397:Homo sapiens over-e	2.53
	435655	AW105663	Hs.6947	(locuslink)NM_014159:Homo sapiens Huntin	2.53
	417686	AA769155	Hs.235498	Hs.235498:hypothetical protein FLJ14075	2.53
	417933	X02308	Hs.82962	NM_001071:Homo sapiens thymidylate synth	2.53
45	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	2.53
	452313	Y00486	Hs.28914	Hs.28914:adenine phosphoribosyltransfera	2.53
	438317	AA826401	Hs.122393	Hs.122393:ESTs	2.53
	409299	AA045650	Hs.53125	NM_004597:Homo sapiens small nuclear rib	2.53
	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	2.53
50	412525	AA581439	Hs.152328	Hs.152328:ESTs	2.53
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.53
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif-	2.53
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	2.53
	434274	AA628539	Hs.57783	Hs.57783:eukaryotic translation initiati	2.53
55	400282		Hs.289101	NM_005313:Homo sapiens glucose regulated	2.53
	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	2.53
	453344	BE349075	Hs.44571	Hs.44571:ESTs	2.53
	449915	NM_004529	Hs.404	NM_004529:Homo sapiens myeloid/lymphoid	2.53
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.52
60	439012	BE383814	Hs.6455	NM_006666:Homo sapiens RuvB-like 2 (E. c	2.52
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.52
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidas	2.52
	442315	AA173992	Hs.7956	Hs.7956:ESTs	2.52
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.52
65	422385	BE549407	Hs.115823	(locuslink)NM_006638:Homo sapiens ribonu	2.52
	433517	AW022133	Hs.189838	Hs.189838:ESTs	2.52
	450230	AW016607	Hs.201582	Hs.201582:ESTs	2.52
	432866	BE395875	Hs.279609	NM_014342:Homo sapiens mitochondrial car	2.52
	433001	AF217513	Hs.279905	NM_016359:Homo sapiens nucleolar protein	2.52
70	440773	AA352702	Hs.37747	NM_022767:Homo sapiens hypothetical prot	2.52
	440587	AL138461	Hs.323084	(locuslink)NM_031209:Homo sapiens tRNA-g	2.52
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	2.52
	424259	AK001776	Hs.143954	(locuslink)NM_018270:Homo sapiens chromo	2.52
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.52
75	453204	R10799	Hs.191990	Hs.191990:ESTs	2.52
	453665	AA626250	Hs.326184	Hs.326184:Homo sapiens nuclear protein p	2.52
	432353	NM_016558	Hs.274411	NM_016558:Homo sapiens SCAN domain conta	2.52
	433271	BE621697	Hs.14317	NM_018648:Homo sapiens nucleolar protein	2.51
	431770	BE221880	Hs.268555	NM_012255:Homo sapiens 5'-3' exoribonuc	2.51
80	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	2.51
	428839	AI767756	Hs.82302	(locuslink)NM_147174:Homo sapiens hepara	2.51
	404826				2.51
	429669	BE185499	Hs.2471	NM_014878:Homo sapiens KIAA0020 gene pro	2.51
	434474	AL042936	Hs.211571	(locuslink)NM_005333:Homo sapiens holocy	2.51
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	2.51
	450422	AA743525	Hs.60300	NM_033414:Homo sapiens hypothetical prot	2.51
	440214	AA247118	Hs.7049	(locuslink)NM_018386:Homo sapiens hypoth	2.51

421168	AF182277	Hs.330780	Hs.330780:cytochrome P450, subfamily IIB	2.51
435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.51
452101	T60298	Hs.10844	NM_052972:Homo sapiens leucine-rich alph	2.51
436043	AW963838	Hs.168830	Hs.168830:Homo sapiens cDNA FLJ12136 fis	2.51
424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	2.51
435677	AA694142	Hs.6685	Hs.6685:thyroid hormone receptor interac	2.51
406363				2.51
452018	AW102941	Hs.211265	Hs.211265:ESTs	2.51
409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.51
421937	AI878857	Hs.109706	NM_016185:Homo sapiens hemalogical and	2.51
416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.51
421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	2.50
434584	D57341	Hs.188361	Hs.188361:Homo sapiens cDNA FLJ12807 fis	2.50
428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	2.50
426053	U68105	Hs.172182	NM_002568:Homo sapiens poly(A) binding p	2.50
432642	BE297635	Hs.3069	NM_004134:Homo sapiens heat shock 70kD p	2.50
452390	AI864142	Hs.29288	(locuslink)NM_022759:Homo sapiens endo-b	2.50
429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	2.50
400076				2.50
420596	NM_002692	Hs.99185	NM_002692:Homo sapiens polymerase (DNA d	2.50
422244	Y08890	Hs.113503	NM_002271:Homo sapiens karyopherin (impo	2.50
410723	AA100683	Hs.372108	Hs.372108:ESTs	2.50
435496	AW840171	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.50
425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	2.50
433626	AF078859	Hs.86347	NM_013341:Homo sapiens hypothetical prot	2.50
448391	H71025	Hs.21075	NM_016328:Homo sapiens GTF2I repeat doma	2.50

TABLE 10B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
406685	0_0	M18728
434414	35978_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175 BF854337
432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG966155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
406708	0_0	AI282759
459306	223120_-4	AW578452
447349	1063443_1	BE743847 AW809603 BM469626 AI375546
441153	264480_3	BE562826 BE378727

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404519	8152000	Plus	12817-13000
406399	9256288	Minus	63448-63554
403220	7630969	Plus	64338-64517
404661	9797073	Plus	33374-33675,33769-34008
402496	9797769	Minus	8615-9103
403055	8748904	Minus	109532-110225
400965	7770576	Minus	173043-173564
403218	7630969	Plus	58039-58149
401866	8018106	Plus	73126-73623
403221	7630969	Plus	66294-66438,66936-67124
401519	6649315	Plus	157315-157950
405451	7622517	Minus	145949-146227
403532	8076842	Minus	81750-81901
402944	9368423	Plus	110411-110716,111173-111640
403219	7630969	Plus	61858-61995
403381	9438267	Minus	26009-26178
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
404684	9797403	Minus	110881-111020
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
405506	6466489	Plus	80014-80401,80593-81125
403739	7630882	Plus	44563-44766,48209-48483,52255-52495

406545	7711510	Plus	145662-145781,147854-147984,148098-14824
401405	7768126	Minus	69276-69452,69548-69958
400750	8119067	Plus	198991-199168,199316-199548
401179	9438647	Plus	113477-113893
400529	9796988	Plus	138232-138423
403817	8962065	Plus	110297-111052
400448	9887687	Minus	177372-177674
406122	9144087	Minus	30940-31386
406180	7283201	Minus	38923-39107
402829	8918414	Plus	101532-101852,102006-102263
400995	8099094	Plus	141186-141601
404826	6572184	Plus	47726-48046
406363	9256114	Plus	14403-14602,17000-17147,17241-17368

Table 11A lists about 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium) that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 3.0, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 11A: 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigenelD	Unigene Title	R1
436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	37.18
406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	31.24
407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	24.81
406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	20.54
431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	20.38
428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	20.13
406667	M12523			19.89
437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	19.68
446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	19.55
423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease i	18.33
421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	17.47
414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	17.37
416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	16.99
422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	15.15
441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefol factor 1	14.23
407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	14.12
422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	13.64
432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.48
424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	13.43
418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, LI c	13.20
453863	X02544	Hs.572	Hs.572:orosomucoid 1	13.06
413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	12.58
436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.34
421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	11.72
409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	11.72
452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	11.49
406399				11.25
414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	11.12
407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	11.01
423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.70
447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	10.69
450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	10.57
427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (10.48
418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	10.20
422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	10.19
423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	9.72
422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	9.70
430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	9.65
406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.52
428355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	9.47
422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	9.41
413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	9.39
422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	9.31
417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 I	9.30

5	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	9.01
	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	8.99
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.80
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	8.71
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	8.67
10	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	8.47
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	8.47
	422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	8.43
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	8.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	8.12
15	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	8.09
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	7.96
	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	7.92
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	7.89
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	7.87
20	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	7.71
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	7.58
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.48
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I isof	7.31
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	7.31
25	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	7.29
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	7.23
	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	7.12
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	7.12
30	414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	7.10
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	7.06
	452194	AI694413	Hs.373599	Hs.373599:EST	7.02
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.97
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.96
35	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	6.96
	403220				6.95
	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	6.87
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	6.87
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	6.80
40	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.78
	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
	422511	AU076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	6.66
	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	6.65
	431301	AA502384	Hs.151529	Hs.151529:ESTs	6.62
45	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	6.59
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	6.56
	431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine deficie	6.54
	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	6.50
50	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.47
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	6.46
	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	6.45
	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.41
	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	6.41
55	419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	6.27
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	6.20
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19
	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	6.19
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	6.18
60	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	6.16
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	6.16
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	6.15
	426174	AA547959	Hs.115838	Hs.115838:ESTs	6.10
	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	6.07
65	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	6.06
	409453	AI885516	Hs.95612	Hs.95612:ESTs	6.06
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	6.03
	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	5.99
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	5.97
70	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif	5.95
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.92
	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	5.90
	428874	W32133	Hs.194366	Hs.194366:transthyretin (prealbumin, amy	5.88
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	5.88
75	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	5.86
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis,	5.82
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	5.77
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	5.75
80	403218				5.74
	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	5.72
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	5.72
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	5.72
	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.72
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	5.71
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	5.70
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	5.70

5	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	5.67
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	5.67
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.63
	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	5.62
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	5.60
10	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	5.59
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.58
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.56
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	5.56
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	5.54
15	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	5.53
	403221				5.52
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	5.52
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.48
20	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	5.44
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.42
	436251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	5.41
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	5.36
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	5.34
25	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	5.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	5.32
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.31
	430680	AW138724	Hs.168974	Hs.168974:ESTs	5.25
	432378	AI493046	Hs.146133	Hs.146133:ESTs	5.25
30	419693	AA133749	Hs.301350	Hs.301350:FXFD domain-containing ion tra	5.24
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	5.21
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	5.21
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	5.21
	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	5.20
35	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	5.20
	428289	M26301	Hs.2253	Hs.2253:complement component 2	5.19
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	5.19
	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	5.15
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	5.13
40	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	5.11
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	5.09
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	5.08
	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	5.08
	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	5.07
45	432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	5.07
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	5.07
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	5.06
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	5.06
	414361	AI086138	Hs.204044	Hs.204044:ESTs	5.04
50	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	5.03
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	5.03
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	5.01
	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	5.00
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.99
55	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	4.99
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.98
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	4.98
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.98
	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.97
60	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	4.97
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.95
	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	4.95
	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.93
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.93
65	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	4.93
	431779	AW971178	Hs.268571	(locuslink)NM_001645:Homo sapiens apolip	4.92
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.91
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.91
	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
70	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.89
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.89
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.88
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	4.88
	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	4.87
75	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (4.87
	405484				4.87
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	4.87
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	4.86
	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	4.83
80	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	4.81
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.79
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.79
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.79
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	4.78
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.77
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.76
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	4.76

	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	4.75
	400529				4.75
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carc	4.75
	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
5	447966	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	4.72
	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.72
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.70
	405556				4.70
10	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.70
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	4.70
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.70
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.70
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, ren	4.65
15	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.64
	403739				4.61
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	4.61
	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	4.61
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	4.60
20	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.60
	447335	BE617695	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.59
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	4.59
	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	4.59
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	4.59
25	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.58
	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	4.57
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.57
	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	4.55
	409964	AW368226	Hs.67928	Hs.67928:ESTs	4.54
30	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	4.54
	432407	AA221036		AF134164:Homo sapiens Human endogenous r	4.54
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.53
	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyro	4.53
	403219				4.53
35	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.52
	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	4.51
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.51
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutas	4.51
40	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.50
	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carc	4.50
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.49
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.48
45	434263	N34895	Hs.79187	Hs.79187:cox sackie virus and adenovirus	4.47
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	4.47
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	4.46
	452299	AW206330	Hs.355663	Hs.355663:ESTs	4.46
50	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.46
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	4.46
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.46
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	4.45
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	4.44
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	4.44
55	419559	Y07828	Hs.91096	NM_007028:Homo sapiens tripartite motif	4.44
	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	4.43
	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.43
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	4.43
	435777	AW4119202	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.42
60	422867	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix prot	4.41
	431350	AI192528	Hs.164537	Hs.164537:ESTs	4.39
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	4.39
	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	4.39
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	4.38
65	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	4.38
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	4.38
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	4.38
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	4.37
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	4.36
70	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alph	4.36
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.35
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.34
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (4.34
	424865	AF011333	Hs.153563	NM_002349:Homo sapiens lymphocyte antige	4.34
75	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	4.33
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	4.32
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.32
	417526	AA558906	Hs.82240	Hs.82240:syntaxin 3A	4.32
80	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	4.31
	436391	AJ227892	Hs.146274	Hs.146274:ESTs	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.29
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.29
	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	4.29

5	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	4.29
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	4.29
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	4.28
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.27
	409636	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	4.27
10	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	4.27
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	4.27
	410199	AW377424	Hs.205126	Hs.205126:Homo sapiens cDNA: FLJ22667 fi	4.24
	431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	4.24
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (4.24
15	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	4.23
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	4.23
	436856	AI469355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	4.23
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	4.23
	426682	AV660038	Hs.2056	Hs.2056:UDP glycosyltransferase 1 family	4.23
20	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	4.22
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	4.22
	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	4.21
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	4.21
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	4.21
25	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	4.20
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
	426427	M86699	Hs.169840	Hs.169840:TTK protein kinase	4.19
	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	4.19
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cispla	4.19
30	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.19
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	4.18
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	4.17
	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	4.17
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	4.17
35	404826				4.17
	414198	AW505308	Hs.75812	NM_004563:Homo sapiens phosphoenolpyruva	4.17
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	4.17
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	4.16
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	4.16
40	420319	AW406289	Hs.96593	NM_019034:Homo sapiens ras homolog gene	4.15
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	4.15
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	4.14
	431890	X17033	Hs.271996	NM_002203:Homo sapiens integrin, alpha 2	4.14
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	4.13
45	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	4.13
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	4.13
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	4.12
	428471	X57348	Hs.184510	Hs.184510:stratifin	4.12
50	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.11
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	4.10
	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	4.10
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	4.10
	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	4.10
55	413835	AI272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	4.09
	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	4.09
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	4.09
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	4.09
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	4.08
60	421190	U95031	Hs.102482	Hs.102482:mucin 5, subtype B, tracheobro	4.08
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	4.08
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	4.06
	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	4.06
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
65	443802	AW504924	Hs.9805	Hs.9805:exportin 5	4.04
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	4.04
	434808	AF155108	Hs.256150	Hs.256150:NY-REN-41 antigen	4.04
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	4.04
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	4.02
70	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	4.02
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	4.02
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.02
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	4.01
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	4.00
75	414812	X72755	Hs.77367	NM_002416:Homo sapiens monokine induced	4.00
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	3.99
	431958	X63629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	3.98
	418661	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription	3.98
	419092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transm	3.98
80	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	3.98
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.97
	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.96
	436485	X59135	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.96
	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.95
	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	3.94
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.94
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	3.94

5	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.94
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	3.93
	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	3.93
	409463	A1458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	3.92
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	3.92
10	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	3.91
	428698	AA852773	Hs.334838	Hs.334838:KIAA1866 protein	3.90
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	3.89
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanine	3.89
	407971	A1469117	Hs.62918	Hs.62918:CDC91 cell division cycle 91-li	3.89
15	440750				3.89
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	3.89
	413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	3.89
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	3.89
	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	3.88
20	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolinate phosph	3.88
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.88
	417129	AI381800	Hs.300684	Hs.300684:calictonin gene-related peptid	3.87
	410268	AA316181	Hs.61635	NM_012449:Homo sapiens six transmembrane	3.87
	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	3.87
25	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	3.86
	449667	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.86
	400298	AA032279	Hs.61635	Hs.61635:six transmembrane epithelial an	3.85
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	3.85
	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	3.85
30	413380	AI904232	Hs.75323	Hs.75323:prohibitin	3.85
	452220	BE158006	Hs.212296	Hs.212296:ESTs	3.85
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	3.85
	433658	L03678	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.84
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	3.84
35	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.84
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	3.84
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens mel transforming	3.84
	427318	AF186081	Hs.175783	NM_014579:Homo sapiens solute carrier fa	3.83
	459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	3.83
40	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.83
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	3.82
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.82
	426514	BE616633	Hs.170195	Hs.170195:bone morphogenetic protein 7 (3.82
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.82
45	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	3.81
	421481	AW391972	Hs.104696	Hs.104696:KIAA1324 protein	3.81
	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	3.80
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	3.80
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	3.80
50	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.80
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diffe	3.80
	410219	T98226	Hs.171952	Hs.171952:occludin	3.80
	407137	T97307			3.78
	430462	AI584156	Hs.105640	Hs.105640:hypothetical protein BC007772	3.78
55	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens interf	3.78
	450010	AW293801	Hs.255052	Hs.255052:ESTs	3.78
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	3.78
	440676	NM_004987	Hs.112378	(locuslink)NM_004987:Homo sapiens LIM an	3.77
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protei	3.77
60	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrid	3.77
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	3.77
	443323	BE560621	Hs.9222	Hs.9222:estrogen receptor binding site a	3.76
	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.76
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	3.76
65	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	3.75
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.74
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	3.74
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.74
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.74
70	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.74
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	3.74
	435886	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.73
	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutat	3.73
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	3.73
75	400419	AF084545		AF084545:Homo sapiens versican Vint isof	3.73
	421357	AK000609	Hs.103808	NM_017896:Homo sapiens chromosome 20 ope	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.73
	452679	Z42387	Hs.83883	(locuslink)NM_020182:Homo sapiens transm	3.72
80	419743	AW408762	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.72
	435730	AB020635	Hs.4984	Hs.4984:KIAA0828 protein	3.72
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.72
	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypoth	3.72
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCTA00142	3.71
	413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjuga	3.71
	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis,	3.71
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	3.71

5	406722	H27498	Hs.293441	Hs.293441:Homo sapiens SNC73 protein (SN	3.71
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	3.71
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.70
	409327	L41162	Hs.53563	NM_001853:Homo sapiens collagen, type IX	3.70
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.70
10	400846				3.70
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.70
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	3.70
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.70
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	3.69
15	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	3.69
	432215	AU076609	Hs.2934	NM_001033:Homo sapiens ribonucleotide re	3.69
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.69
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (3.69
	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.68
20	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.68
	401179				3.67
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.67
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.67
	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-ral simian leuk	3.66
25	409402	AF208234	Hs.695	Hs.695:cystatin B (stefin B)	3.66
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.66
	432633	AI796390	Hs.210667	Hs.210667:ESTs	3.66
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.66
	453857	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.65
30	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.65
	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	3.65
	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	3.64
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.64
	441128	AA570256	Hs.348504	Hs.348504:hypothetical protein BC014072	3.64
35	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.64
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	3.63
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.62
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.62
	452098	AI858183		BF755039:QV0-CT0583-181000-428-f07 CT058	3.62
40	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	3.62
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.61
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.61
	400847				3.60
	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	3.60
45	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.60
	404854				3.60
	400448				3.60
	453331	AI240665	Hs.352537	Hs.352537:Homo sapiens cDNA FLJ13066 fis	3.60
	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.60
50	417389	BE260964	Hs.82045	Hs.82045:midline (neurite growth-promoti	3.59
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.59
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	3.59
	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.59
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	3.59
55	426722	U53823	Hs.171952	NM_002538:Homo sapiens occludin (OCLN)	3.58
	420531	AI652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.58
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	3.57
	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.57
	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.57
60	424241	AW995948	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, i	3.57
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.57
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.56
	434224	AA380731	Hs.84	NM_000206:Homo sapiens interleukin 2 rec	3.56
	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.56
65	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.56
	413859	AW992356	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, i	3.56
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.55
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	3.55
	411704	AI499220	Hs.71573	(locuslink)NM_017988:Homo sapiens hypoth	3.55
70	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.54
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.54
	453323	AF034102	Hs.32951	NM_001532:Homo sapiens solute carrier fa	3.54
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.54
	452488	N74921	Hs.184389	Hs.184389:ESTs, Moderately similar to S1	3.54
75	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.54
	426811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.53
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.53
	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.53
	428582	BE336699	Hs.185055	Hs.185055:BENE protein	3.53
80	446147	AL133064	Hs.14051	(locuslink)NM_145698:Homo sapiens endoze	3.53
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.52
	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.52
	442007	AA301116	Hs.142838	NM_032390:Homo sapiens MKI67 (FHA domain	3.52
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.52
	421642	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	3.51
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.51
	421340	F07783	Hs.1369	NM_000574:Homo sapiens decay acceleratin	3.50

	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	3.50
	452862	AW378065	Hs.8687	Hs.8687:ESTs	3.50
	442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.50
5	404240				3.50
	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	3.50
	429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	3.50
	445937	AI452943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.49
10	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.49
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.49
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associat	3.49
	456534	X91195	Hs.100623	NM_138689:Homo sapiens protein phosphata	3.49
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.49
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.49
15	439841	AF038961	Hs.6710	NM_004870:Homo sapiens mannose-P-dolicho	3.49
	428390	AI640377	Hs.350077	NM_000982:Homo sapiens ribosomal protein	3.48
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alpha	3.48
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	3.48
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	3.48
20	457635	AV660976	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.48
	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.48
	454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypoth	3.48
	402829				3.47
	451707	AW051061	Hs.60973	Hs.60973:Homo sapiens cDNA FLJ40829 fis,	3.47
25	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.47
	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.47
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976 fis	3.47
	439223	AW238299	Hs.250618	NM_025217:Homo sapiens UL16 binding prot	3.46
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.46
30	450273	AW296454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	3.46
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	3.46
	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	3.46
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.45
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif	3.45
35	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfait 4 (SURF4)	3.45
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.45
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	3.45
	410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.45
	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	3.44
40	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.44
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.44
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.44
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (3.44
	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	3.44
45	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	3.44
	448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.44
	420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	3.44
	412420	AL035668	Hs.73853	NM_001200:Homo sapiens bone morphogeneti	3.43
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	3.43
50	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prostatic)	3.43
	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	3.43
	428093	AW594506	Hs.104830	Hs.104830:ESTs	3.43
	428293	BE250944	Hs.183556	Hs.183556:solute carrier family 1 (neutr	3.42
55	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.42
	442821	BE391929	Hs.8752	Hs.8752:transmembrane protein 4	3.42
	427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.42
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.41
	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.41
	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	3.41
60	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	3.41
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	3.41
	423323	AI951628	Hs.127007	NM_003740:Homo sapiens potassium channel	3.41
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	3.41
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.40
65	422256	M64673	Hs.1499	NM_005526:Homo sapiens heat shock transc	3.40
	451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.40
	400205		Hs.81848	NM_006265:Homo sapiens RAD21 homolog (S.	3.40
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.39
	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.39
70	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.39
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.39
	406363				3.39
	444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methyl	3.39
	423309	BE006775	Hs.126782	NM_014467:Homo sapiens sushi-repeat prot	3.38
75	426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	3.38
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.38
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.38
	457670	AF119666	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.38
	400125		Hs.125078	(locuslink)NM_004152:Homo sapiens ornith	3.38
80	429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylation	3.37
	410293	AK000047	Hs.61960	NM_018992:Homo sapiens hypothetical prot	3.37
	434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.37
	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.37
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	3.37

	446715	AI337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	3.36
	426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.36
	429747	M87507	Hs.2490	Hs.2490:caspase 1, apoptosis-related cys	3.36
5	406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.36
	439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.36
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.36
	421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	3.36
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.36
10	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	3.36
	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	3.36
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	3.35
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.35
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.35
15	457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	3.35
	432169	Y00971	Hs.2910	NM_002765:Homo sapiens phosphoribosyl py	3.35
	412525	AA581439	Hs.152328	Hs.152328:ESTs	3.35
	416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	3.35
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	3.35
20	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	3.34
	400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.34
	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	3.34
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	3.34
	450506	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.34
25	437296	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	3.34
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.34
	439246	AI498072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.34
30	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	3.34
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.34
	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	3.34
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.34
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	3.33
35	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.33
	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	3.33
	414271	AK000275	Hs.75871	(locuslink)NM_012408:Homo sapiens protei	3.33
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.33
	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	3.32
40	430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.32
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	3.32
	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	3.32
	430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripar	3.32
45	402104				3.32
	446620	AA128808	Hs.179902	(locuslink)NM_022109:Homo sapiens CDw92	3.32
	443425	AI056776	Hs.133397	Hs.133397:ESTs	3.32
	414883	AA926960	Hs.348669	Hs.348669:CDK28 protein kinase 1	3.31
50	413063	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.31
	451564	AU076698	Hs.132760	(locuslink)NM_001467:Homo sapiens glucos	3.31
	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	3.31
	441866	BE464341	Hs.21201	Hs.21201:nectin 3	3.31
	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.31
	422192	AA305159	Hs.113019	NM_015931:Homo sapiens fis485 (LOC51066)	3.31
55	446506	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.31
	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytosol	3.31
	449644	AW960707	Hs.148324	Hs.148324:ESTs	3.31
	422611	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosy	3.31
	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	3.30
60	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	3.30
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.30
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.30
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	3.30
	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	3.30
65	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.29
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	3.29
	442772	AW503680	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.29
	430281	AI878842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.29
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.29
70	420332	NM_001756	Hs.1305	NM_001756:Homo sapiens serine (or cystei	3.29
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	3.29
	412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	3.28
	427308	D26067	Hs.174905	Hs.174905:KIAA0033 protein	3.28
	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.28
75	449199	AI990122	Hs.196988	Hs.196988:ESTs	3.28
	442739	NM_007274	Hs.8679	(locuslink)NM_007274:Homo sapiens cytosol	3.28
	422051	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	3.28
	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	3.28
	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.28
80	402260				3.28
	409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multid	3.28
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.28
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.27
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.27

5	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.27
	434521	NM_002267	Hs.3886	Hs.3886:karyopherin alpha 3 (importin al	3.27
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.27
	445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	3.27
	448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	3.26
10	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	3.26
	440286	U29589	Hs.7138	NM_000740:Homo sapiens cholinergic recep	3.26
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	3.26
	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	3.26
	426520	BE545684	Hs.343566	Hs.343566:KIAA0251 protein	3.26
15	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.26
	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	3.26
	425966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.25
	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	3.25
	449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.25
20	424381	AA285249	Hs.146329	NM_007194:Homo sapiens CHK2 checkpoint h	3.25
	426784	U03749	Hs.172216	NM_001275:Homo sapiens chromogranin A (p	3.25
	420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.25
	438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	3.24
	419216	AU076718	Hs.164021	NM_002993:Homo sapiens small inducible c	3.24
25	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.24
	458376	AB023179	Hs.9059	Hs.9059:KIAA0962 protein	3.24
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	3.24
	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.24
	435640	AF220053	Hs.64960	NM_018468:Homo sapiens uncharacterized h	3.23
30	427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	3.23
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	3.23
	430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	3.23
	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.23
	432731	R31178	Hs.287820	Hs.287820:fibronectin 1	3.23
35	410340	AW182833	Hs.112188	(locuslink)NM_021826:Homo sapiens hypoth	3.23
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	3.23
	430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	3.23
	425907	AA365752	Hs.155965	Hs.155965:ESTs	3.23
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	3.22
40	403912				3.22
	429782	NM_005754	Hs.220689	Hs.220689:Ras-GTPase-activating protein	3.22
	416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	3.22
	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.22
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	3.22
45	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	3.22
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.22
	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	3.22
	450770	AA019924	Hs.28803	Hs.28803:ESTs	3.22
	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	3.22
50	414172	AW954324	Hs.75790	(locuslink)NM_002642:Homo sapiens phosph	3.21
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	3.21
	432078	BE314877	Hs.24553	(locuslink)NM_022369:Homo sapiens hypoth	3.21
	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.21
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	3.21
55	409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	3.21
	400836				3.20
	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	3.20
	414343	AL036166	Hs.75914	NM_006815:Homo sapiens coated vesicle me	3.20
	447096	BE539199	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	3.20
60	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.20
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.20
	407736	NA1744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.20
	400845				3.20
	407082	Z47055			3.20
65	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kinesi	3.20
	403217				3.20
	414249	AI797994	Hs.279929	(locuslink)NM_017510:Homo sapiens gp25L2	3.19
	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.19
	417777	AI823763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis,	3.19
70	457274	AW674193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	3.19
	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XIII	3.19
	430280	AA361258	Hs.237868	Hs.237868:Homo sapiens mRNA; cDNA DKFZp6	3.19
	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	3.19
	422938	NM_001809	Hs.1594	NM_001809:Homo sapiens centromere protei	3.18
75	435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.18
	449704	AK000733	Hs.23900	Hs.23900:Rac GTPase activating protein 1	3.18
	426925	NM_001196	Hs.172894	Hs.172894:BH3 interacting domain death a	3.18
	414814	D14697	Hs.77393	(locuslink)NM_002004:Homo sapiens farnes	3.18
	405387				3.18
80	444108	R55784	Hs.140942	Hs.140942:Homo sapiens cDNA FLJ38396 fis	3.18
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2-I	3.17
	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.17
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	3.17
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	3.17
	447032	AK000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.17
	410663	AA194952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.17

	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3-)-glycopro	3.17
	451032	W03692	Hs.323079	Hs.323079:Homo sapiens mRNA; cDNA DKFZp5	3.17
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	3.17
5	417018	M16038	Hs.80887	Hs.80887:v-yes-1 Yamaguchi sarcoma viral	3.16
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.16
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	3.16
	432728	NM_006979	Hs.278721	NM_006979:Homo sapiens HLA class II regi	3.16
10	442643	U82756	Hs.374973	(locuslink)NM_004697:Homo sapiens PRP4 p	3.16
	418462	BE001596	Hs.85266	Hs.85266:integrin, beta 4	3.16
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	3.16
	429556	AW139399	Hs.314807	Hs.314807:hypothetical protein MGC2655	3.15
	418127	BE243982	Hs.83532	(locuslink)NM_002389:Homo sapiens membra	3.15
15	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	3.15
	435968	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens integr	3.15
	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.15
	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	3.15
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.14
20	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	3.14
	407961	AW672939	Hs.41694	Hs.41694:origin recognition complex, sub	3.14
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-II	3.14
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.14
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	3.14
25	450295	AI766732	Hs.210628	Hs.210628:ESTs	3.14
	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
	452695	AW780199	Hs.30327	NM_003668:Homo sapiens mitogen-activated	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.13
30	424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (renal a	3.13
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	3.13
	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	3.12
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	3.12
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	3.12
35	438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
	424727	AW590378	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.12
	435975	AL118990	Hs.373554	(locuslink)NM_130786:Homo sapiens alpha-	3.12
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	3.12
	412326	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
40	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	3.12
	428699	AW578252	Hs.190161	Hs.190161:LRB protein	3.12
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	3.12
	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.12
	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	3.12
45	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	3.12
	410240	AL157424	Hs.61289	Hs.61289:synaptojanin 2	3.12
	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	3.11
	406865	AI025931	Hs.181357	Hs.181357:laminin receptor 1 (67kD, ribo	3.11
	405203				3.11
50	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	3.11
	417211	T97617	Hs.269092	Hs.269092:ESTs	3.11
	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	3.11
	429824	AA296363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.11
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	3.11
55	408805	H69912	Hs.48269	NM_003384:Homo sapiens vaccinia related	3.10
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	3.10
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	3.10
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	3.10
	429597	NM_003816	Hs.2442	Hs.2442:a disintegrin and metalloprotein	3.10
60	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.10
	429238	NM_002849	Hs.198288	NM_002849:Homo sapiens protein tyrosine	3.10
	433409	AI278802	Hs.25661	Hs.25661:ESTs, Moderately similar to hyp	3.10
	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.10
	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.10
65	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	3.10
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic I	3.10
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	3.10
70	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.10
	433435	BE545277	Hs.340959	NM_005726:Homo sapiens Ts translation el	3.09
	408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	3.09
	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-fl	3.09
	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	3.09
75	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.09
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	3.09
	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	3.09
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	3.09
	430066	AI929659	Hs.237825	Hs.237825:signal recognition particle 72	3.09
80	428044	AA093322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	3.09
	426989	AI815205	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (3.08
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	3.08
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	3.08
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	3.08

	410668	BE379794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	3.08
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.08
	419757	AA773820	Hs.63970	Hs.63970:ESTs	3.08
5	427725	U66839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	3.08
	424408	AI754813	Hs.146428	Hs.146428:collagen, type V, alpha 1	3.08
	453914	NM_000507	Hs.574	NM_000507:Homo sapiens fructose-1,6-bisph	3.08
	420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	3.08
10	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	3.07
	411423	AW845987	Hs.68864	(locuslink)NM_139248:Homo sapiens membra	3.07
	449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	3.07
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to choli	3.07
	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antimicr	3.07
15	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 l	3.07
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	3.07
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	3.07
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	3.07
	436553	AW407157	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.06
20	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	3.06
	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	3.06
	418062	AW630656	Hs.83383	NM_006406:Homo sapiens peroxiredoxin 4 (3.06
	407223	H96850		H96850:yw03b12.s1 Soares melanocyte 2NbH	3.06
	418641	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.06
25	450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXYD d	3.06
	408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	3.06
	435550	AI224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	3.06
	421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.05
	440246	W52010	Hs.191379	Hs.191379:ESTs	3.05
30	446770	AV660309	Hs.154986	Hs.154986:ESTs, Weakly similar to PLLP_H	3.05
	440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	3.05
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	3.05
	453830	AA534296	Hs.20953	Hs.20953:hypothetical protein BC010003	3.05
	412867	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	3.05
35	422032	AA476966	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	3.05
	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	3.05
	408524	D87942	Hs.46328	Hs.46328:fucosyltransferase 2 (secretor	3.05
	408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	3.05
	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	3.04
40	432281	AK001239	Hs.274263	Hs.274263:hypothetical protein FLJ10377	3.04
	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	3.04
	423570	AW838306	Hs.129819	NM_018344:Homo sapiens hypothetical prot	3.04
	443653	AA137043	Hs.9663	NM_013374:Homo sapiens programmed cell d	3.04
45	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	3.04
	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	3.04
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	3.04
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.04
	453450	AW797627	Hs.347459	Hs.347459:Homo sapiens cDNA FLJ13900 fis	3.04
50	412708	R26830	Hs.106137	Hs.106137:Homo sapiens mRNA for OK/SW-CL	3.04
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	3.04
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	3.03
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	3.03
	412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	3.03
	444309	U83236	Hs.10803	Hs.10803:calcium and integrin binding 1	3.03
55	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	3.03
	430354	AA954810	Hs.239784	Hs.239784:scribble	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	3.03
	421179	U72664	Hs.148495	NM_002810:Homo sapiens proteasome (proso	3.02
60	451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	3.02
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	3.02
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.02
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.02
	417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	3.02
65	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	3.02
	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis,	3.01
	414421	AI521130	Hs.355126	(locuslink)NM_144686:Homo sapiens hypoth	3.01
	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Not56 (D. melanog	3.01
	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	3.01
70	437651	BE560672	Hs.13543	(locuslink)NM_145214:Homo sapiens tripar	3.01
	436540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	3.00
	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protei	3.00
	415697	AI365603	Hs.279696	Hs.279696:DKFZP566I1024 protein	3.00
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	3.00
75	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	3.00
	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	3.00
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.00
	406868	AA505445	Hs.300697	Hs.300697:immunoglobulin heavy constant	3.00
	424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	3.00
80	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	3.00
	417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rh-related antige	3.00

TABLE 11B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	406685	0_0	M18728
10	432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748884 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
15	459306	223120_-4	AW578452
	452098	161393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 AI858183
	451129	1495511_1	BE072881 AI762181 BE072946

TABLE 11C

20 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 25 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
	406399	9256288	Minus	63448-63554
30	403220	7630969	Plus	64338-64517
	403218	7630969	Plus	58039-58149
	403221	7630969	Plus	66294-66438,66936-67124
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
	400529	9796988	Plus	138232-138423
35	405556	1552511	Plus	163497-163623,164715-164968,165369-16550
	403739	7630882	Plus	44563-44766,48209-48483,52255-52495
	403219	7630969	Plus	61858-61995
	404826	6572184	Plus	47726-48046
	400750	8119067	Plus	198991-199168,199316-199548
40	400846	9188605	Plus	39310-39474
	401179	9438647	Plus	113477-113893
	400847	9188605	Plus	44643-44835
	404854	7143420	Plus	14260-14537
	400448	9887687	Minus	177372-177674
45	404240	5002624	Minus	116132-116407,116653-116922
	402829	8918414	Plus	101532-101852,102006-102263
	406363	9256114	Plus	14403-14602,17000-17147,17241-17368
	402104	8119072	Plus	122409-122600
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
50	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	400836	8954179	Plus	677-1188
	400845	9188605	Plus	34428-34612
	403217	7630969	Plus	54089-54163,55427-55623
	405387	6587915	Minus	3769-3833,5708-5895
55	405203	7230116	Plus	125295-125463

60 Table 12A lists about 1006 genes up-regulated in cervical cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" cervical cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" cervical cancer level was set to the 93rd percentile value amongst cervical cancers. The "average" normal adult tissue level was set to the 93rd percentile value amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 12A: 1006 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES

65 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 70 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
75	402075	U19557	Hs.123035	squamous cell carcinoma antigen 2 (SCCA2)	81.1
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	43.6
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial coll	38.9
	435094	AI560129	Hs.329062	EST	30.3
	439606	W79123	Hs.58561	G protein-coupled receptor 87	28.8
80	452240	AI591147	Hs.61232	ESTs	27.0
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin bi	26.0
	417034	NM_006183	Hs.80962	neurotensin	25.5
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, cl	24.5
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	23.7

	435505	AF200492	Hs.211238	interleukin-1 homolog 1	21.2
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	20.5
	418345	AJ001696	Hs.241407	serine proteinase inhibitor 13 (PI13; serpin	20.1
5	452461	N78223	Hs.108106	transcription factor	19.8
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor, cl	19.2
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	17.5
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-type,	16.4
	435243	AW292886	Hs.261373	hypothetical protein dJ434O14.3	16.3
10	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.2
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-C	15.9
	421373	AA808229	Hs.167771	ESTs	15.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	15.4
	441459	AI919142	Hs.214233	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.6
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	13.8
15	412719	AW016610	Hs.129911	ESTs	13.4
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	13.3
	431753	X76029	Hs.2841	neuromedin U	13.2
	438817	AI023799	Hs.163242	ESTs	13.1
20	404996			Target Exon	13.1
	443211	AI128388	Hs.143655	ESTs	12.9
	414764	AW013887	Hs.72047	ESTs	12.9
	428618	AA885360	Hs.160199	Target CAT	12.7
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.7
25	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribosomal	12.6
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.6
	432666	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein produ	12.6
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaphyseal	12.6
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin D 24	12.3
30	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.2
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	11.6
	415989	AI267700	Hs.317584	ESTs	11.5
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	11.4
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	11.3
35	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	11.0
	449260	AA741180	Hs.29879	ESTs	11.0
	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN HOMEOB	10.7
	406467			Target Exon	10.5
40	439926	AW014875	Hs.137007	ESTs	10.2
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, pr	10.2
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	10.2
	414422	AA147224	Hs.337232	Homeo box A13	10.2
	442660	AW138174	Hs.130651	ESTs	10.1
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu or sig	10.0
45	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN ALU SU	9.9
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clo	9.8
	400195	NM_007057		NM_007057:Homo sapiens ZW10 interactor (ZW1N	9.8
	422426	W79117	Hs.58559	ESTs	9.7
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical p	9.7
50	458194	AW393618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN ALU SU	9.4
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR/MRP)	9.4
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothetical p	9.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	9.1
55	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT2RP40	9.1
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.0
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.0
	426427	M86699	Hs.169840	TTK protein kinase	9.0
60	429538	BE182592	Hs.11261	small proline-rich protein 2A	9.0
	446232	AI281848	Hs.194691	retinoic acid induced 3	8.9
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	8.9
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDNA clo	8.9
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	8.9
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	8.9
65	430486	BE062109	Hs.241551	chloride channel, calcium activated, family m	8.7
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	8.7
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	8.7
	407642	AW178963		gb:MR0-ST0032-200899-001-b11 ST0032 Homo sapi	8.7
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily, m	8.7
70	458027	L49054	Hs.85195	myeloid leukemia factor 1	8.4
	424086	AI351010	Hs.102267	lysyl oxidase	8.3
	420092	AA814043	Hs.88045	ESTs	8.3
	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	8.3
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human, odont	8.2
75	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	8.2
	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adren	8.2
	440834	AA907027	Hs.128606	ESTs	8.2
	452724	R84810	Hs.30464	cyclin E2	8.1
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (from c	8.1
80	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine h	8.0
	429228	AI553633	Hs.337139	ESTs	7.9
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome region 14	7.9
	425710	AF030880	Hs.159275	solute carrier family, member 4	7.8
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	7.8

	435159	AA668879	Hs.116649	ESTs	7.7
	439232	N48590	Hs.46693	ESTs	7.7
	437616	AI797163	Hs.207954	ESTs	7.6
	406554			Target Exon	7.4
5	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	7.4
	424098	AF077374	Hs.139322	small proline-rich protein 3	7.3
	418134	AA397769	Hs.86617	ESTs	7.2
	446364	AB006624	Hs.14912	KIAA0286 protein	7.2
10	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (yeast	7.1
	414148	BE084049		gb:PM0-BT0651-270400-003-f02 BT0651 Homo sapi	7.0
	429548	AW138872	Hs.135288	ESTs	7.0
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	7.0
	450192	AA263143	Hs.24596	RAD51-interacting protein	7.0
15	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila ho	6.9
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone COL0454	6.9
	427821	AA470158	Hs.98202	ESTs	6.9
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794 prote	6.9
	425761	AW664214	Hs.196729	ESTs	6.9
20	450028	AI912012	Hs.200737	ESTs	6.8
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated protein N	6.8
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	6.8
	413573	AI733859	Hs.149089	ESTs	6.8
	422330	D30783	Hs.115263	epiregulin	6.8
25	454988	AW850140		gb:IL3-CT0219-261099-023-D11 CT0219 Homo sapi	6.8
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010317E2	6.8
	403471			Target Exon	6.7
	409041	AB033025	Hs.50081	KIAA1199 protein	6.7
	407839	AA045144	Hs.161566	ESTs	6.6
30	415652	T79213	Hs.272073	ESTs	6.6
	420900	AL045633	Hs.44269	ESTs	6.6
	444271	AW452569	Hs.149804	ESTs	6.6
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	6.5
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.5
35	431622	AW979271	Hs.293184	ESTs	6.5
	457405	AA504860		gb:ab03a10.s1 Stratagene fetal retina 937202	6.4
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	6.4
	414812	X72755	Hs.77367	monokine induced by gamma interferon	6.4
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase	6.3
40	446435	AW206737	Hs.253582	ESTs	6.3
	421948	L42583	Hs.334309	keralin 6A	6.3
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	6.3
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-protein	6.2
	406747	AI925153	Hs.217493	annexin A2	6.2
45	453884	AA355925	Hs.36232	KIAA0186 gene product	6.2
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapiens c	6.2
	421773	W69233	Hs.112457	ESTs	6.2
	457435	AW972024	Hs.142653	ret finger protein	6.1
50	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HEMBB10	6.1
	427043	AA397679	Hs.3991	ESTs	6.1
	409723	AW885757	Hs.257862	ESTs	6.1
	459462	AA481396	Hs.105167	ESTs	6.1
	423244	AL038379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	6.0
	427217	AA399272	Hs.144341	ESTs	6.0
55	441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein [H.s	6.0
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferritin a	6.0
	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	5.9
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein [H.s	5.9
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	5.9
60	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced prote	5.9
	414299	AA142989	Hs.71730	ESTs	5.8
	439292	AA090421	Hs.5555	hypothetical protein MGC5347	5.8
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin (140	5.8
	413625	AW451103	Hs.71371	ESTs	5.8
65	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	5.8
	415064	AA159804	Hs.149305	hypothetical protein MGC2603	5.7
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor ty	5.7
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	5.7
	415900	Z43758	Hs.26037	ESTs	5.7
70	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.7
	449611	AI970394	Hs.197075	ESTs	5.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo sapi	5.7
	438639	AI278360	Hs.31409	ESTs	5.7
	414972	BE263782	Hs.77695	KIAA0008 gene product	5.7
75	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1	5.6
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone COL0042	5.6
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	5.6
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	5.5
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase 3)	5.5
80	451307	AW293207	Hs.211516	ESTs	5.5
	441531	AW291239	Hs.271111	ESTs	5.5
	418663	AK001100	Hs.41690	desmocollin 3	5.5
	410659	AI080175	Hs.68826	ESTs	5.5
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo sapi	5.5

	431255	AA497043	Hs.115685	ESTs	5.5
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	5.5
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	5.4
5	418502	R99288	Hs.35152	ESTs	5.4
	440320	AA879294		gb:nw86e09.s1 NCL_CGAP_Pr12 Homo sapiens cDNA	5.4
	439579	AF086400		gb:Homo sapiens full length insert cDNA clone	5.4
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7 (gale	5.4
	408536	AW381532	Hs.135188	ESTs	5.4
10	408758	NM_003686	Hs.47504	exonuclease 1	5.4
	451411	AA017492	Hs.135655	EST	5.4
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.3
	407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	5.3
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin 6)	5.2
	420026	AI831190	Hs.166676	ESTs	5.2
15	427356	AW023482	Hs.97849	ESTs	5.2
	420440	NM_002407	Hs.97644	mammaglobin 2	5.2
	430082	AW514083	Hs.190135	ESTs	5.2
	445259	AI798994	Hs.152923	ESTs	5.2
	457345	AI699933	Hs.192175	ESTs	5.2
20	453161	AA628608	Hs.61656	ESTs	5.2
	445019	AI205540	Hs.281295	ESTs	5.2
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	5.2
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSO	5.2
25	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	5.2
	443179	AI928402	Hs.6933	hypothetical protein FLJ12684	5.2
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, choline, al	5.2
	441020	W79283	Hs.35962	ESTs	5.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	5.1
30	419520	AB009303	Hs.90800	matrix metalloproteinase 16 (membrane-inserte	5.1
	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	5.1
	405547			NM_018833*:Homo sapiens transporter 2, ATP-bi	5.1
	435206	AI432364	Hs.160594	ESTs	5.1
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	5.1
35	439223	AW238299	Hs.250618	UL16 binding protein 2	5.1
	413251	AI932903	Hs.211535	ESTs	5.1
	426320	W47595	Hs.169300	transforming growth factor, beta 2	5.1
	458829	AI557388		gb:PT2.1_6_G03.r tumor2 Homo sapiens cDNA 3',	5.0
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	5.0
40	432473	AI202703	Hs.152414	ESTs	5.0
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino acid	5.0
	423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	5.0
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, protein-gl	5.0
	432867	AW016936	Hs.233364	ESTs	5.0
45	449448	D60730	Hs.57471	ESTs	5.0
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (from c	4.9
	406547			C7000246:gil72477 pir DVHY1C multidrug resis	4.9
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromosomes 1	4.9
	446704	AI337228	Hs.197083	ESTs	4.9
50	443476	AA631492	Hs.23921	hypothetical protein DKFZp547A023	4.9
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypothetic	4.9
	421155	H87879	Hs.102267	lysyl oxidase	4.9
	443335	T89697	Hs.16645	ESTs	4.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell growt	4.8
55	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	4.8
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage elast	4.8
	441720	AI346487	Hs.28739	ESTs	4.8
	442980	AA857025	Hs.8878	kinesin-like 1	4.8
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12	4.8
60	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosome seg	4.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosyltran	4.8
	418939	AW630803	Hs.89497	lamin B1	4.7
	417235	AA810278	Hs.24250	ESTs	4.7
	411958	AA099020		gb:zn45h01.s1 Stratagene HeLa cell s3 937216	4.7
65	433858	N69243	Hs.192974	hypothetical protein FLJ12735	4.7
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	4.7
	418379	AA218940	Hs.137516	fidgetin-like 1	4.7
	401747			Homo sapiens keratin 17 (KRT17)	4.7
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clo	4.7
70	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	4.7
	457465	AW301344	Hs.122908	DNA replication factor	4.6
	433159	AB035893	Hs.150587	kinesin-like protein 2	4.6
	412333	AW937485		gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapi	4.6
	401137			Target Exon	4.6
75	401575			Target Exon	4.6
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL0667	4.6
	421978	AJ243662	Hs.110196	NICE-1 protein	4.6
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	4.6
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PLACE10	4.6
80	450510	AA010056	Hs.242998	ESTs	4.6
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.6
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, type II	4.6
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino acid	4.5
	449416	AI651016	Hs.246311	ESTs	4.5

	416168	H23687		gb:yn72d12.r1 Soares adult brain N2b5HB55Y Ho	4.5
	447033	AI357412	Hs.157601	ESTs	4.5
	446353	AI290919	Hs.153661	ESTs	4.5
5	443715	AI583187	Hs.9700	cyclin E1	4.5
	454707	AW814989		gb:MR1-ST0206-170400-024-g05 ST0206 Homo sapi	4.5
	435435	T89473	Hs.192328	ESTs	4.5
	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	4.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	4.4
10	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.4
	430919	AA489041	Hs.295448	ESTs	4.4
	435313	AI769400	Hs.189729	ESTs	4.4
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	4.4
	433322	H50621	Hs.134156	ESTs, Weakly similar to I38022 hypothetical p	4.4
15	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (p150)	4.4
	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.4
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein ho	4.4
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	4.4
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor, cl	4.4
20	418216	AA662240	Hs.283099	AF15q14 protein	4.4
	446252	AI283125	Hs.150009	ESTs	4.4
	447519	U46258	Hs.339665	ESTs	4.4
	425916	NM_006786	Hs.162200	urotensin 2	4.3
	408420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalinin (10	4.3
25	416320	H47867	Hs.34024	ESTs	4.3
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth facto	4.3
	441582	BE550200	Hs.127197	ESTs	4.3
	414132	AI801235	Hs.48480	ESTs	4.3
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homology to	4.3
30	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (RHAMM)	4.3
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.3
	428613	AB037749	Hs.186928	KIAA1328 protein	4.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter tra	4.3
	447078	AW685727	Hs.301570	ESTs	4.3
35	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	4.3
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.3
	405708			Target Exon	4.3
	433405	AW157566	Hs.156892	ESTs	4.3
	456443	AW967500	Hs.133543	ESTs	4.3
40	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	4.2
	448621	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	4.2
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequence	4.2
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.2
	455365	AW948343		gb:RC0-MT0015-130400-031-c01 MT0015 Homo sapi	4.2
45	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypothetical p	4.2
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypothetical p	4.2
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	4.2
	427666	AI791495	Hs.180142	calmodulin-like skin protein	4.2
	444602	AI174456	Hs.271925	ESTs, Moderately similar to I38022 hypothetic	4.2
50	417791	AW965339	Hs.111471	ESTs	4.2
	444266	AI424984	Hs.125465	ESTs	4.2
	439394	AA149250	Hs.56105	ESTs	4.2
	457336	AW969657	Hs.291029	ESTs	4.2
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypothetical p	4.2
55	404440			NM_021048:Homo sapiens melanoma antigen, fami	4.2
	449228	AJ403107	Hs.148590	protein related with psoriasis	4.2
	437144	AL049466	Hs.7859	ESTs	4.2
	448599	AW860912		gb:QV0-CT0387-170200-121-c05 CT0387 Homo sapi	4.2
	431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like protein	4.2
60	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.2
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	4.2
	458116	AW977549	Hs.47367	KIAA1785 protein	4.1
	444105	AW189097	Hs.166597	ESTs	4.1
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	4.1
65	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor, cl	4.1
	408096	BE250162	Hs.83765	dihydrofolate reductase	4.1
	457620	AA602711	Hs.336753	EST	4.1
	402048			Target Exon	4.1
	427025	AA397589	Hs.97523	ESTs	4.1
70	423515	AA327017	Hs.162204	ESTs	4.1
	423891	AK002042	Hs.134795	Homo sapiens cDNA FLJ11180 fis, clone PLACE10	4.1
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo sapi	4.1
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	4.1
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	4.1
75	423738	AB002134	Hs.132195	airway trypsin-like protease	4.1
	448243	AW369771	Hs.52620	integrin, beta 8	4.1
	411559	BE144081		gb:MR0-HT0165-030200-007-d06 HT0165 Homo sapi	4.1
	423553	AA405635	Hs.96854	ESTs, Weakly similar to DYLC_HUMAN CYTOPLASMI	4.1
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	4.1
80	424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypothetical p	4.1
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PLACE10	4.1
	424745	AA214618	Hs.152759	activator of S phase kinase	4.0
	433384	AI021992	Hs.124244	ESTs	4.0
	448995	AI613276	Hs.5662	guanine nucleotide binding protein (G protein	4.0

	448504	AI858128	Hs.171136	ESTs	4.0
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (from c	4.0
	432441	AW292425	Hs.163484	ESTs	4.0
5	424794	M85646	Hs.210696	ESTs	4.0
	432184	AW971125		gb:EST383212 MAGE resequences, MAGL Homo sapi	4.0
	408321	AW405882	Hs.44205	cortistatin	4.0
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like repeat d	4.0
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.0
10	447724	AW298375	Hs.24477	ESTs	4.0
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y79AA10	4.0
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.0
	420252	AW270404	Hs.193161	ESTs	4.0
	412811	H06382	Hs.21400	ESTs	4.0
15	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	4.0
	438390	AI422017		gb:tt45f12.x1 NCL_CGAP_Brn23 Homo sapiens cDN	4.0
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	4.0
	429900	AA460421	Hs.30875	ESTs	4.0
	421270	H56037	Hs.108146	ESTs	3.9
20	430733	AW975920	Hs.283361	ESTs	3.9
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo sapi	3.9
	424131	AA335714	Hs.199665	ESTs	3.9
	457059	BE561665	Hs.177677	exosome component Rrp40	3.9
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	3.9
25	404959			NM_025001*:Homo sapiens hypothetical protein	3.9
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.9
	428536	AI143139	Hs.2288	visinin-like 1	3.9
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H.sapi	3.9
	432757	AF113013	Hs.278919	PRO0806 protein	3.9
30	418686	Z36830	Hs.87268	annexin A8	3.9
	437845	AA769578	Hs.90488	ESTs	3.9
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein produ	3.9
	419312	AA831850	Hs.58149	hypothetical protein MGC14136	3.9
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	3.9
35	410553	AW016824	Hs.255527	hypothetical protein MGC14128	3.9
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.9
	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HEMBB10	3.9
	442163	AI791749	Hs.128896	ESTs	3.9
	438656	H85310	Hs.209456	ESTs, Weakly similar to NG22 [H.sapiens]	3.9
40	406560			ENSP00000016943*:cDNA	3.8
	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33)	3.8
	404132			Target Exon	3.8
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	3.8
	439238	N47305	Hs.46668	ESTs	3.8
45	433289	AF005258		gb:Homo sapiens laminin alpha 3b chain mRNA,	3.8
	436149	AI754308	Hs.159452	ESTs	3.8
	446292	AF081497	Hs.279682	Rh type C glycoprotein	3.8
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-bind	3.8
	405545			(MDR/TAP) (TAP2)	3.8
50	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	3.8
	409687	T51125	Hs.8493	ESTs	3.8
	407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo sapie	3.8
	415532	R14780	Hs.12826	ESTs	3.8
	402047	AK001921	Hs.169575	hypothetical protein MGC2550	3.8
55	415317	Z43388		gb:HSC1AF121 normalized infant brain cDNA Hom	3.8
	438777	AA825487	Hs.142179	ESTs	3.8
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolysis bu	3.7
	405943			Target Exon	3.7
60	430686	NM_001942	Hs.2633	desmoglein 1	3.7
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP024	3.7
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	3.7
	418582	BE244318	Hs.213194	hypothetical protein MGC10895	3.7
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	3.7
65	433849	BE465884	Hs.280728	ESTs	3.7
	449592	AI655494	Hs.195718	ESTs	3.7
	453028	AB006532	Hs.31442	RecQ protein-like 4	3.7
	435612	AA693537	Hs.321411	ESTs	3.7
	417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clone 22d	3.7
70	418735	N48769	Hs.44609	ESTs	3.7
	444707	AI188613	Hs.41690	desmocollin 3	3.7
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.7
	450613	AI702055		gb:tg20g10.x1 NCL_CGAP_U11 Homo sapiens cDNA	3.7
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	3.7
75	432837	AA310693	Hs.87329	HSPC072 protein	3.7
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN ALU SU	3.7
	423441	R68649	Hs.278359	absent in melanoma 1 like	3.7
	449978	AI806335	Hs.200829	ESTs, Weakly similar to T30171 ninein - mouse	3.7
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo sapi	3.7
80	409582	R27430	Hs.271565	ESTs	3.6
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANTIGEN	3.6
	458446	AW394104	Hs.43744	ESTs, Moderately similar to I54374 gene NF2 p	3.6
	433040	H70423	Hs.300511	ESTs	3.6
	452193	AA987351	Hs.184993	ESTs	3.6

	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed-rect	3.6
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.6
	459575	BE080825		gb:QV1-BT0631-180200-078-c08 BT0631 Homo sapi	3.6
5	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.6
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	3.6
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.6
	427131	AA448460	Hs.112017	GE36 gene	3.6
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	3.6
10	420373	AW968228		gb:EST380198 MAGE resequences, MAGJ Homo sapi	3.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromosomes 2	3.6
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.6
	424639	AI917494	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HEMBA10	3.6
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.6
15	434321	AA629368		gb:zu78a11.s1 Soares_testis_NHT Homo sapiens	3.6
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	3.6
	427335	AA448542	Hs.251677	G antigen 7B	3.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	3.6
20	426749	AI623718	Hs.105618	ESTs	3.6
	443899	AW842283	Hs.79933	cyclin I	3.6
	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H.sapi	3.6
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	mammaglobin 1	3.5
25	408867	AA437199	Hs.656	cell division cycle 25C	3.5
	428508	BE252383	Hs.184668	SBB131 protein	3.5
	431120	AA492588		gb:ng99c08.s1 NCI_CGAP_Thy1 Homo sapiens cDNA	3.5
	401780			NM_005557*:Homo sapiens keratin 16 (focal non	3.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sapiens	3.5
30	456671	AB011142	Hs.114293	KIAA0570 gene product	3.5
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP10 (HT	3.5
	435244	N77221	Hs.187824	ESTs	3.5
	436246	AW450963	Hs.119991	ESTs	3.5
	431917	D16181	Hs.2868	peripheral myelin protein 2	3.5
35	443113	AI040686	Hs.132908	ESTs	3.5
	443341	AW631480	Hs.8688	ESTs	3.5
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.5
	418347	AA216419		gb:nc16e03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA	3.5
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo sapi	3.5
40	408633	AW963372	Hs.46677	PRO2000 protein	3.5
	427878	C05766	Hs.181022	CGI-07 protein	3.5
	419945	AW290975	Hs.118923	ESTs	3.5
	448372	AW445166	Hs.170802	ESTs	3.5
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen 1NFLS	3.5
45	411274	NM_002776	Hs.69423	kallikrein 10	3.5
	400666			NM_002425:Homo sapiens matrix metalloproteina	3.5
	426920	AA393351	Hs.132121	ESTs	3.5
	402639			Target Exon	3.4
50	454891	AW837349		gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapi	3.4
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet-de	3.4
	456296	AA829976	Hs.239114	mannosidase, alpha, class 1A, member 2	3.4
	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.4
	429274	AI379772	Hs.99206	ESTs	3.4
	430704	AW813091	Hs.335799	ESTs	3.4
55	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo sapi	3.4
	451778	AI826131	Hs.71243	ESTs, Weakly similar to zinc finger protein [3.4
	430397	AI924533	Hs.105607	bicarbonate transporter related protein 1	3.4
	432113	AA935065	Hs.152385	ESTs	3.4
	449722	BE280074	Hs.23960	cyclin B1	3.4
60	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapi	3.4
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.4
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.4
	417009	AA191719	Hs.314714	ESTs	3.4
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moiety X	3.4
65	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen induci	3.4
	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PLACE20	3.4
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	3.4
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens cDNA	3.4
	403274			Target Exon	3.4
70	435360	AF105366	Hs.4876	solute carrier family 12 (potassium/chloride	3.4
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2 prote	3.4
	443462	AI054690	Hs.171176	ESTs	3.3
	444910	AI201849		gb:qs76g04.x1 NCI_CGAP_Pr28 Homo sapiens cDNA	3.3
75	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (from c	3.3
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	3.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE066	3.3
	419751	AW195581	Hs.93121	KIAA0761 protein	3.3
80	404782			C7001692*:gil6724096[gb]AAF26844.1 (AF195021	3.3
	415613	R20233		gb:yg18h11.r1 Soares infant brain 1NIB Homo s	3.3
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypothetical p	3.3
	406599			Target Exon	3.3
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.3

5	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo sapi	3.3
	421107	AA283822	Hs.55606	ESTs, Weakly similar to S47072 finger protein	3.3
	436985	AA740946	Hs.150895	ESTs	3.3
	443903	AI220547	Hs.135223	ESTs	3.3
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (from c	3.3
	447153	AA805202	Hs.315562	ESTs	3.3
	450769	AA057418	Hs.33654	ESTs	3.3
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-C	3.3
10	402481			NM_001821*:Homo sapiens choroideremia-like (R	3.3
	459394	BE409894	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, complete	3.3
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-1 [H.	3.3
	417708	N74392	Hs.50495	ESTs	3.3
	414869	AA157291	Hs.21479	ubiquitin 1	3.3
15	441690	R81733	Hs.33106	ESTs	3.3
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.3
	412246	AI160873	Hs.69233	zinc finger protein	3.3
	412903	BE007967	Hs.155795	ESTs	3.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placental)	3.3
20	451177	AI969716	Hs.13034	ESTs	3.3
	409990	AA079337		gb:zm95b09.r1 Stratiagene colon HT29 (937221)	3.3
	418462	BE001596	Hs.85266	integrin, beta 4	3.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92k	3.3
	405196			C2000662*:gi 7512792 pir T12482 hypothetical	3.3
25	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA libra	3.3
	432917	NM_014125	Hs.279812	PRO0327 protein	3.3
	448251	BE280486	Hs.84045	hypothetical protein FLJ20288	3.3
	415025	AW207091	Hs.72307	ESTs	3.3
	420218	AW958037	Hs.286	ribosomal protein L4	3.2
30	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fis, clone HEMBB10	3.2
	447762	AI939461	Hs.161370	ESTs	3.2
	414147	BE091634		gb:IL2-BT0731-240400-069-C03 BT0731 Homo sapi	3.2
	445038	AI635444	Hs.143917	dJ467N11.1 protein	3.2
	448666	NM_014953	Hs.323346	KIAA1008 protein	3.2
35	402800			Target Exon	3.2
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated	3.2
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cere	3.2
	455203	AW865450		gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapi	3.2
	459666	W27362		gb:30g7 Human retina cDNA randomly primed sub	3.2
40	401458			Target Exon	3.2
	432361	AI378562	Hs.159585	ESTs	3.2
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLICING F	3.2
	405336			Target Exon	3.2
	446563	BE326588	Hs.141454	ESTs	3.2
45	449276	AW241510	Hs.252713	ESTs	3.2
	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo sapi	3.2
	420591	X53655	Hs.99171	neurotrophin 3	3.2
	401486			C4000647*:gi 4758508 ref NP_004253.1 airway	3.2
50	432979	AA573263	Hs.120860	ESTs	3.2
	413833	Z15005	Hs.75573	centromere protein E (312kD)	3.2
	438325	AA804258	Hs.123229	ESTs	3.2
	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha-1C-a	3.2
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cysteine-r	3.2
	421777	BE562088	Hs.108196	HSPC037 protein	3.2
55	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone ADKA02	3.2
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone LNG004	3.2
	402337			Target Exon	3.2
	420930	AW888650		gb:CM4-NT0007-130500-551-f06 NT0007 Homo sapi	3.2
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HEMBA10	3.2
60	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.1
	437641	AA811452	Hs.291911	ESTs	3.1
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.1
	434208	T92641	Hs.127648	hypothetical protein PRO2176	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.1
65	452934	AA581322	Hs.4213	hypothetical protein MGC16207	3.1
	458923	Y12812	Hs.24422	regulatory factor X-associated protein	3.1
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A receptor, ep	3.1
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDNA clo	3.1
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevisiae,	3.1
70	445885	AI734009	Hs.127699	KIAA1603 protein	3.1
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP010	3.1
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine protein k	3.1
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo sapi	3.1
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription factor	3.1
75	455987	BE178323		gb:RC3-HT0600-240400-023-g05 HT0600 Homo sapi	3.1
	421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA, part	3.1
	423887	AL080207	Hs.134585	DKFZP434G232 protein	3.1
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.1
	447815	AI432199	Hs.247084	ESTs	3.1
80	441974	AI683782	Hs.128245	ESTs	3.1
	446474	AI301227	Hs.150186	hypothetical protein DKFZp566K1946	3.1
	452166	AI948607	Hs.264680	ESTs	3.1
	451659	BE379761	Hs.14248	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1

	447701	BE619526	Hs.255527	hypothetical protein MGC14128	3.1
	443648	AI085377	Hs.143610	ESTs	3.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.1
5	449441	AI656040	Hs.196532	ESTs	3.1
	458145	AI239457	Hs.130794	ESTs	3.1
	444588	AI221321	Hs.167559	ESTs	3.1
	450832	AW970602	Hs.105421	ESTs	3.1
	449425	AW103433	Hs.195684	ESTs	3.1
10	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT2RP30	3.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	3.1
	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB55Y Ho	3.1
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S. cere	3.1
	404107			Target Exon	3.1
15	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.1
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (from c	3.1
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM040	3.1
	442824	BE178065	Hs.144081	ESTs	3.1
	435061	AI651474	Hs.163944	ESTs	3.1
20	420589	AA419360	Hs.192708	ESTs	3.0
	434569	AI311295	Hs.8294	KIAA0196 gene product	3.0
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B, membe	3.0
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional act	3.0
	402892			Target Exon	3.0
25	406087			Target Exon	3.0
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	3.0
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbHPU Ho	3.0
	435990	AI015862	Hs.131793	ESTs	3.0
	442577	AA292998	Hs.163900	ESTs	3.0
30	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitter tra	3.0
	458154	AW816379	Hs.335018	ESTs	3.0
	416809	N67253	Hs.271691	ESTs	3.0
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	3.0
	437938	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapiens cDN	3.0
35	413281	AA861271	Hs.222024	transcription factor BMAL2	3.0
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810027O1	3.0
	445505	AI971156	Hs.148891	ESTs	3.0
	425005	AI565851		gb:tn07g03.x1 NCI_CGAP_Bm25 Homo sapiens cDN	3.0
40	435673	AF202961	Hs.284200	Homo sapiens uncharacterized gastric protein	3.0
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA	3.0
	453509	AL040021	Hs.252674	ESTs, Weakly similar to alternatively spliced	3.0
	455750	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapi	3.0
	407777	AA161071	Hs.71465	squalene epoxidase	3.0
	424441	X14850	Hs.147097	H2A histone family, member X	3.0
45	417734	Z42667	Hs.6724	ESTs	3.0
	449676	AW380579	Hs.209657	ESTs	3.0
	445425	AI223511	Hs.300722	ESTs	3.0
	427061	AB032971	Hs.173392	KIAA1145 protein	3.0
	433584	AW295399		gb:Ul-H-BI2-ahv-h-03-0-Ul.s1 NCI_CGAP_Sub4 Ho	3.0
50	444477	AI150548	Hs.23155	ESTs	3.0
	446255	AI283257	Hs.257090	ESTs	3.0
	400612			C10001034:gil7513113 pir T13078 KIAA0992 pro	3.0
	450841	AI741466	Hs.270515	ESTs	3.0
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	3.0
55	433871	W02410	Hs.205555	ESTs	3.0
	401994			Target Exon	3.0
	449272	AW137656	Hs.197645	ESTs	3.0
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 kD)	3.0
	400250			Eos Control	3.0
60	408015	AW136771	Hs.244349	epidermal differentiation complex protein lik	3.0
	436414	BE264633	Hs.143638	WD repeat domain 4	3.0
	432220	AI571306	Hs.232224	ESTs	3.0
	420831	AA280824	Hs.190035	ESTs	3.0
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_UI2 Homo sapiens cDNA	3.0
65	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG repeat r	3.0
	428262	AI651324	Hs.7298	biphenyl hydrolase-like (serine hydrolase; br	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone COL070	3.0
	417308	H60720	Hs.81892	KIAA0101 gene product	3.0
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	3.0
70	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2 (dihy	3.0
	423556	R72694	Hs.7720	dynein, cytoplasmic, heavy polypeptide 1	3.0
	426890	AA393167	Hs.41294	ESTs	2.9
	436333	AA709270	Hs.136672	EST	2.9
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.9
75	402556			C1001383*:gil538695 pir A61183 hypothetical	2.9
	411098	AW817238		gb:QV0-ST0247-090200-105-b07 ST0247 Homo sapi	2.9
	435399	AA679463		gb:ac50c03.s1 Stratagene hNT neuron (937233)	2.9
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.9
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone HEP016	2.9
80	410658	AW105231	Hs.192035	ESTs	2.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	2.9
	412279	BE245511		gb:TCBAP1D3235 Pediatric pre-B cell acute lym	2.9
	405277			ENSP00000211621*:Keratin, type II cytoskeleta	2.9
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapiens c	2.9

	455319	AW895387		gb:QV4-NN0038-300300-157-c10 NN0038 Homo sapi	2.9
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	2.9
	413306	AW303544	Hs.118654	ESTs	2.9
5	432215	AJ076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.9
	434423	NM_006769	Hs.3844	LIM domain only 4	2.9
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	2.9
	412367	AW945964		gb:QV0-ET0001-050500-228-e09 ET0001 Homo sapi	2.9
10	436148	BE005252	Hs.321583	Homo sapiens cDNA FLJ20779 fis, clone COL0507	2.9
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.9
	404981			ENSP00000252242::Keratin, type II cytoskeleta	2.9
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced by tu	2.9
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA, part	2.9
	401760			Target Exon	2.9
15	443859	NM_013409	Hs.9914	folliculin	2.9
	404253			NM_021058::Homo sapiens H2B histone family, m	2.9
	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	2.9
	435867	AA954229	Hs.114052	ESTs	2.9
	429035	BE549781	Hs.270475	ESTs	2.9
20	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega-hydr	2.9
	446417	AJ299050		gb:qn14d12.x1 NCLCGAP_Lu5 Homo sapiens cDNA	2.9
	437637	AJ003029	Hs.65792	syntrophin, gamma 2	2.9
	452452	BE393822	Hs.29645	Homo sapiens mRNA; cDNA DKFZp761C029 (from cl	2.9
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	2.9
25	450698	W31489	Hs.95044	ESTs, Weakly similar to I38022 hypothetical p	2.9
	439430	AF124250	Hs.6564	cervical cancer anti-estrogen resistance 3	2.9
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	2.9
	438268	AA782163	Hs.293502	ESTs	2.9
	401781			Target Exon	2.9
30	439625	AF086453	Hs.58611	ESTs	2.9
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothetical p	2.9
	410743	AA089474	Hs.272153	ESTs	2.9
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog o	2.9
	449746	AI688594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOCHROME	2.9
35	443479	AF027219	Hs.9443	zinc finger protein 202	2.9
	442601	AI684969	Hs.46772	ESTs	2.9
	405932			C15000305:gi 3806122 gb AAC69198.1 (AF097887	2.9
	405454			C12000541:gi 5729884 ref NP_006539.1 IGF-II	2.9
40	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	2.9
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, parti	2.9
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransf	2.9
	414581	AA256213	Hs.72010	ESTs	2.9
	411268	AK000512	Hs.69388	hypothetical protein FLJ20505	2.9
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_1NFLS	2.9
45	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	2.9
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	2.9
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.9
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein produ	2.9
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothetical p	2.9
50	435711	AF226667	Hs.58553	CTP synthase II	2.9
	419088	AI538323	Hs.52620	integrin, beta 8	2.8
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clone IF	2.8
	429299	AI620463	Hs.293984	hypothetical protein MGC13102	2.8
	451702	AW665452	Hs.246503	ESTs	2.8
55	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	2.8
	405281			NM_002864::Homo sapiens pregnancy-zone protein	2.8
	438161	BE089028	Hs.20158	ESTs, Weakly similar to S34159 transcription	2.8
	409103	AF251237	Hs.112208	XAGE-1 protein	2.8
	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.8
60	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mis5, S	2.8
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.8
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-like	2.8
	452730	AA027952	Hs.165216	ESTs	2.8
	413083	BE064528		gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapi	2.8
65	437030	AA742577	Hs.303781	EST	2.8
	438113	AI467908	Hs.8882	ESTs	2.8
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone LNG096	2.8
	440994	AI160011	Hs.193341	ESTs	2.8
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HEMBA10	2.8
70	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	2.8
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin, tissu	2.8
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.8
	433788	AI810534	Hs.161275	ESTs	2.8
	403806			Target Exon	2.8
75	437182	AL080098		gb:Homo sapiens mRNA; cDNA DKFZp564C1072 (fro	2.8
	453955	AW579207	Hs.304666	ESTs, Weakly similar to I78885 serine/threoni	2.8
	420795	AA323037	Hs.128645	sorting nexin 16	2.8
	452696	AI826645	Hs.211534	ESTs	2.8
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.8
80	438052	AA776564	Hs.41891	zinc finger 1111	2.8
	441755	AW450826	Hs.127786	ESTs	2.8
	427961	AW293165	Hs.143134	ESTs	2.8
	449785	AI225235	Hs.288300	hypothetical protein FLJ23231	2.8
	450451	AW591528	Hs.202072	ESTs	2.8

	406831	N73448	Hs.50272	ESTs, Weakly similar to RS1A_HUMAN 40S RIBOSO	2.8
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A receptor, pi	2.8
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.8
5	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.8
	448979	AI611378	Hs.192610	ESTs	2.8
	409143	AW025980	Hs.138965	ESTs, Weakly similar to I38022 hypothetical p	2.8
	410664	NM_006033	Hs.65370	lipase, endothelial	2.8
	444550	BE250716	Hs.87614	ESTs	2.8
10	422109	S73265	Hs.1473	gastrin-releasing peptide	2.8
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.8
	445941	AI267371	Hs.172636	ESTs	2.8
	459719	AW749511	Hs.301554	ESTs, Weakly similar to AF133298 1 cytochrome	2.8
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT2RP20	2.8
15	456456	AA477609	Hs.89563	nuclear cap binding protein subunit 1, 80kD	2.8
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothetical p	2.8
	403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	2.8
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	2.8
	439846	T63959	Hs.228320	hypothetical protein FLJ23537	2.8
20	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	2.8
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	2.8
	455091	BE079752		gb:RC6-BT0627-140200-011-A04 BT0627 Homo sapi	2.8
	410049	AW579475		gb:RC0-DT0076-110100-031-d10 DT0076 Homo sapi	2.8
	452571	W31518	Hs.34665	ESTs	2.8
25	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	2.8
	426343	NM_014642	Hs.169387	KIAA0036 gene product	2.8
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-associated	2.8
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromosomes 4	2.7
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.7
30	429128	AA446869	Hs.119316	ESTs	2.7
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MAMMA10	2.7
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.7
	403763			NM_001059*:Homo sapiens tachykinin receptor 3	2.7
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypothetic	2.7
35	406753	AA505665	Hs.217493	annexin A2	2.7
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sapiens	2.7
	419875	AA853410	Hs.93557	proenkephalin	2.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical p	2.7
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.7
40	456181	L36463	Hs.1030	ras inhibitor	2.7
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen 1NFLS	2.7
	417995	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICROTUBUL	2.7
	435347	AW014873	Hs.116963	ESTs	2.7
	457339	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC FINGE	2.7
45	417398	N78541	Hs.177366	ESTs	2.7
	408380	AF123050	Hs.44532	diubiquitin	2.7
	437724	AW444828	Hs.184323	ESTs	2.7
	408680	AK000093	Hs.46821	hypothetical protein FLJ20086	2.7
	454202	AW178363		gb:RC3-HT0105-010999-002-H05 HT0105 Homo sapi	2.7
50	414362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli RecA ho	2.7
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.7
	406092			Target Exon	2.7
	447748	AI422023	Hs.161338	ESTs	2.7
	443236	AI079496	Hs.134169	ESTs	2.7
55	433743	AF075312	Hs.236760	Homo sapiens clone HQ0262	2.7
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related protein	2.7
	405675			Target Exon	2.7
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila inaD-like)	2.7
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	2.7
60	448592	N69546	Hs.44563	hypothetical protein	2.7
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MAMMA10	2.7
	407287	AI678812		gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA	2.7
	448275	BE514434	Hs.20830	kinesin-like 2	2.7
	412977	AA125910	Hs.191461	ESTs	2.7
65	431721	AB032996	Hs.268044	KIAA1170 protein	2.7
	417357	AF260257	Hs.131917	retinitis pigmentosa GTPase regulator interac	2.7
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the p	2.7
	416294	D86980	Hs.79170	KIAA0227 protein	2.7
	458201	AI989961	Hs.233477	ESTs, Moderately similar to A Chain A, Cyclop	2.7
70	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolog 2	2.7
	401230			NM_014191*:Homo sapiens sodium channel, volta	2.7
	422058	AA862231	Hs.334443	ESTs	2.7
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.7
	430152	AB001325	Hs.234642	aquaporin 3	2.7
75	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.7
	443500	AV646388	Hs.93961	Homo sapiens mRNA; cDNA DKFp667D095 (from cl	2.7
	418030	BE207573	Hs.83321	neuromedin B	2.7
	445640	AW989626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	2.7
80	418869	AW516565		gb:xq01d05.x1 Soares_NHCeC_cervical_tumor Hom	2.7
	431688	AA513906		gb:ng67c08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	2.7
	427579	AA366143	Hs.179669	hypothetical protein FLJ20637	2.7
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.7
	414737	AI160386	Hs.125087	ESTs	2.7
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.7

	446659	AI335361	Hs.226376	ESTs	2.7
	419833	AA251131	Hs.220697	ESTs	2.7
	411819	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo sapi	2.6
5	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypothetical p	2.6
	446102	AW168067	Hs.252956	ESTs	2.6
	441408	AI733249	Hs.126897	ESTs	2.6
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse transc	2.6
	416283	NM_005429	Hs.79141	vascular endothelial growth factor C	2.6
10	421470	R27496	Hs.1378	annexin A3	2.6
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	2.6
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.6
	431832	AW276866	Hs.192715	ESTs	2.6
	426698	AA394104	Hs.97489	ESTs	2.6
	433288	AI368873	Hs.271257	ESTs, Weakly similar to I38022 hypothetical p	2.6
15	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.6
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypothetical p	2.6
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo sapi	2.6
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein [H.s	2.6
20	401260			C1001031*:gij7305041[ref]NP_038876.1} erythro	2.6
	435136	R27299	Hs.10172	ESTs	2.6
	412108	AA100293	Hs.185043	ESTs	2.6
	434442	AA737415	Hs.152826	ESTs	2.6
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	2.6
25	419667	AU077005	Hs.92208	a disintegrin and metalloproteinase domain 15	2.6
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	2.6
	409594	AA076118		gb:zm18e06.s1 Stratagene pancreas (937208) Ho	2.6
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (937208) Ho	2.6
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.6
30	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth factor	2.6
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.6
	434444	AI765276	Hs.101257	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	2.6
	411465	AW847663		gb:IL3-CT0213-280100-056-F02 CT0213 Homo sapi	2.6
35	408625	AW243323	Hs.266785	ESTs	2.6
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.6
	439245	NM_013381	Hs.6510	thyrotropin-releasing hormone degrading ectoe	2.6
	431890	XI7033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit of	2.6
	414747	U30872	Hs.77204	centromere protein F (350/400kD, milosin)	2.6
40	401050			NM_014155*:Homo sapiens HSPC063 protein (HSPC	2.6
	405897			Target Exon	2.6
	451153	BE092900		gb:CM2-BT0742-100400-147-h04 BT0742 Homo sapi	2.6
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC FINGE	2.6
	440159	AI637599	Hs.126127	ESTs	2.6
45	404184			NM_030903*:Homo sapiens olfactory receptor, f	2.6
	428552	AW274560	Hs.129520	ESTs	2.6
	401367			Target Exon	2.6
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
50	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated fac	2.6
	449432	AW451361	Hs.196529	ESTs	2.6
	425062	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger protein)	2.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PLACE10	2.6
	450705	U90304	Hs.25351	iroquois homeobox protein 5	2.6
55	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	2.6
	408391	AW859276		gb:MR1-CT0352-240200-105-d02 CT0352 Homo sapi	2.6
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mouse)	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to ARL-	2.6
60	453331	AI240665	Hs.8895	ESTs	2.6
	447175	AI365208	Hs.293606	ESTs	2.6
	451878	AI821027	Hs.8429	ESTs	2.6
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	2.6
	418282	AA215535	Hs.98133	ESTs	2.6
65	434557	AW855466	Hs.271866	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.6
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.6
	420894	AA744597	Hs.88854	ESTs	2.6
	435663	AI023707	Hs.134273	ESTs	2.6
	448037	AW195634	Hs.170401	ESTs	2.6
70	418067	AI127958	Hs.83393	cystatin E/M	2.6
	439524	BE542950	Hs.155548	ESTs	2.6
	402298			Target Exon	2.6
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.6
75	407471	D55644		gb:Human spleen PABL (pseudautosomal boundar	2.6
	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, complete	2.6
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from c	2.6
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothetical p	2.6
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (from c	2.6
	425415	M13903	Hs.157091	involucrin	2.6
80	444826	AI674482	Hs.148441	ESTs	2.6
	413331	BE083950		gb:PM0-BT0651-260200-001-b11 BT0651 Homo sapi	2.6
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.6
	405041			C3001706*:gij1345652[sp]P15989[CA36_CHICK COL	2.6
	413864	BE175582		gb:RC5-HT0580-100500-022-C01 HT0580 Homo sapi	2.6

	438746	AI885815	Hs.184727	ESTs	2.5
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo sapi	2.5
	433365	AF026944	Hs.293797	ESTs	2.5
5	412723	AA648459	Hs.335951	hypothetical protein AF301222	2.5
	422656	AI870435	Hs.1569	LIM homeobox protein 2	2.5
	411171	AW820260		gb:QV2-ST0296-150200-040-c10 ST0296 Homo sapi	2.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapi	2.5
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telencepha	2.5
10	414883	AA926960	Hs.334883	CDC28 protein kinase 1	2.5
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.5
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (from cl	2.5
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associated fac	2.5
	455549	AW994222		gb:RC3-BN0036-250200-012-e02 BN0036 Homo sapi	2.5
15	409676	AA077118	Hs.197298	NS1-binding protein	2.5
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	2.5
	429413	NM_014058	Hs.201877	DESC1 protein	2.5
	424420	BE614743	Hs.146688	prostaglandin E synthase	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypep	2.5
20	452834	AI638627	Hs.105685	KIAA1688 protein	2.5
	424354	NM_014314	Hs.145612	RNA helicase	2.5
	455095	AW855598		gb:CM1-CT0278-031199-032-e08 CT0278 Homo sapi	2.5
	431241	AA496799	Hs.36958	ESTs	2.5
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (connexin	2.5
25	427239	BE270447	Hs.174070	ubiquitin carrier protein	2.5
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.5
	458175	AW296024	Hs.150434	ESTs	2.5
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein type	2.5
	453379	AA035261	Hs.61753	ESTs	2.5
30	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothetical p	2.5
	412313	AW936832		gb:PM2-DT0023-050400-003-h03 DT0023 Homo sapi	2.5
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro	2.5
	443757	H05479	Hs.62314	ESTs	2.5
	449300	AI656959	Hs.222165	ESTs	2.5
35	434913	AW872860	Hs.11056	RALBP1 protein	2.5
	448946	AI652855	Hs.23363	hypothetical protein FLJ10983	2.5
	437327	AL353942	Hs.306504	Homo sapiens mRNA; cDNA DKFZp761L23121 (from	2.5
	450262	AW409872	Hs.184846	Homo sapiens, Similar to zinc finger protein	2.5
	453204	R10799	Hs.191990	ESTs	2.5
40	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	2.5
	449344	AI640355	Hs.312691	ESTs	2.5
	439436	BE140845	Hs.57868	ESTs	2.5
	449867	AI672379	Hs.122970	hypothetical protein FLJ21579	2.5
	452220	BE158006	Hs.212296	ESTs	2.5
45	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.5
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapien	2.5
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	2.5
	415030	D31118	Hs.191735	hypothetical protein MGC10520	2.5
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	2.5
50	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	2.5
	400301	X03635	Hs.1657	estrogen receptor 1	2.5
	429386	AK001795	Hs.201179	hypothetical protein FLJ10933	2.5
	423949	AI014546	Hs.130912	ESTs	2.5
	411768	NM_013371	Hs.71979	interleukin 19	2.5
55	436961	AW375974	Hs.156704	ESTs	2.5
	431124	AF284221	Hs.59506	doublesex and mab-3 related transcription fac	2.5
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	2.5
	418717	AI334430	Hs.86984	ESTs	2.5
	443270	NM_004272	Hs.337737	Homer, neuronal immediate early gene, 1B	2.5
60	448454	NM_005879	Hs.21254	TRAF interacting protein	2.5
	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogene hom	2.5
	442966	AI394036	Hs.132237	ESTs, Weakly similar to DUS8_HUMAN DUAL SPECI	2.5
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN ALU SU	2.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription factor	2.5
65	440381	AA917808	Hs.190495	ESTs	2.5
	403983			Target Exon	2.5
	451340	AW936273		gb:QV0-DT0020-090200-107-g07 DT0020 Homo sapi	2.5
	447888	BE620911	Hs.126889	ESTs	2.5
	441794	AW197794	Hs.253338	ESTs	2.5
70	424153	AA451737	Hs.141496	MAGE-like 2	2.5
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.5
	435647	AI653240	Hs.49823	ESTs	2.5
	428780	AI478578	Hs.50636	ESTs	2.5
	439108	AW163034	Hs.6467	synaptogyrin 3	2.5
75	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fascin h	2.5
	428054	AI948688	Hs.266619	ESTs	2.5
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	2.5
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S. cere	2.5
	443362	AI053464	Hs.166505	ESTs	2.5
80	433183	AF231338	Hs.222024	transcription factor BMAL2	2.5
	438214	H06076	Hs.26320	TRABID protein	2.5
	446745	AW118189	Hs.156400	ESTs	2.5
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.5
	426333	AW269088	Hs.118183	hypothetical protein FLJ22833	2.5

TABLE 12B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
407642	1007175_1	AW178963 AW845721 BE141041 AW806977 AW845690 AW845691 AW845724 AW176564 AW845705 AW845603 AW845729 AW845722 AW178966 AW845693 AW845585 AW845707 BE141053 BE141046 AW845570 AW845575 BE141043 BE141039 BE141070 AW062443 AW806980 AW845643 AW806969 AW845686 BE141054 BE141040 BE141044 BE141042 AW845571 AW845604 BE141047 BE141071 AW062442 AW845633 AW178968
408391	1055687_1	AW859276 AW859274 AW190959 T91463
408690	107490_1	AW864542 AA056567 AW882724
409594	114249_1	AA076118 AA975618 AA076220
409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
409990	116644_1	AA079337 AA079338 AW272100
410008	116812_1	AA079552 BE142525 BE142527
410049	1172307_1	AW579475 AW939654 AW939655
410784	1221005_1	AW803201 BE079700 BE062940
411098	1232093_1	AW817238 AW993985 AW993998
411171	1234393_1	AW820260 AW820332 R94405
411465	1246768_1	AW847663 AW847861 AW861080
411559	1249417_1	BE144081 BE144190 AW851155
411819	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
411958	126717_1	AA099020 AW751275 AW751276 AW751289
412279	1287332_1	BE245511 BE246133 AW935247
412313	1288355_1	AW936832 AW936609 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW936760 AW936819 AW937485 AW937589 AW937658 AW937654 AW937492
412333	1289037_1	AW945964 AW946020 AW946034 AW946027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016 AW946039
412367	1291505_1	AW946045 AW946028 AW946036
412879	1334272_1	BE092219 BE092361 BE006789
413083	1348639_1	BE064528 BE064589 BE064561
413331	1361726_1	BE083950 BE084017 BE084016
413864	1395788_1	BE175582 BE175514 BE175505 BE175591 BE175530
414147	142127_1	BE091634
414148	142133_1	BE084049 AW292907 AA135984
415317	1533847_1	Z43388 F05453 R19673 R20275 H06917
415613	1540602_1	R20233 F12901 T74740
415747	155189_1	AA381209 AA381245 AA167683
416120	1571266_1	H46739 H51513 H19779
416168	1574545_1	H23687 H46460 H40239
416548	1600181_1	H62953 N76608 N72413
417742	1696282_1	R64719 Z44680 R12451
418347	174149_1	AA216419 F03238 AA229517
418869	179863_1	AW516565 AA229762 AA230035
419807	188252_1	R77402 AA262462 AA250988 R06794
420373	193194_1	AW968228 AA259146 W01465
420637	195241_1	AW976153 AA278945 AA747691
420930	197736_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
422689	219896_1	AW856665 AA315006 AW954733
423733	231476_1	AA330281 AA330232 AW962521
423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA649496
423841	232507_1	AW753967 AA370795 AA331630 AW962550
425005	245908_1	AI565851 AA349656 R24798
429163	300543_1	AA884766 AW974271 AA592975 AA447312
431120	328264_1	AA492588 AA492498 AA492571
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
431688	336609_1	AA513906 AA847734 AI357044
432184	342677_1	AW971125 AA527731 N52655 AI821508 AA532420
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432869	355475_1	AW974094 AA569074 AA602574
433289	36202_1	AF005258
433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
433644	371919_1	AW342028 AA641080 AA603282
434321	383473_1	AA629368 AW849574 AW849573
435399	405576_1	AA679463 AW813779 AW813709
437182	43421_1	AL080098 AL037472 AA432051
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005 AI422017 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AI423279 AI423645 AI424090 AI359637 AL044732 D17003
438390	45662_1	AW979074 AA834841 AA828650
438966	467436_1	AA828995 AA834879 AI926361
438993	467651_1	

439579 47404_1 AF086400 W79232 W73990
 440320 491930_1 AA879294 N67538 AI474541
 444910 624951_1 AI201849 BE069007 AW946544
 446417 676384_1 AI299050 BE256910
 447197 711623_1 R36075 AI366546 R36167
 448599 770766_1 AW860912 AI540866
 449034 794817_1 AI624049 AW117770 AI858360
 450024 82296_1 AA005129 AA679084 AA694399
 450613 840016_1 AI702055 R89204 R86260
 451105 859083_1 AI761324 AW880941 AW880937
 451153 86054_1 BE092900 AA015877 AA018521
 451340 86640_1 AW936273 AW340350 AA017208
 454202 1050507_1 AW178363 AW846011 AW845964 AW845988 AW845977 AW846002
 454241 1067807_1 BE144666 BE184942 AW238414 BE184946
 454707 1230250_1 AW814989 AW814852 AW814808
 454891 1239217_1 AW837349 AW837355 AW882717
 454988 1248607_1 AW850140 AW850195 AW850192
 455091 1252939_1 BE079752 BE079868 BE148989 AW855532 BE148818 BE148815 BE148796
 455092 1252971_1 BE152428 AW855572 AW855607
 455095 1252987_1 AW855598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855601 AW855605
 455203 1259973_1 AW865450 AW865119 AW865452 AW865461 AW865325 AW865114 AW865116 AW865321 AW865590 AW865390
 455310 1278158_1 AW893961 AW893998 AW894034 AW894019
 455319 1279172_1 AW895387 AW895547 AW895564 AW895323 AW895405 AW895539 AW895538
 455365 1284681_1 AW948343 AW948341 AW902855 AW984737
 455549 1324696_1 AW994222 AW994377
 455666 1349545_1 BE065813 BE065788 BE065889 BE065832
 455750 1355998_1 BE075114 BE075283 BE075118
 455838 1374605_1 BE145808 BE145807 BE181883
 455987 1397735_1 BE178323 BE177978
 457405 333127_1 AA504860 AA504911
 458829 773443_1 AI557388 BE158936
 459267 966605_1 AJ003631 AJ003650 AJ003651

TABLE 12C

Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400612	9929646	Minus	151513-151662
400666	8118496	Plus	17982-18115,20297-20456
401050	8117628	Minus	78449-79425
401137	2547238	Minus	598-1009
401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
401260	8076883	Minus	86008-86355
401367	9796198	Minus	145356-145807
401458	9187886	Plus	76485-77597
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
401575	7229804	Minus	76253-76364
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402048	8072512	Plus	43936-44078
402298	6598824	Plus	36758-37953
402337	6957691	Plus	4116-4286,16811-16973,17107-17256,19715-20040,22029-22205
402481	9797406	Plus	87891-88991
402556	9863723	Plus	13579-14026
402639	9958129	Minus	20167-22383
402800	6010175	Plus	43921-44049,46181-46273
402892	8086844	Minus	194384-194645
403274	8072441	Minus	104069-104179,105683-105859
403471	9930659	Minus	85867-85983
403763	7229888	Minus	43575-43887
403806	8140491	Plus	146390-146678
403983	8576059	Minus	82441-82701
404107	8099028	Minus	201699-202363
404132	6981900	Plus	11307-12434
404184	4581418	Minus	12652-13548
404253	9367202	Minus	55675-56055
404440	7528051	Plus	80430-81581
404782	9910094	Minus	15455-15589
404959	7407964	Plus	45243-45368
404981	4432779	Minus	20626-20770,22513-22721
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405041	7547195	Plus	121230-121714
405196	7230083	Minus	135716-135851

405277	3980473	Plus	23471-23572
405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
405336	6094635	Plus	33267-33563
405454	7656675	Plus	133807-134053
405545	1054740	Plus	118677-118807,119091-119296,121626-121823
405547	1054740	Plus	124361-124520,124914-125050
405657	4827303	Minus	104132-104293
405675	4557087	Plus	70304-70630
405708	4156182	Plus	55030-55604
405897	6758795	Plus	59828-60535
405932	7767812	Minus	123525-123713
405943	6758796	Plus	20605-20812
406087	9123919	Minus	7234-7626
406092	9123919	Plus	251370-251797,252168-252882
406467	9795551	Plus	182212-182958
406554	7711566	Plus	106956-107121
406560	7711569	Minus	35162-35292
406599	8248616	Plus	10933-11086

TABLE 13A: 465 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES, LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 13A lists about 465 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 12A, except that the ratio was greater than or equal to 1.7, and the 96th percentile value amongst cervical cancers was greater than or equal 100 units, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 PPDomains: Predicted Protein Domains
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigenelD	PPDomains	Unigene Title	R1
425650	NM_001944	Hs.1925	TM,cadherin,Cadherin_C_term	desmoglein 3 (pemphigus vulgaris antigen)	43.6
418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interstitial)	38.9
439606	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87	28.8
452240	AI591147	Hs.61232	TM	ESTs	27.0
424046	AF027866	Hs.138202	SS,TM,serpin	serine (or cysteine) proteinase inhibitor	24.5
400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (stromelysin	20.5
418345	AJ001696	Hs.241407	SS,TM,serpin	serine proteinase inhibitor 13(P113; se	20.1
423017	AW178761	Hs.227948	SS,serpin	serine (or cysteine) proteinase inhibitor	19.2
428227	AA321649	Hs.2248	SS,TM,IL8	small inducible cytokine subfamily B (Cys	15.9
447164	AF026941	Hs.17518	TM,IBR	Homo sapiens cig5 mRNA, partial sequence	13.8
414764	AW013887	Hs.72047	TM	ESTs	12.9
416661	AA634543	Hs.79440	TM	IGF-II mRNA-binding protein 3	12.7
427585	D31152	Hs.179729	SS,C1q,Collagen	collagen, type X, alpha 1 (Schmid metaphy	12.6
406467			TM,elfhand	Target Exon	10.5
428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromelysin 1	10.2
418882	NM_004996	Hs.89433	TM,ABC_membrane,ABC_tran	ATP-binding cassette, sub-family C (CFTR/	9.4
419247	S65791	Hs.89764	TM,KH-domain	fragile X mental retardation 1	9.1
446232	AI281848	Hs.194691	TM,7tm_3Ribosomal_L13	retinoic acid induced 3	8.9
424905	NM_002497	Hs.153704	TM,kinase	NIMA (never in mitosis gene a)-related ki	8.9
422420	U03398	Hs.1524	TM,tubulin,TNF	tumor necrosis factor (ligand) superfamil	8.7
427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA1794 p	6.9
444342	NM_014398	Hs.10887	Lamp	similar to lysosome-associated membrane g	6.8
422330	D30783	Hs.115263	SS,TM,EGF	epiregulin	6.8
447342	AI199268	Hs.19322	SS,lipocalin	Homo sapiens, Similar to RIKEN cDNA 20103	6.8
407839	AA045144	Hs.161566	TM,cadherin,Cadherin_C_term	ESTs	6.6
410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
414812	X72755	Hs.77367	SS,TM,IL8	monokine induced by gamma interferon	6.4
421773	W69233	Hs.112457	SS	ESTs	6.2
413385	M34455	Hs.840	TM,IDO	indoleamine-pyrrole 2,3 dioxygenase	5.9
413753	U17760	Hs.75517	SS,laminin_EGF,laminin_Nterm,adh_short	laminin, beta 3 (nicein (125kD), kalinin	5.8
432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collagenase	5.5
418663	AK001100	Hs.41690	TM,cadherin	desmocollin 3	5.5
407366	AF026942		TM,IBR	gb:Homo sapiens cig33 mRNA, partial seque	5.5
433091	Y12642	Hs.3185	SS,TM,UPAR_LY6	lymphocyte antigen 6 complex, locus D	5.4
408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Cation_ATPase_C, N	ESTs	5.4
420440	NM_002407	Hs.97644	SRCRUteroglobin	mammaglobin 2	5.2
437044	AL035864	Hs.69517	TM	cDNA for differentially expressed CO16 ge	5.1
405547			SS,TM,ABC_membrane,ABC_tran,ig	NM_018833*:Homo sapiens transporter 2, AT	5.1
439223	AW238299	Hs.250618	SS	UL16 binding protein 2	5.1
426320	W47595	Hs.169300	SS,TM,TGF-beta,TGFb_propeptide	transforming growth factor, beta 2	5.1
423634	AW959908	Hs.1690	TM	heparin-binding growth factor binding pro	5.0
426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 3 (E polypeptide, protei	5.0
409744	AW675258	Hs.56265	TM,metalthio,Kelch	Homo sapiens mRNA; cDNA DKFZp586P2321 (fr	4.9

	444461	R53734	Hs.25978	TM	ESTs, Weakly similar to 2109260A B cell g	4.8
	410361	BE391804	Hs.62661	SS,TM,GBP	guanylate binding protein 1, interferon-i	4.8
	423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrophage e	4.8
5	450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep,Repolysin	a disintegrin and metalloproteinase domai	4.8
	401575	NA		TM	Target Exon	4.6
	428484	AF104032	Hs.184601	TM	solute carrier family 7 (cationic amino a	4.5
	425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, iodothyronine, type II	4.4
	431808	M30703	Hs.270833	SS,TM,EGF	amphiregulin (schwannoma-derived growth f	4.3
10	434699	AA643687	Hs.149425	TM,Nucleoside_tra2	Homo sapiens cDNA FLJ11980 fis, clone HEM	4.3
	406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprotein 9	4.2
	404440			TM,MAGE	NM_021048:Homo sapiens melanoma antigen,	4.2
	449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
	444105	AW189097	Hs.166597	TM,cadherin	ESTs	4.1
15	409632	W74001	Hs.55279	SS,serpin	serine (or cysteine) proteinase inhibitor	4.1
	423515	AA327017	Hs.162204	SS,TM,UPAR_LY6	ESTs	4.1
	423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
	423553	AA405635	Hs.96854	TM	ESTs, Weakly similar to DYLL_HUMAN CYTOPL	4.1
	445537	AJ245671	Hs.12844	TM,ras	EGF-like-domain, multiple 6	4.0
20	446989	AK001898	Hs.16740	TM	hypothetical protein FLJ11036	4.0
	428536	AI143139	Hs.2288	TM,efhand,Syndecan	visinin-like 1	3.9
	413801	M62246	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	3.9
	429441	AJ224172	Hs.204096	Uteroglobulin	lipophilin B (uteroglobulin family member),	3.9
	409601	AF237621	Hs.80828	TM,filamentfilament,C2	keratin 1 (epidermolytic hyperkeratosis)	3.8
25	439238	N47305	Hs.46668	TM	ESTs	3.8
	446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
	405545			SS,TM,proteasome,ig,ABC_memb,tranABC_tran,	(MDR/TAP) (TAP2)	3.8
	422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	SS,TM,fn3,vwa,Collagen,Kunitz_BPTI	collagen, type VII, alpha 1 (epidermolyti	3.7
30	430686	NM_001942	Hs.2633	SS,TM,cadherin,Cadherin_C_term	desmoglein 1	3.7
	444707	AI188613	Hs.41690	TM,cadherin	desmocollin 3	3.7
	409582	R27430	Hs.271565	TM	ESTs	3.6
	408771	AW732573	Hs.47584	TM,K_tetra,ion_trans	potassium voltage-gated channel, delayed-	3.6
	400441	M15530	Hs.99879	TM,G-alpha	B-cell growth factor 1 (12kD)	3.6
35	413278	BE563085	Hs.833	TM,ubiquitinlaminin_G,laminin_EGF,kazal	interferon-stimulated protein, 15 kDa	3.6
	426514	BE616633	Hs.170195	SS,TGFb_propeptide,TGF-beta	bone morphogenetic protein 7 (osteogenic	3.6
	424927	AW973666	Hs.153850	SS	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	SS,TM,Uteroglobulin	mammaglobin 1	3.5
	407756	AA116021	Hs.38260	SS,UCH-1,UCH-2	ubiquitin specific protease 18	3.5
40	407137	T97307		TM,GDA1_CD39	gb:ye53h05.s1 Soares fetal liver spleen 1	3.5
	411274	NM_002776	Hs.69423	trypsin	kallikrein 10	3.5
	400666			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metalloprot	3.5
	412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Cam_acyltransf	endothelial cell growth factor 1 (platele	3.4
45	450650	T65617	Hs.101257	TM	hypothetical protein MGC3295	3.4
	451778	AI826131	Hs.71243	ig	ESTs, Weakly similar to zinc finger prote	3.4
	430397	AI924533	Hs.105607	SS,TM	bicarbonate transporter related protein 1	3.4
	449722	BE280074	Hs.23960	TM,cyclin	cyclin B1	3.4
	422487	AJ010901	Hs.198267	TM,vwd	mucin 4, tracheobronchial	3.4
	449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
50	418994	AA296520	Hs.89546	SS,TM,lectin_c,sushi,EGF	selectin E (endothelial adhesion molecule	3.3
	421379	Y15221	Hs.103982	SS,TM,IL8	small inducible cytokine subfamily B (Cys	3.3
	414774	X02419	Hs.77274	SS,kringle,trypsin	plasminogen activator, urokinase	3.3
	431958	X63629	Hs.2877	SS,TM,Cadherin_C_term,cadherin	cadherin 3, type 1, P-cadherin (placental	3.3
	418462	BE001596	Hs.85266	SS,TM,integrin_B,fn3	integrin, beta 4	3.3
55	424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatinase B,	3.3
	401486	NA		SS,TM,trypsin	C4000647*gi4758508 ref NP_004253.1 air	3.2
	408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, clone AD	3.2
	427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	3.2
	452934	AA581322	Hs.4213	SS,TM,ig	hypothetical protein MGC16207	3.1
60	448988	Y09763	Hs.22785	SS,TM	gamma-aminobutyric acid (GABA) A receptor	3.1
	439750	AL359053	Hs.57664	TM,Integrin_B,Ricin_B_lectinrrm	Homo sapiens mRNA full length insert cDNA	3.1
	414696	AF002020	Hs.76918	SS,TM,Patched	Niemann-Pick disease, type C1	3.1
	435604	AA625279	Hs.26892	TM	uncharacterized bone marrow protein BM040	3.1
	453883	AI638516	Hs.22630	TM,Ets,SAM_PNT	cofactor required for Sp1 transcriptional	3.0
65	448733	NM_005629	Hs.187958	SS,TM,SNF,ABC_tran,isodh,pkinase,DSPC,Ribosomal_	solute carrier family 6 (neurotransmitter	3.0
	444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
	437938	AI950087		TM,histone,ig,MHC_I	gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapiens	3.0
	424441	X14850	Hs.147097	TM,histone	H2A histone family, member X	3.0
	427061	AB032971	Hs.173392	TM	KIAA1145 protein	3.0
70	409703	NM_006187	Hs.56009	SS	2'-5'-oligoadenylate synthetase 3 (100 kD	3.0
	447313	U92981	Hs.18081	TGF-beta	Homo sapiens clone DT1P1B6 mRNA, CAG repe	3.0
	431070	AW408164	Hs.249184	ABC_tran	transcription factor 19 (SC1)	2.9
	446269	AW263155	Hs.14559	TM	hypothetical protein FLJ10540	2.9
	421190	U95031	Hs.102482	TM,vwd	mucin 5, subtype B, tracheobronchial	2.9
75	452732	BE300078	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.9
	443859	NM_013409	Hs.9914	SS,kazal	folistatin	2.9
	446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid omega-	2.9
	449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOCH	2.9
	418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
80	414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kinase,SCO1-SenC	ESTs	2.9
	431629	AU077025	Hs.265827	SS,iRNA_antSH2,SH3,pkinase	interferon, alpha-inducible protein (clon	2.8
	445873	AA250970	Hs.251946	SS,rrm,PABPpkinase,14-3-3,rrm	poly(A)-binding protein, cytoplasmic 1-li	2.8
	438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
	410310	J02931	Hs.62192	SS,TM,Tissue_fac	coagulation factor III (thromboplastin, t	2.8

	411558	AA102670	Hs.70725	SS,TM	gamma-aminobutyric acid (GABA) A receptor	2.8
	413273	U75679	Hs.75257	TM,ig,pkinase	stem-loop (histone) binding protein	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product	2.8
5	433345	AI681545	Hs.152982	SS	hypothetical protein FLJ13117	2.7
	452234	AW084176	Hs.223296	TM	ESTs, Weakly similar to I38022 hypothetic	2.7
	456181	L36463	Hs.1030	TM,RA,VPS9	ras inhibitor	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor,sushi	diubiquitin	2.7
	422278	AF072873	Hs.114218	TM,Frizzled,Fz	frizzled (Drosophila) homolog 6	2.7
10	446839	BE091926	Hs.16244	TM	mitotic spindle coiled-coil related prote	2.7
	416250	AA581386	Hs.73452	TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Claudin	hypothetical protein MGC10791	2.7
	407287	AI678812		TM,rascadherin	gb:tu59d08.x1 NCL_CGAP_Gas4 Homo sapiens	2.7
	412977	AA125910	Hs.191461	TGF-beta	ESTs	2.7
	400298	AA032279	Hs.61635	TM	six transmembrane epithelial antigen of t	2.7
15	425483	AF231022	Hs.158159	EGF,cadherin,laminin_G	FAT tumor suppressor (Drosophila) homolog	2.7
	430152	AB001325	Hs.234642	SS,TM,MIP	aquaporin 3	2.7
	444006	BE395085	Hs.10086	SS,TM	type I transmembrane protein Fn14	2.7
	418869	AW516565		TM,RasGAP,IQ,WW	gb:xq01d05.x1 Soares_NHCeC_cervical_tumor	2.7
	416658	U03272	Hs.79432	SS,TM,EGF,TB	fibrillin 2 (congenital contractural arac	2.6
20	410290	AA402307	Hs.322844	SS,TM,Sema,TIG,Plexin_repeat	hypothetical protein DKFZp564A176	2.6
	419667	AU077005	Hs.92208	SS,TM,disintegrin,Repolyisin,Pep_M12B_propep	a disintegrin and metalloproteinase domai	2.6
	406671	AA129547	Hs.285754	TM,pkinase,Plexin_repeat,Sema,TIG,LIM	met proto-oncogene (hepatocyte growth fac	2.6
	434444	AI765276	Hs.101257	TM	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	TM,ABC_tran,ABC_membrane,Rhomboid	ATP-binding cassette, sub-family C (CFTR/	2.6
25	431890	X17033	Hs.271986	vwa,FG-GAP,integrin_A	integrin, alpha 2 (CD49B, alpha 2 subunit	2.6
	452281	T93500	Hs.28792	TGF-beta,TGFB_propeptide	Homo sapiens cDNA FLJ11041 fis, clone PLA	2.6
	421506	BE302796	Hs.105097	TM,TK	thymidine kinase 1, soluble	2.6
	453331	AI240665	Hs.8895	TM,disintegrin,Pep_M12B_propep,Repolyisin	ESTs	2.6
	447197	R36075		TM,SDF	gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.5
30	459688	U72671	Hs.151250	SS,TM,ig	intercellular adhesion molecule 5, telenc	2.5
	437412	BE069288	Hs.34744	TM,ABC_tran,ABC_membrane,Rhomboid	Homo sapiens mRNA; cDNA DKFZp547C136 (fro	2.5
	429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
	424420	BE614743	Hs.146688	TM,MAPEG	prostaglandin E synthase	2.5
	427239	BE270447	Hs.174070	TM,UQ_con	ubiquitin carrier protein	2.5
35	407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170	2.5
	431130	NM_006103	Hs.2719	SS,TM,wap	epididymis-specific, whey-acidic protein	2.5
	453379	AA035261	Hs.61753	PAN,kringle,trypsin	ESTs	2.5
	421733	AL119671	Hs.1420	SS,TM,ig,pkinase	fibroblast growth factor receptor 3 (acho	2.5
	452220	BE158006	Hs.212296	TM,integrin_A,FG-GAP	ESTs	2.5
40	417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	2.5
	440381	AA917808	Hs.190495	TM	ESTs	2.5
	441794	AW197794	Hs.253338	TM	ESTs	2.5
	439108	AW163034	Hs.6467	SS,TM	synaptogyrin 3	2.5
	401103	NA		TM,vwd	C12001233:gil7305361[ref NP_038652.1] oto	2.4
45	430630	AW269920	Hs.2621	TM,cystatin	cystatin A (stefin A)	2.4
	430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
	416621	AI648602	Hs.55468	TM,histone,Sec1sugar_tr	ESTs	2.4
	402745			SS,TM,EGF,ldl_recepLb,thyroglobulin_1	NM_002508:Homo sapiens nidogen (enactin)	2.4
	407758	D50915	Hs.38365	SS,TM	KIAA0125 gene product	2.4
50	457570	AA579426		TM	gb:nf37c09.s1 NCL_CGAP_Pr2 Homo sapiens c	2.4
	429574	BE268321	Hs.208912	SS,TM	hypothetical protein MGC861	2.4
	431211	M86849	Hs.323733	SS,TM,connexin	gap junction protein, beta 2, 26kD (conne	2.4
	452865	AI924046	Hs.119567	SS,TM,PMP22_Claudin	ESTs, Weakly similar to A47582 B-cell gro	2.4
	420511	AF052692	Hs.98485	SS,TM,connexin	gap junction protein, beta 3, 31kD (conne	2.4
55	437897	AA770561	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969	2.4
	437846	AA773866	Hs.244569	TM	esophagus cancer-related gene-2	2.4
	418432	M14156	Hs.85112	Insulin	insulin-like growth factor 1 (somatomedin	2.3
	438108	AI471795	Hs.287776	TM	vanilloid receptor-related osmotically ac	2.3
	453406	AI192987	Hs.61784	pkinase,Furin-like,Recep_L_domain	hypothetical protein FLJ14451	2.3
60	435542	AA687376	Hs.269533	pkinase,RhoGEF,ig,PH,SH3	ESTs	2.3
	434517	AA635690	Hs.337251	TM	hypothetical protein MGC2487	2.3
	431630	NM_002204	Hs.265829	SS,TM,FG-GAP,integrin_A	integrin, alpha 3 (antigen CD49C, alpha 3	2.3
	422310	AA316622	Hs.98370	SS,TM,fn3,ig,pkinase,Ribosomal_L36e,p450	cytochrome P450, subfamily IIS, polypepti	2.3
	441954	AI744935	Hs.8047	TM,Band_7,AAA,cdc48_N	Fanconi anemia, complementation group G	2.3
65	416091	AF295370	Hs.283082	SS,TM,Defensin_beta	defensin, beta 3	2.3
	429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membrane-ins	2.3
	409402	AF208234	Hs.695	TM,cystatin	cystatin B (stefin B)	2.3
	432284	AA532807	Hs.105822	TM,pkinase	ESTs	2.3
	408243	Y00787	Hs.624	SS,TM,IL8	interleukin 8	2.3
70	423229	AC003965	Hs.125532	SS,trypsin	protease, serine, 26	2.3
	408713	NM_001248	Hs.47042	GDA1_CD39	ectonucleoside triphosphate diphosphohydr	2.3
	440502	AI824113	Hs.78281	RGS,GoLoco,RBD	regulator of G-protein signalling 12	2.3
	429929	AB014583	Hs.226275	TM	KIAA0683 gene product	2.3
	439963	AW247529	Hs.6793	TM,p450Ets	platelet-activating factor acetylhydrolas	2.3
75	428953	AA306610	Hs.194676	SS,TM,TNFR_c6,arf,Statthmin,DEAD	tumor necrosis factor receptor superfamil	2.3
	439398	AA284267	Hs.221504	SS	ESTs	2.2
	440371	BE268550	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.2
	452203	X57522	Hs.158164	SS,TM,ABC_tran,ABC_membrane	transporter 1, ATP-binding cassette, sub-	2.2
80	407811	AW190902	Hs.40098	SS	cysteine knot superfamily 1, BMP antagoni	2.2
	432078	BE314877	Hs.24553	TM	hypothetical protein FLJ12541 similar to	2.2
	429113	D28235	Hs.196384	SS,TM,EGF	prostaglandin-endoperoxide synthase 2 (pr	2.2
	452755	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypothetic	2.2
	428434	AW363590	Hs.65551	SS	Homo sapiens, Similar to DNA segment, Chr	2.2
	429922	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0	2.2

5	417903	NM_002342	Hs.1116	SS,TM,ASC,TNFR_c6	lymphotoxin beta receptor (TNFR superfami	2.2
	422012	AW403423	Hs.110746	SS,homeobox,pou	HCR (a-helix coiled-coil rod homologue)	2.2
	433090	AI720050	Hs.145362	SS,TM	immortalization-upregulated protein	2.2
	417576	AA339449	Hs.82285	TM,AIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltransfera	2.2
	409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor; SREC	2.2
	417433	BE270266	Hs.82128	SS,TM,LRRCT,LRRNT,LRR	5T4 oncofetal trophoblast glycoprotein	2.2
	416763	AI908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators of di	2.2
	425999	AW513051	Hs.332981	TM,FAD_binding_2,P53PA,Ribosomal_S2,FAD_bindi	ESTs, Weakly similar to I38022 hypothetic	2.2
10	452799	AI948829	Hs.213786	TM	ESTs	2.2
	414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficient (S.	2.2
	448153	Y10805	Hs.20521	SS,TM,Na_Ca_Ex	HMT1 (hnRNP methyltransferase, S. cerevis	2.2
	428969	AF120274	Hs.194689	SS	artemin	2.2
	443171	BE281128	Hs.9030	SS,TM,7tm_1,rm	TONDU	2.2
15	408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
	409533	AW969543	Hs.21291	TM	mitogen-activated protein kinase kinase k	2.2
	408201	AK000568	Hs.43654	TM	hypothetical protein FLJ20561	2.1
	408996	AI979168	Hs.82226	TM	glycoprotein (transmembrane) nmb	2.1
	417900	BE250127	Hs.82906	TM,WD40,pro_isomerase	CDC20 (cell division cycle 20, S. cerevis	2.1
20	437191	NM_006846	Hs.331555	SS,TM,kazal	serine protease inhibitor, Kazal type, 5	2.1
	412834	R77123	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	2.1
	431117	AF003522	Hs.250500	SS,TM,DSL,EGF	delta (Drosophila)-like 1	2.1
	447674	BE270640	Hs.19192	TM,kinaseras,arf	cyclin-dependent kinase 2	2.1
	409651	H96643	Hs.283565	bZIPcofilin_ADF,EGF	FOS-like antigen-1	2.1
25	440495	AA887212	Hs.14161	TM,NSFNa_Ca_Ex	hypothetical protein DKFZp4341930	2.1
	429415	NM_002593	Hs.202097	SS,CUB,NTR,MAM,TIL,TiLa,vwd,EPO_TPO	procollagen C-endopeptidase enhancer	2.1
	421013	M62397	Hs.1345	TM	mutated in colorectal cancers	2.1
	447827	U73727	Hs.19718	SS,TM,Y_phosphatase,fn3,ig,MAM	protein tyrosine phosphatase, receptor ty	2.1
	449224	AW995911	Hs.299883	fn3	hypothetical protein FLJ23399	2.1
30	452679	Z42387	Hs.83883	TM	transmembrane, prostate androgen induced	2.1
	409956	AW103364	Hs.727	SS,TGF-beta,TGFb_propeptide	inhibin, beta A (activin A, activin AB al	2.1
	438580	AA811262	Hs.299202	TM,kinasesugar_tr	ESTs	2.1
	406400			SS,TM,trypsin	NM_007196:Homo sapiens kallikrein 8 (neur	2.1
	424965	AW956282	Hs.144609	TM	Homo sapiens, Similar to RIKEN cDNA 57305	2.1
35	412270	AC005262	Hs.73797	TM,G-alpha	guanine nucleotide binding protein (G pro	2.1
	428471	X57348	Hs.184510	TM,14-3-3	stratifin	2.1
	427375	AL035460	Hs.177536	SS,Zn_carbOpept,hormone5Reprolysin	metallocarboxypeptidase CPX-1	2.1
	416498	U33632	Hs.79351	TM	potassium channel, subfamily K, member 1	2.1
	423453	AW450737	Hs.128791	SS,Granin,CDP-OH_P_transf	CGI-09 protein	2.1
40	417944	AU077196	Hs.82985	SS,COLFI,Collagen,vwc	collagen, type V, alpha 2	2.1
	424197	AF096834	Hs.142989	SS,TM,CSD	germ cell specific Y-box binding protein	2.1
	446163	AA026880	Hs.25252	TM,fn3	prolactin receptor	2.1
	417331	AW411297	Hs.81972	TM,SH2,PID	SHC (Src homology 2 domain-containing) tr	2.1
	430413	AW842182	Hs.241392	IL8,PX	small inducible cytokine A5 (RANTES)	2.1
45	421685	AF189723	Hs.106778	TM,E1-E2_ATPase,HydrolaseE1-E2_ATPase	ATPase, Ca transporting, type 2C, member	2.1
	407305	AA715284		TM,kinase,Sema,Plaxin_repeat,TIG,LIM	gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens c	2.1
	407792	AI077715	Hs.39384	SS	putative secreted ligand homologous to f	2.0
	418695	AA447014	Hs.193261	SS	hypothetical protein MGC2991	2.0
50	439738	BE246502	Hs.9598	TM,RasGAP,IQ,VWV	sema domain, immunoglobulin domain (lg),	2.0
	433398	AW843150	Hs.112412	TM,PMP22_Claudin	ESTs	2.0
	456327	H68741	Hs.38774	TM,Glyco_transf_8	ESTs	2.0
	446872	X97058	Hs.16362	TM	pyrimidinergic receptor P2Y, G-protein co	2.0
	419726	U50330	Hs.1274	SS,TM,Astacin,CUB,EGF	bone morphogenetic protein 1	2.0
	410116	AW630671	Hs.58636	SS,TM	squamous cell carcinoma antigen recognize	2.0
55	426500	NM_014638	Hs.170156	TM	KIAA0450 gene product	2.0
	452194	AI694413	Hs.332649	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily I	2.0
	418140	BE613836	Hs.83551	TM,E1-E2_ATPase	microfibrillar-associated protein 2	2.0
	425855	AF135025	Hs.159679	SS,trypsin	kallikrein 12	2.0
	434346	AA630445	Hs.116773	TM,Ferric_reduct	ESTs	2.0
60	426274	D38122	Hs.2007	TM,TNF	tumor necrosis factor (ligand) superfamil	2.0
	440008	AW051683	Hs.277686	TM,RhoGEF,FYVE,PH	ESTs	2.0
	424634	NM_003613	Hs.151407	ig,tsp_1	cartilage intermediate layer protein, nuc	2.0
	446641	AL049229	Hs.15787	TM,kinase,rm	Homo sapiens mRNA; cDNA DKFZp564O1016 (fr	2.0
	418851	AI417828	Hs.192435	TM	ESTs	2.0
65	440351	AF030933	Hs.7179	TM,Rad1,Cadherin_C_tern	RAD1 (S. pombe) homolog	2.0
	439496	BE616501	Hs.32343	SS	Homo sapiens, Similar to RIKEN cDNA 11100	2.0
	454197	BE140966		TM,Ammonium_transpkinasin,Ammonium_transp	gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
	433573	AF234887	Hs.57652	TM,7tm_2,GPSIRNA-synt_2b,Seryl_IRNA_N	cadherin, EGF LAG seven-pass G-type recep	2.0
	429211	AF052693	Hs.198249	TM,connexin	gap junction protein, beta 5 (connexin 31	2.0
70	420737	L08096	Hs.99899	SS,TM,TNF	tumor necrosis factor (ligand) superfamil	2.0
	455333	AW897851		TM,Glyco_hydro_2	gb:RC1-NN0063-100500-022-c08 NN0063 Homo	2.0
	414784	NM_000344	Hs.288986	SS,TM,BIR	survival of motor neuron 1, telomeric	2.0
	435836	AW292532	Hs.250175	TM,GNS1_SUR4	homolog of yeast long chain polyunsaturat	2.0
	411789	AF245505	Hs.72157	TM,ig,LRRCT	DKFZP564I1922 protein	2.0
	441455	AJ271671	Hs.7854	TM,ras,DENN	zinc/iron regulated transporter-like	2.0
75	426068	AF029778	Hs.166154	SS,TM,DSL,EGF,NUDIX	jagged 2	2.0
	439733	AL365412	Hs.107203	TM,Sm	hypothetical protein from EUROIMAGE 17593	2.0
	435014	BE560898	Hs.10026	TM,Ribosomal_L17	mitochondrial ribosomal protein L17	1.9
	457819	AA057484	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	1.9
80	422737	M26939	Hs.119571	SS,Collagen,COLFI	collagen, type III, alpha 1 (Ehlers-Danlo	1.9
	431104	AW970859	Hs.313503	Sema,ig	ESTs	1.9
	432210	AI567421	Hs.273330	TM,laminin_G,laminin_EGF,kazalubiquitin	Homo sapiens, clone IMAGE:3544662, mRNA,	1.9
	436511	AA721252	Hs.291502	TM,disintegrin,Reprolysin,Pep_M12B_propep,kinase,	ESTs	1.9
	419216	AU076718	Hs.164021	SS,IL8	small inducible cytokine subfamily B (Cys	1.9

	432169	Y00971	Hs.2910	TM,Pribosyltran	phosphoribosyl pyrophosphate synthetase 2	1.9
	441128	AA570256	Hs.54628	TM,ras	ESTs, Weakly similar to T23273 hypothetic	1.9
	447160	AA330310	Hs.24181	TM	ESTs	1.9
5	419138	U48508	Hs.89631	TM,RYDR,ITPR,RyR,SPRY	ryanodine receptor 1 (skeletal)	1.9
	457817	AA247751	Hs.79572	TM,hemopexin,Peptidase_M10	cathepsin D (lysosomal aspartyl protease)	1.9
	431009	BE149762	Hs.48956	SS,TM,connexin	gap junction protein, beta 6 (connexin 30)	1.9
	428957	NM_003881	Hs.194679	SS,TM,vwc,IGFBP,isp_1	WNT1 inducible signaling pathway protein	1.9
	418546	AA224827		TM,vwa,FG-GAP,integrin_A	gb:nc32g04.s1 NCL_CGAP_Pr2 Homo sapiens c	1.9
10	400749			SS,TM,ldl_recept_a,fn3,ldl_recept_b	NM_003105*:Homo sapiens sortilin-related	1.9
	408369	R38438	Hs.182575	F-protein	solute carrier family 15 (H???) transporte	1.9
	422765	AW409701	Hs.1578	TM,BIR	baculoviral IAP repeat-containing 5 (surv	1.9
	417409	BE272506	Hs.82109	TM,Syndecan	syndecan 1	1.9
	407720	AB037776	Hs.38002	TM,calponin,CH	KIAA1355 protein	1.9
15	418830	BE513731	Hs.88959	TM,CDP-OH_P_transf,MCM	hypothetical protein MGC4816	1.9
	434769	AA648884	Hs.134278	TM,CDP-OH_P_transf,MCM	Homo sapiens cDNA FLJ12676 fis, clone NT2	1.9
	421593	NM_017436	Hs.105956	SS,TM	globotriaosylceramide/CD77 synthase; Gb3/	1.9
	426064	BE387014	Hs.166146	TM,WH1	Homer, neuronal immediate early gene, 3	1.9
	404604	NA		TM	Target Exon	1.9
20	422753	AI928995	Hs.1575	SS,TM,Sm	small nuclear ribonucleoprotein D3 polype	1.9
	422739	H20106	Hs.119591	SS,Clal_adaptor_s	adaptor-related protein complex 2, sigma	1.9
	433068	NM_006456	Hs.288215	SS,Pribosyltran	sialyltransferase	1.9
	419594	AA013051	Hs.91417	TM	topoisomerase (DNA) II binding protein	1.9
	428188	M98447	Hs.22	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 1 (K polypeptide epiderm	1.9
25	428343	AL043021	Hs.12705	TM,Rhomboid,HMG_boxTPR	ESTs	1.9
	429592	AB029041	Hs.209646	Troponin	KIAA1118 protein	1.9
	431620	AA126109	Hs.264981	C2,PH,RasGAP,NTP_transf_2	2'-5'-oligoadenylate synthetase 2 (69-71	1.9
	424670	W61215	Hs.116651	ig	epithelial V-like antigen 1	1.9
	428373	AI751656	Hs.183986	SS,TM,ig	poliovirus receptor-related 2 (herpesviru	1.9
30	453449	W16752	Hs.32981	SS,ig,Sema	sema domain, immunoglobulin domain (Ig),	1.9
	432304	AA932186	Hs.69297	TM,7tm_1	ESTs	1.9
	432673	AB028859	Hs.278605	TM,DnaJ,DnaJ_CDnaJ	DnaJ (Hsp40) homolog, subfamily B, member	1.9
	416207	NM_014745	Hs.336433	SS,TM,zf-DHHC	Homo sapiens, clone MGC:2908, mRNA, compl	1.9
	408988	AL119844	Hs.49476	TM,Plexin_repeat,Sema,isp_1	Homo sapiens clone TUA8 Cri-du-chat regio	1.9
35	417426	NM_002291	Hs.82124	SS,laminin_EGF,laminin_Nterm	laminin, beta 1	1.9
	443883	AA114212	Hs.9930	SS,TM,serpin,Marek_A	serine (or cysteine) proteinase inhibitor	1.9
	433328	AW298159	Hs.23644	SS,TM	ESTs, Weakly similar to S65824 reverse tr	1.9
	419981	AA897581	Hs.128773	TM,Skl_Sno	ESTs	1.8
	420931	AF044197	Hs.100431	SS,TM,IL8	small inducible cytokine B subfamily (Cys	1.8
40	415023	AA932146	Hs.133494	TM,Ribosomal_S17Ribosomal_L13	Homo sapiens clone TCCCA00164 mRNA seque	1.8
	413644	BE154910	Hs.278793	TM,Glyco_hydro_2	ESTs, Weakly similar to Z195_HUMAN ZINC F	1.8
	449987	AW079749	Hs.184719	TM,ABC_tran,ABC_membraneion_trans	ESTs, Weakly similar to ALU1_HUMAN ALU SU	1.8
	421340	F07783	Hs.1369	SS,sushi	decay accelerating factor for complement	1.8
	417866	AW067903	Hs.82772	SS,TM,Collagen,COLFI,TSPN	collagen, type XI, alpha 1	1.8
45	430259	BE550182	Hs.127826	TM,transmembrane4RasGEF,RA	RaIGEF-like protein 3, mouse homolog	1.8
	432998	AA835948	Hs.153307	TM,SDF	ESTs	1.8
	431671	NM_016937	Hs.267289	TM,NA	polymerase (DNA directed), alpha	1.8
	411773	NM_006799	Hs.72026	trypsin	protease, serine, 21 (testisin)	1.8
	425247	NM_005940	Hs.155324	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 11 (stromelysin	1.8
50	422976	AU076657	Hs.1600	TM,cpn60_TCP1,Sema	chaperonin containing TCP1, subunit 5 (ep	1.8
	425159	NM_004341	Hs.154868	SS,TM,GATase,OTCace,CPSase_L_chain,Dihydrooro	carbamoyl-phosphate synthetase 2, asparta	1.8
	447776	AI525625	Hs.130181	Ricin_B_lectin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.8
	426908	AW815163	Hs.172851	SS,TM,fusion_gly,Myosin_tailadh_short	arginase, type II	1.8
	408116	AA251393	Hs.289052	TM,Na_Ca_ExCam_acyltransf	Homo sapiens, Similar to RIKEN cDNA 54304	1.8
55	417847	AI521558	Hs.7331	Uteroglobulin	hypothetical protein FLJ22316	1.8
	415791	H09366	Hs.78853	SS,TM,UNG	uracil-DNA glycosylase	1.8
	407903	AI287341	Hs.154029	TM,ubiquitin,laminin_G,laminin_EGF,kazal	bHLH factor Hes4	1.8
	422511	AU076442	Hs.117938	TM,p450	collagen, type XVII, alpha 1	1.8
	414117	W88559	Hs.1787	TM,ion_trans,K_tetra	proteolipid protein 1 (Pelizaeus-Merzbach	1.8
60	426841	AI052358	Hs.193726	TM,asp	ESTs	1.8
	415272	AA164215	Hs.203186	TM,TPR,pkinase,Ig,B56	ESTs	1.8
	426440	BE382756	Hs.169902	TM,sugar_tr,Fork_head	solute carrier family 2 (facilitated gluc	1.8
	419488	AA316241	Hs.90691	FGF	nucleophosmin/nucleoplasm 3	1.8
	418452	BE379749	Hs.85201	SS,TM,lectin_c	C-type (calcium dependent, carbohydrate-r	1.8
65	431363	M86528	Hs.266902	SS,NGF	neurotrophin 5 (neurotrophin 4/5)	1.8
	440975	AW499914	Hs.7579	SS,TM	hypothetical protein FLJ10402	1.8
	438962	BE046594		TGF-beta,bZIP	gb:hn41c11.x1 NCL_CGAP_RDF2 Homo sapiens	1.8
	414602	AW630088	Hs.76550	SS	Homo sapiens mRNA; cDNA DKFZp564B1264 (fr	1.8
	418054	NM_002318	Hs.83354	TM,mito_carr,Lysyl_oxidase	lysyl oxidase-like 2	1.8
70	440501	AA887391	Hs.202229	TM,Galactosyl_T	ESTs	1.8
	449309	AW589823	Hs.224189	TM	ESTs	1.8
	421461	AW291023	Hs.97255	TM,Lysyl_oxidase,SCP2,Band_7	ESTs, Weakly similar to A46010 X-linked r	1.8
	412584	X54870	Hs.74085	TM,lectin_c	DNA segment on chromosome 12 (unique) 248	1.8
	441565	AW953575	Hs.303125	TM	p53-induced protein PIGPC1	1.8
75	431837	T79326	Hs.326553	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily I	1.8
	436251	BE515065	Hs.296585	SS,Y_phosphataseTIG	nucleolar protein (KKE/D repeat)	1.8
	448633	AA311426	Hs.21635	TM,EGF,laminin_G,fibrinogen_C,F5_F8_type_C,tubulin	tubulin, gamma 1	1.8
	424291	AL120051	Hs.144700	TM,Ephrin,Hist_deacetyl	ephrin-B1	1.8
	415388	AF018081	Hs.78409	SS,TM,TSPN,Collagen	collagen, type XVIII, alpha 1	1.8
80	435550	AI224456	Hs.4934	TM,LRR,LRRCT	H.sapiens polyA site DNA	1.8
	448568	AA149121	Hs.71947	TM,LRRCT	ESTs	1.8
	439246	AI498072	Hs.77783	SS,TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Cla	membrane-associated tyrosine- and threoni	1.8
	410001	AB041036	Hs.57771	SS,TM,trypsin	kallikrein 11	1.8
	417312	AW888411	Hs.81915	SS,Stathmin	leukemia-associated phosphoprotein p18 (s	1.8

5	444152	AI125694	Hs.149305	TM	hypothetical protein MGC2603	1.8
	453454	AW052006	Hs.8551	TM	PRP4/STK/WD splicing factor	1.8
	449320	AB030835	Hs.23476	SS,adenylatekinase	Cip1-interacting zinc finger protein	1.8
	428329	AA426091	Hs.98453	TM,Gal-bind,Jectin	ESTs, Moderately similar to R27328 2 [H.s	1.8
	452875	BE275760	Hs.30928	TM,Apolipoproteinig	DNA segment on chromosome 19 (unique) 117	1.8
	444031	BE271513	Hs.25303	TM,Peptidase_M10,hemopexin	hypothetical protein FLJ13154	1.8
	443534	AI076123		TM	gb:oy92e04.x1 Soares_fetal_liver_spleen_1	1.8
10	413313	NM_002047	Hs.75280	TM,WHEP-TRS,7tm_2	glycyl-IRNA synthelase	1.8
	452874	AK001061	Hs.30925	SS	hypothetical protein FLJ10199	1.8
	453140	AA032238	Hs.170531	TM	ESTs	1.8
	418641	BE243136	Hs.86947	SS,TM,disintegrin,Pep_M12B_propep,Repolyisin	a disintegrin and metalloproteinase domai	1.8
	432925	AA878324	Hs.192734	SS	ESTs	1.8
	453857	AL080235	Hs.35861	TM	DKFZP586E1621 protein	1.8
15	457663	AW371946	Hs.337459	TM	ESTs	1.8
	452873	AK001247	Hs.30922	TM	hypothetical protein FLJ10385	1.8
	436396	AI683487	Hs.152213	SS,wnt	wingless-type MMTV integration site famil	1.8
	452835	AK001269	Hs.30738	TM	hypothetical protein FLJ10407	1.7
	459647	R34107	Hs.198287	ig	pregnancy specific beta-1-glycoprotein 11	1.7
20	418245	AA088767	Hs.83883	TM,PEPCK	transmembrane, prostate androgen induced	1.7
	448484	BE613340	Hs.334725	TM	Homo sapiens, Similar to RIKEN cDNA 94300	1.7
	431369	BE184455	Hs.251754	SS,wap	secretory leukocyte protease inhibitor (a	1.7
	434877	AW974792	Hs.292171	TM	ESTs	1.7
	428923	BE047698	Hs.188785	TM	ESTs	1.7
25	402915	NA		TM,HCO3_cotransp	ENSP00000202587*:Bicarbonate transporter-	1.7
	420185	AL044056	Hs.158047	TM	ESTs	1.7
	445739	AW136354	Hs.145303	TM	ESTs	1.7
	409435	AI810721	Hs.95424	TM,p450	ESTs	1.7
	408688	AI634522	Hs.152925	TM	KIAA1268 protein	1.7
30	420085	AI741909	Hs.44680	TM	hypothetical protein FLJ20979	1.7
	433933	AI754389	Hs.133494	TM,Ribosomal_S17Ribosomal_L13	Homo sapiens clone TCCIA00164 mRNA seque	1.7
	430965	AA489732	Hs.154918	hormone_rec,Prog_receptor,zf-C4	ESTs	1.7
	414703	BE243877	Hs.76941	SS,TM,Na_K-ATPaseE2F_TDP	ATPase, Na? transporting, beta 3 polypept	1.7
	423464	NM_016240	Hs.128856	TM,Collagen	CSR1 protein	1.7
35	416737	AF154335	Hs.79691	SS,TM,LIM,PDZsugar_lr,PDZ,LIM	LIM domain protein	1.7
	409012	AL117435	Hs.49725	TM,RhoGEFzf-DHHC,adh_short	DKFZP434I216 protein	1.7
	423804	AW403448	Hs.1706	TM,IRF	interferon-stimulated transcription facto	1.7
	410418	D31382	Hs.63325	SS,TM,trypsin,Idl_recept_a	transmembrane protease, serine 4	1.7
	440028	AW473675	Hs.125843	TM	ESTs, Weakly similar to T17227 hypothetic	1.7
40	457646	AA725650	Hs.112948	TM,SPRY	ESTs	1.7
	445439	BE243084	Hs.12719	SS,TGF-beta	regulator of nonsense transcripts 1	1.7
	420426	AA262045	Hs.36567	TM,Galactosyl_T_2ATP-synt_C	Homo sapiens cDNA FLJ14227 fis, clone NT2	1.7
	431341	AA307211	Hs.251531	TM,proteasome	proteasome (prosome, macropain) subunit,	1.7
	412338	AA151527	Hs.69485	TM,Sema,Plexin_repeatTIG,Plexin_repeat	hypothetical protein FLJ12436	1.7
45	414799	AI752416	Hs.77326	SS,thyroglobulin_1,IGFBP	insulin-like growth factor binding protei	1.7
	452700	AI859390	Hs.288940	TM,DIX,RGS,thiored	five-span transmembrane protein M83	1.7
	430877	NM_005269	Hs.2693	GST_C,IRNA-synt_1,WHEP-TRS,TGF-beta	glioma-associated oncogene homolog (zinc	1.7
	428624	AI125222	Hs.98712	TM,thiored,Y_phosphatase,MAM,ig,fn3MSP_domain	hypothetical protein DKFZp434H0311	1.7
	444065	AW449415	Hs.10260	TM,ion_trans	Homo sapiens cDNA FLJ11341 fis, clone PLA	1.7
50	416319	AI815601	Hs.79197	SS,TM,ig	CD83 antigen (activated B lymphocytes, im	1.7
	429367	AB007867	Hs.278311	Sema,Plexin_repeat,TIG	plexin B1	1.7
	430425	AA531428	Hs.241412	TM	apolipoprotein L, 2	1.7
	441668	AI611973	Hs.127525	TM,Ammonium_transp	ESTs	1.7
	418469	U34879	Hs.85279	SS,TM,adh_short	hydroxysteroid (17-beta) dehydrogenase 1	1.7
55	450835	BE262773	Hs.25584	TM,ArfGap	hypothetical protein FLJ10767	1.7
	418859	AA229558		TM	gb:nc15d10.s1 NCL_CGAP_Pr1 Homo sapiens c	1.7
	425304	AA463844	Hs.31339	TM,ig,ITAM	fibroblast growth factor 11	1.7
	423635	X85019	Hs.130181	TM,Ricin_B_Jectin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.7
	414820	AA371931	Hs.77422	TM,ion_trans,LIM,Synaptophysin	proteolipid protein 2 (colonic epithelium	1.7
60	440654	AW014242	Hs.159998	TM,connexin	ESTs	1.7
	412276	BE262621	Hs.73798	SS,MIF	macrophage migration inhibitory factor (g	1.7
	422087	X58968	Hs.111301	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 2 (gelatinase A,	1.7
	407151	H25836	Hs.301527	SS,TNF	ESTs, Moderately similar to unknown [H.sa	1.7
	410726	AI623859	Hs.15936	TM,PX	ESTs	1.7
65	452012	AA307703	Hs.279766	TM,kinesin	kinesin family member 4A	1.7
	433627	AF078866	Hs.284296	TM,SURF4,SURF1,DEADlipocalin	Homo sapiens cDNA: FLJ22993 fis, clone KA	1.7
	409220	BE243323	Hs.51233	TM,death,TNFR_c6	tumor necrosis factor receptor superfamil	1.7
	427082	AB037858	Hs.173484	TM,mito_carr	hypothetical protein FLJ10337	1.7
	426410	BE298446	Hs.305890	TM,Bcl-2,BH4	BCL2-like 1	1.7
70	433598	AI762836	Hs.271433	TM,Cytidylyltransf,SIR27tm_2	ESTs, Moderately similar to ALU2_HUMAN AL	1.7
	436495	BE258948	Hs.290874	TM,Armaddillo_seg	ESTs, Weakly similar to ALU8_HUMAN ALU SU	1.7
	422032	AA476966	Hs.110857	TM,TFIIS,RNA_POL_M_15KDserpin,hormone_rec,zf-C4	polymerase (RNA) III (DNA directed) polyp	1.7
	429736	AF125304	Hs.212680	SS,TNFR_c6	tumor necrosis factor receptor superfamil	1.7
	427600	AW630918	Hs.179774	TM,Transglutamin_C,Transglutamin_N,Transglut_core	proteasome (prosome, macropain) activator	1.7
75	431981	AA664069	Hs.115779	laminin_B,laminin_EGF	ESTs	1.7
	407736	N41744	Hs.19978	TM,Sulfatase	CGI-30 protein	1.7
	420187	AK001714	Hs.95744	TM	hypothetical protein similar to ankyrin r	1.7
	424620	AA101043	Hs.151254	SS,TM,trypsin	kalikrein 7 (chymotryptic, stratum come	1.7
	430488	D19589	Hs.13453	TM	hypothetical protein FLJ14753	1.7
80	423393	R37772	Hs.21420	TM,thioredpkinase	p21-activated protein kinase 6	1.7
	444051	N48373	Hs.10247	SS,ig		

TABLE 13B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
408344	105240_1	AA053843 BE162213
418546	176677_1	AA224827 T59708 T59843 BE156903
418859	179717_1	AA229558 AA345492 AA229582
418869	179863_1	AW516565 AA229762 AA230035
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875
		AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
		AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062
		AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642
		AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499
		AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996
		AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531
		H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
438962	467390_1	BE046594 BE046667 AA828585 AI207343
443534	572957_1	AI076123 AI244834 AI695239
447197	711623_1	R36075 AI366546 R36167
454197	1050392_1	BE140966 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969
		BE141673 BE141650 BE141674 BE141550 BE141688 AW178241 BE140994 BE141666 BE140998 BE141008 BE140988 BE141011 BE140975
		BE141667 BE141675 BE141657 BE141681 BE141656 BE141672 BE141680 AW178237 BE141012 BE140990 BE141658 BE141648 BE141013
		BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646
		BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671
		AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141556
455333	1281044_1	AW897851 AW897852
457570	357443_1	AA579426 AA579436 AA573735

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400666	8118496	Plus	17982-18115,20297-20456
400749	7331445	Minus	9162-9293
401103	8568122	Minus	98330-98449
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
401575	7229804	Minus	76253-76364
402745	9212200	Minus	76516-76690
402915	7406502	Minus	140-276
404440	7528051	Plus	80430-81581
404604	9212537	Minus	72019-72509
405545	1054740	Plus	118677-118807,119091-119296,121626-121823
405547	1054740	Plus	124361-124520,124914-125050
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406467	9795551	Plus	182212-182958

TABLE 14A: 209 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES THAT ARE LIKELY TO ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES

Table 14A lists about 209 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 12A, except that the ratio was greater than or equal to 2.0, and the 96th percentile value amongst cervical cancers was greater than or equal 40 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulatable by small molecules (e.g. pkinase, peptidase, phosphatase, ATPase, or ion_transporter domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 PPDomains: Predicted Protein Domains
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigenelD	PPDomains	Unigene Title	R1
418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interst	38.9
439606	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87	28.8
400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (stroma	20.5
415817	U88967	Hs.78867	SS,TM,Y_phosphatase,carb_anhyd	protein tyrosine phosphatase, recep	16.4
416209	AA236776	Hs.79078	TM,HORMA	MAD2 (mitotic arrest deficient, yea	15.4
404996	NM_001333	Hs.87417	Peptidase_C1	CTSL2 Cathepsin L2	13.1

	428618	AA885360	Hs.160199	pkinese	Target CAT	12.7
	429486	AF155827	Hs.203963	helicase_C,SNF2_Nhelicase_C	hypothetical protein FLJ10339	12.6
	419183	U60669	Hs.89663	p450	cytochrome P450, subfamily XXIV (vi	12.3
5	428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromel	10.2
	420759	T11832	Hs.127797	helicase_C	Homo sapiens cDNA FLJ11381 fis, clo	10.2
	458194	AW383618	Hs.265459	p450	ESTs, Moderately similar to ALU2_HU	9.4
	446232	AI281848	Hs.194691	TM,7tm_3Ribosomal_L13	retinoic acid induced 3	8.9
	424905	NM_002497	Hs.153704	TM,PKinase	NIMA (never in mitosis gene a)-rela	8.9
10	452291	AF015592	Hs.28853	TM,PKinase	CDC7 (cell division cycle 7, S. cer	8.7
	424086	AI351010	Hs.102267	Lysyl_oxidase	lysyl oxidase	8.3
	425710	AF030880	Hs.159275	TM,Sulfate_transp,STAS	solute carrier family, member 4	7.8
	433133	AB027249	Hs.104741	TM,Collagen,PKinase	PDZ-binding kinase; T-cell original	7.4
	447254	NM_004153	Hs.17908	SS,AAA,BAH	origin recognition complex, subunit	7.1
15	431941	AK000106	Hs.272227	PKinase,Furin-like,Recep_L_dom	Homo sapiens cDNA FLJ20099 fis, clo	6.9
	427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
	436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA	6.9
	403471	NA		SS,TM,trypsin	Target Exon	6.7
	410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
20	457405	AA504860		TM,7tm_2	gb:ab03a10.s1 Stratagene fetal reti	6.4
	421948	L42583	Hs.334309	filament,HCO3_cotranspfilament	keratin 6A	6.3
	439292	AA090421	Hs.5555	TM,AAA,Ferric_reduct	hypothetical protein MGC5347	5.8
	413625	AW451103	Hs.71371	TM,E1-E2_ATPase,Hydrolase	ESTs	5.8
	425695	NM_005401	Hs.159238	TM,Band_41,Y_phosphatase	protein tyrosine phosphatase, non-r	5.7
25	438394	BE379623	Hs.27693	SS,pro_isomerase	peptidylprolyl isomerase (cyclophil	5.6
	432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collag	5.5
	408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Cation_ATPa	ESTs	5.4
	432226	AW182766	Hs.273558	Cytidylyltransf	phosphate cytidylyltransferase 1, c	5.2
	419520	AB009303	Hs.90800	TM,hemopexin,Peptidase_M10	matrix metalloproteinase 16 (membra	5.1
30	426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutam	transglutaminase 3 (E polypeptide,	5.0
	421155	H87879	Hs.102267	SS,Lysyl_oxidase,Aldose_epim,E	lysyl oxidase	4.9
	423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrop	4.8
	450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep	a disintegrin and metalloproteinase	4.8
	418379	AA218940	Hs.137516	AAA	fidgetin-like 1	4.7
35	457465	AW301344	Hs.122908	Pribosyltran,Sulfatase	DNA replication factor	4.6
	412333	AW937485		TM,7tm_1	gb:QV3-DT0044-221299-045-b09 DT0044	4.6
	450510	AA010056	Hs.242998	DNA_topoisomI,DNA_topoisomIVGF	ESTs	4.6
	436291	BE568452	Hs.5101	abhydrolase	protein regulator of cytokinesis 1	4.6
	446353	AI290919	Hs.153661	HECTPKinase	ESTs	4.5
40	435435	T89473	Hs.192328	lipase,PLAT	ESTs	4.5
	425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, iodothyronine, type II	4.4
	433322	H50621	Hs.134156	TM,ion_transNB-ARC,CARD_mito_c	ESTs, Weakly similar to I38022 hypo	4.4
	408908	BE296227	Hs.250822	TM,PKinase	serine/threonine kinase 15	4.4
	444781	NM_014400	Hs.11950	PH,lactamase_B	GPI-anchored metastasis-associated	4.4
45	428479	Y00272	Hs.184572	PKinase	cell division cycle 2, G1 to S and	4.2
	406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprot	4.2
	423035	AW449679	Hs.156739	TM,Glyco_transf_8	H.sapiens XG mRNA (clone PEP11)	4.2
	449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
	423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
50	457030	AI301740	Hs.173381	TM,Dihydroorotase	dihydropyrimidinase-like 2	4.1
	448995	AI613276	Hs.5662	adenylatekinase	guanine nucleotide binding protein	4.0
	415857	AA866115	Hs.127797	helicase_C	Homo sapiens cDNA FLJ11381 fis, clo	4.0
	438390	AI422017		TM,DSL,7tm_17tm_1	gb:tf45f12.x1 NCI_CGAP_Brn23 Homo s	4.0
	429900	AA460421	Hs.30875	PKinase	ESTs	4.0
55	446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
	422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
	408771	AW732573	Hs.47584	TM,K_tetra,ion_trans	potassium voltage-gated channel, de	3.6
	424296	AI631874	Hs.155140	PKinase	casein kinase 2, alpha 1 polypeptid	3.6
	436246	AW450963	Hs.119991	connexinhormone_rec,zf-C4	ESTs	3.5
60	411274	NM_002776	Hs.69423	trypsin	kalikrein 10	3.5
	400666			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metal	3.5
	426920	AA393351	Hs.132121	PDEase	ESTs	3.5
	412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Carn_acy	endothelial cell growth factor 1 (p	3.4
	430704	AW813091	Hs.335799	Epimerase	ESTs	3.4
65	455092	BE152428		Sulfatase	gb:CM0-HT0323-151299-126-b04 HT0323	3.4
	453775	NM_002916	Hs.35120	AAA,PI3_P14_kinase,PI3Ka,PI3K_	replication factor C (activator 1)	3.4
	438993	AA828995		integrin_B	gb:od77b08.s1 NCI_CGAP_Ov2 Homo sap	3.4
	426572	AB037783	Hs.170623	hormone_rec,zf-C4	hypothetical protein FLJ11183	3.4
	449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
70	427660	AI741320	Hs.114121	hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23228 fis, cl	3.3
	402481			TM,GDI,7tm_1	NM_001821*:Homo sapiens choroiderem	3.3
	414774	X02419	Hs.77274	SS,kringle,trypsin	plasminogen activator, urokinase	3.3
	412246	AI160873	Hs.69233	SulfotransferACOX	zinc finger protein	3.3
	418462	BE001596	Hs.85266	SS,TM,Integrin_B,fn3	integrin, beta 4	3.3
75	424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatin	3.3
	401486	NA		SS,TM,trypsin	C4000647*:gij4758508[ref]NP_004253.	3.2
	408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, cl	3.2
	427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, cl	3.2
80	402337			SS,p450	Target Exon	3.2
	420930	AW888650		ribonuclease_T2	gb:CM4-NT0007-130500-551-f06 NT0007	3.2
	443426	AF098158	Hs.9329	PKinase	chromosome 20 open reading frame 1	3.1
	439750	AL359053	Hs.57664	TM,Integrin_B,Ricin_B_tectinrr	Homo sapiens mRNA full length inser	3.1
	420039	NM_004605	Hs.94581	CARD,SulfotransferDAGKc	sulfotransferase family, cytosolic,	3.0
	448733	NM_005629	Hs.187958	SS,TM,SNF,ABC_tran,isodh,pkina	solute carrier family 6 (neurotrans	3.0

	444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
	450841	AI741466	Hs.270515	pro_isomerase	ESTs	3.0
	428262	AI651324	Hs.7298	death,pkinase	biphenyl hydrolase-like (serine hyd	3.0
5	435399	AA679463		pkinase	gb:ac50c03.s1 Stratagene hNT neuron	2.9
	446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid	2.9
	449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN	2.9
	418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
	414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kin	ESTs	2.9
10	431629	AU077025	Hs.265827	SS,iRNA_antiSH2,SH3,pkinase	interferon, alpha-inducible protein	2.8
	445873	AA250970	Hs.251946	SS,rm,PABPpkinase,14-3-3,rm	poly(A)-binding protein, cytoplasmic	2.8
	438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
	422689	AW856665		helicase_C,SNF2_Nhelicase_C	gb:RC3-CT0297-290100-013-d03 CT0297	2.8
	439453	BE264974	Hs.6566	SS,AAA	thyroid hormone receptor interactor	2.8
15	413582	AW295647	Hs.71331	carb_anhydrase	hypothetical protein MGC5350	2.8
	410664	NM_006033	Hs.65370	TM,lipase,PLAT	lipase, endothelial	2.8
	456456	AA477609	Hs.89563	FBPase	nuclear cap binding protein subunit	2.8
	413273	U75679	Hs.75257	TM,lg,pkinase	stem-loop (histone) binding protein	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product	2.8
20	403763			TM,7tm_1	NM_001059*:Homo sapiens tachykinin	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor	diubiquitin	2.7
	401230			SS,TM,ion_trans,IQ	NM_014191*:Homo sapiens sodium chan	2.7
	418030	BE207573	Hs.83321	SS,TM,Peptidase_S26,Bombesin	neuromedin B	2.7
	445640	AW969626	Hs.31704	TM,alpha-amylase	ESTs, Weakly similar to KIAA0227 [H	2.7
25	432865	AI753709	Hs.152484	TM,ion_transNB-ARC,CARD,WD40,m	ESTs, Weakly similar to I38022 hypo	2.6
	419667	AU077005	Hs.92208	SS,TM,disintegrin,Reprolysin,P	a disintegrin and metalloproteinase	2.6
	406671	AA129547	Hs.285754	TM,pkinase,Flexin_repeat,Sema,	met proto-oncogene (hepatocyte grow	2.6
	412530	AA766268	Hs.266273	abhydrolase	hypothetical protein FLJ13346	2.6
	431890	X17033	Hs.271986	vwa,FG-GAP,integrin_A	integrin, alpha 2 (CD49B, alpha 2 s	2.6
30	404184	NA		SS,TM,7tm_1	NM_030903*:Homo sapiens olfactory r	2.6
	428450	NM_014791	Hs.184339	pkinase,KA1	KIAA0175 gene product	2.6
	425698	NM_016112	Hs.159241	TM,pkinase,ion_trans	polycystic kidney disease 2-like 1	2.6
	453331	AI240665	Hs.8895	TM,disintegrin,Pep_M12B_propep	ESTs	2.6
	444826	AI674482	Hs.148441	pkinase,SAM	ESTs	2.6
35	414987	AA524394	Hs.294022	connexinhormone_rec,zf-C4,conn	hypothetical protein FLJ14950	2.6
	438746	AI885815	Hs.184727	Ribosomal_S2,transferrin	ESTs	2.5
	429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
	407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170	2.5
	453379	AA035261	Hs.61753	PAN,kringle,trypsin	ESTs	2.5
40	421733	AL119671	Hs.1420	SS,TM,lg,pkinase	fibroblast growth factor receptor 3	2.5
	452220	BE158006	Hs.212296	TM,integrin_A,FG-GAP	ESTs	2.5
	417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	2.5
	400301	X03635	Hs.1657	TM,Oest_recep,zf-C4,hormone_re	estrogen receptor 1	2.5
	408938	AA059013	Hs.22607	Y_phosphatase	ESTs	2.4
45	411643	AI924519	Hs.192570	DEAD,helicase_C	hypothetical protein FLJ22028	2.4
	446638	AL133063	Hs.15783	TM,pkinase	Homo sapiens mRNA; cDNA DKFZp434P11	2.4
	430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
	417655	AA780791	Hs.14014	Peptidase_M41,AAApkinase	hypothetical protein FLJ14813	2.4
	448005	AW207437	Hs.170378	pkinase	ESTs	2.4
50	423973	AF038461	Hs.136574	TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase, 12R t	2.4
	437897	AA770561	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969	2.4
	425397	J04088	Hs.156346	DNA_topoisomII,DNA_topoisolVIGF	topoisomerase (DNA) II alpha (170kD	2.4
	432777	AA564991	Hs.269477	alpha-amylase	ESTs	2.4
	421247	BE391727	Hs.102910	TM,iRNA-synt_1,SPRYF5_F8_type_	general transcription factor IIH, p	2.4
55	425465	L18964	Hs.1904	TM,pkinase,DAG_PE-bind,OPR,pki	protein kinase C, iota	2.4
	419281	H96452	Hs.42189	TM,E1-E2_ATPase,HMA,Hydrolase	ESTs	2.4
	434205	AF119861	Hs.283032	SH3,effhand,C2,PH,RhoGEF,AAA,PG	hypothetical protein PRO2015	2.4
	453406	AI192987	Hs.61784	pkinase,Furin-like,Recep_L_dom	hypothetical protein FLJ14451	2.3
	435542	AA687376	Hs.269533	pkinase,RhoGEF,lg,PH,SH3	ESTs	2.3
60	443151	AI827193	Hs.132714	DNA_mis_repair,HATPase_cAcylph	ESTs	2.3
	431630	NM_002204	Hs.265829	SS,TM,FG-GAP,integrin_A	integrin, alpha 3 (antigen CD49C, a	2.3
	422310	AA316622	Hs.98370	SS,TM,fn3,jg,pkinase,Ribosomal	cytochrome P450, subfamily IIS, pol	2.3
	441954	AI744935	Hs.8047	TM,Band_7,AAA,cdo48_N	Fanconi anemia, complementation gro	2.3
	414907	X90725	Hs.77597	SS,TM,pkinase,POLO_box	polo (Drosophila)-like kinase	2.3
65	439810	AL109710	Hs.85568	aconitase,Aconitase_C	EST	2.3
	429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membra	2.3
	432284	AA532807	Hs.105822	TM,pkinase	ESTs	2.3
	452947	AW130413		alpha-amylase	gb:xf50f04.x1 NCI_CGAP_Gas4 Homo sa	2.3
	423229	AC003965	Hs.125532	SS,trypsin	protease, serine, 26	2.3
70	453941	U39817	Hs.36820	DEAD,HRDC,helicase_C	Bloom syndrome	2.3
	439963	AW247529	Hs.6793	TM,p450Ets	platelet-activating factor acetylhy	2.3
	424439	AA579635	Hs.1770	DNA_ligase	ligase I, DNA, ATP-dependent	2.2
	452755	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypo	2.2
	429922	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0	2.2
75	434149	Z43829	Hs.19574	TM,EPH_lbd,fn3,pkinase,SAM	hypothetical protein MGC5469	2.2
	417576	AA339449	Hs.82285	TM,AlRS,formyl_transf,GARS	phosphoribosylglycinamide formyltra	2.2
	409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor, SREC	2.2
	416763	AI908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators	2.2
	414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficien	2.2
80	443171	BE281128	Hs.9030	SS,TM,7tm_1,rm	TONDU	2.2
	430637	BE160081	Hs.256290	S_100Peptidase_M16	S100 calcium-binding protein A11 (c	2.2
	452367	U71207	Hs.29279	SS,Hydrolase	eyes absent (Drosophila) homolog 2	2.2
	408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
	417900	BE250127	Hs.82906	TM,WD40,pro_isomerase	CDC20 (cell division cycle 20, S. c	2.1

5	424490	AJ278016	Hs.55565	TM, pkinase, ank	ankyrin repeat domain 3	2.1
	412834	R77123	Hs.79881	TM, 7Im_1	Homo sapiens cDNA: FLJ23006 fis, cl	2.1
	410855	X97795	Hs.66718	SNF2_N, helicase_C	RAD54 (S.cerevisiae)-like	2.1
	418804	AA809632		HATPase_c, HSP90, PHD, zf-C2H2	gb:nz17n04.s1 NCL_CGAP_GCB1 Homo sa	2.1
	447674	BE270640	Hs.19192	TM, pkinaseras, arf	cyclin-dependent kinase 2	2.1
	450663	H43540	Hs.25292	SS, TM, RNase_HIII	ribonuclease HI, large subunit	2.1
	408805	H69912	Hs.48269	TM, pkinase	vaccinia related kinase 1	2.1
	429415	NM_002593	Hs.202097	SS, CUB, NTR, MAM, TIL, TILa, vwd, EP	procollagen C-endopeptidase enhance	2.1
10	447827	U73727	Hs.19718	SS, TM, Y_phosphatase, fn3, ig, MAM	protein tyrosine phosphatase, recep	2.1
	428273	AI867228	Hs.303211	Glycos_transf_2	ESTs	2.1
	404274			SS, TM, pkinase, fn3	NM_002944*:Homo sapiens v-ros avian	2.1
	403133			pkinae, K_tetra, Band_41, RhoGEF	Target Exon	2.1
	440249	AI246590	Hs.337275	VHL, TatD_DNase	ESTs	2.1
15	438580	AA811262	Hs.299202	TM, pkinasesugar_tr	ESTs	2.1
	406400			SS, TM, trypsin	NM_007196:Homo sapiens kalikrein 8	2.1
	427375	AL035460	Hs.177536	SS, Zn_carbOpept, hormone5ReproI	metallocarboxypeptidase CPX-1	2.1
	423453	AW450737	Hs.128791	SS, Granin, CDP-OH_P_transf	CGI-09 protein	2.1
	433716	AA608808	Hs.225118	Acylphosphatase	ESTs	2.1
20	420757	X78592	Hs.99915	TM, hormone_rec, Androgen_recep,	androgen receptor (dihydrotestoster	2.1
	425018	BE245277	Hs.154196	DNase_I, K_tetra	E4F transcription factor 1	2.1
	421685	AF189723	Hs.106778	TM, E1-E2_ATPase, HydrolaseE1-E2	ATPase, Ca transporting, type 2C, m	2.1
	457288	AA521458	Hs.192738	pro_isomerase	ESTs	2.1
	407305	AA715284		TM, pkinase, Sema, Plexin_repeat,	gb:nv35f03.r1 NCL_CGAP_Br5 Homo sap	2.1
25	456327	H68741	Hs.38774	TM, Glyco_transf_8	ESTs	2.0
	422429	AA310527		pkinae, RGS, PHpkinase, PH, RGS	gb:EST181333 Jurkat T-cells V Homo	2.0
	402974	NM_001501	Hs.129715	GnRHhormone5, hormone4	gonadotropin-releasing hormone 2	2.0
	458016	AW188099	Hs.131813	pkinae	ESTs	2.0
	452194	AI694413	Hs.332649	TM, 7Im_3, ANF_receptor, sushi	olfactory receptor, family 2, subfa	2.0
30	428028	U52112	Hs.182018	TM, pkinase, MBD	interleukin-1 receptor-associated k	2.0
	427747	AW411425	Hs.180655	pkinae, lipoxigenase, PLATilipox	serine/threonine kinase 12	2.0
	452841	T17431	Hs.65412	TM, DEAD, helicase_C	DEAD/H (Asp-Glu-Ala-Asp/His) box po	2.0
	449539	W80363	Hs.58446	pkinae, Furin-like, Recep_L_dom	ESTs	2.0
	418140	BE613836	Hs.83551	TM, E1-E2_ATPase	microfibrillar-associated protein 2	2.0
35	430076	AA465115	Hs.318773	AAA, BAH	KIAA1836 protein	2.0
	425749	AW328587	Hs.159448	Ribosomal_L7Ae, LRR, LRRCT, pkina	surfeit 2	2.0
	425855	AF135025	Hs.159679	SS, trypsin	kalikrein 12	2.0
	400135	L40027	Hs.118890	pkinae	glycogen synthase kinase 3 alpha	2.0

40 TABLE 14B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

45	Pkey	CAT number	Accessions
			*
50	412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492
	418804	179138_1	AA809632 AI917245 AI701732 AA228406
	420930	197736_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
	422429	216469_1	AA310527 AW962295 Z44865 H05641
	422689	219896_1	AW856665 AA315006 AW954733
	435399	405576_1	AA679463 AW813779 AW813709
55	438390	45662_1	AI422017 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AI423279 AI423645 AI424090 AI359637 AL044732 D17003
	438993	467651_1	AA828995 AA834879 AI926361
	452947	939810_1	AW130413 AI932362
	455092	1252971_1	BE152428 AW855572 AW855607
	457405	333127_1	AA504860 AA504911

60 TABLE 14C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NT_position: Indicates nucleotide positions of predicted exons.

70	Pkey	Ref	Strand	NT_position
	400666	8118496	Plus	17982-18115, 20297-20456
	401230	9929527	Minus	33835-34006, 34539-34592, 36461-36745, 48925-49098, 52604-52758
	401486	7341763	Plus	32585-32756, 36281-36540, 40791-40933, 44018-44179
75	402337	6957691	Plus	4116-4286, 16811-16973, 17107-17256, 19715-20040, 22029-22205
	402481	9797406	Plus	87891-88991
	403133	7331427	Plus	38314-38634
	403471	9930659	Minus	85867-85983
	403763	7229888	Minus	43575-43887
80	404184	4581418	Minus	12652-13548
	404274	9885189	Plus	104127-104318
	406400	9256298	Plus	1553-1712, 1878-2140, 4252-4385, 5922-6077

TABLE 15A: 752 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

Table 15A lists about 752 genes up-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 12A, except that the ratio was greater than or equal to 7.0, the denominator was the median value for three non-malignant cervical specimens, and the 96th percentile value amongst cervical cancers was greater than or equal 80 units.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of cervical cancer to normal cervix

Pkey	ExAccn	UnigenelD	Unigene Title	R1
414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	58.3
411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HEMBA1004341	36.2
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-Cys), mem	35.6
421508	NM_004833	Hs.105115	absent in melanoma 2	33.6
443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit, beta type, 1	32.0
454390	AB020713	Hs.56966	KIAA0906 protein	30.5
416065	BE267931	Hs.78996	proliferating cell nuclear antigen	30.4
433226	AW503733	Hs.9414	KIAA1488 protein	30.0
413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein,	29.4
411669	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	28.9
414132	AI801235	Hs.48480	ESTs	28.3
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	28.1
448569	BE382657	Hs.21486	signal transducer and activator of transcription 1, 9	27.4
432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	27.2
418963	BE304571	Hs.89529	aldo-keto reductase family 1, member A1 (aldehyde red	26.9
439963	AW247529	Hs.6793	platelet-activating factor acetylhydrolase, isoform I	26.5
449722	BE280074	Hs.23960	cyclin B1	26.2
414812	X72755	Hs.77367	monokine induced by gamma interferon	25.3
408405	AK001332	Hs.44672	hypothetical protein FLJ10470	25.1
432917	NM_014125	Hs.279812	PRO0327 protein	24.6
412530	AA766268	Hs.266273	hypothetical protein FLJ13346	23.6
457465	AW301344	Hs.122908	DNA replication factor	23.1
408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone COL06049	22.9
429083	Y09397	Hs.227817	BCL2-related protein A1	22.9
401405			Target Exon	22.8
426272	AW450671	Hs.189284	ESTs	22.7
424878	H57111	Hs.221132	ESTs	22.6
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakbinesin 6)	22.5
444371	BE540274	Hs.239	forkhead box M1	22.2
418030	BE207573	Hs.83321	neuromedin B	22.0
452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolog)-	21.6
400196			Eos Control	21.3
416795	AI497778	Hs.20509	HBV pX associated protein-8	21.2
424865	AF011333	Hs.153563	lymphocyte antigen 75	21.0
438011	BE466173	Hs.145696	splicing factor (CC1.3)	20.7
428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, progelatin	20.3
436923	AW293704	Hs.122658	ESTs	20.2
415791	H09366	Hs.78853	uracil-DNA glycosylase	20.0
448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moiety X)-type m	19.6
435647	AI653240	Hs.49823	ESTs	19.6
431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene trap PA	19.5
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	19.5
428433	AA521410	Hs.41371	ESTs	19.4
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK2-associated	19.3
417308	H60720	Hs.81892	KIAA0101 gene product	19.2
429574	BE268321	Hs.208912	hypothetical protein MGC861	19.2
407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	19.0
408901	AK001330	Hs.48855	hypothetical protein FLJ10468	19.0
438899	AF085833	Hs.135624	ESTs	19.0
456362	AW973003	Hs.179909	hypothetical protein FLJ22995	18.9
438598	AI805943	Hs.326067	hypothetical protein MGC5178	18.8
408908	BE296227	Hs.250822	serine/threonine kinase 15	18.8
427488	M91401	Hs.178658	RAD23 (S. cerevisiae) homolog B	18.6
400195			NM_007057*:Homo sapiens ZW10 interactor (ZWINT), tran	18.5
414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin)	18.4
410324	AW292539	Hs.30177	ESTs	18.3
453028	AB006532	Hs.31442	RecQ protein-like 4	18.1
410608	AI538438	Hs.159087	ESTs	18.1
432503	AA551196	Hs.188952	ESTs	17.9
430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	17.7
430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo sapiens cDNA	17.6
449962	AA004879	Hs.187820	ESTs	17.3
425408	AB002375	Hs.156814	KIAA0377 gene product	17.1
440774	AI420611	Hs.127832	ESTs	16.8
408201	AK000568	Hs.43654	hypothetical protein FLJ20561	16.7
436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothetical protein [16.7
426897	AW976570	Hs.97387	ESTs	16.5
447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical protein F	16.5

	433159	AB035898	Hs.150587	kinesin-like protein 2	16.3
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	16.3
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional activation,	16.3
	453941	U39817	Hs.36820	Bloom syndrome	16.1
5	438461	AW075485	Hs.286049	phosphoserine aminotransferase	16.0
	407999	AI126271	Hs.49433	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTE	16.0
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12951 fis, clone NT2RP2006454	15.7
	407720	AB037776	Hs.38002	KIAA1355 protein	15.6
10	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1 protein - mou	15.6
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage elastase)	15.5
	419777	D60134	Hs.270975	ESTs	15.3
	453886	R66282	Hs.20247	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	15.2
	443715	AI583187	Hs.9700	cyclin E1	15.2
	407786	AA687538	Hs.38972	tetraspan 1	15.2
15	431910	AK000142	Hs.101774	hypothetical protein FLJ23045	15.2
	417634	W27202	Hs.82327	glutathione synthetase	15.1
	432692	AW974944	Hs.200577	ESTs	15.1
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cys-Cys), membe	15.1
20	427999	AI435128	Hs.181369	ubiquitin fusion degradation 1-like	15.0
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	15.0
	431629	AI077025	Hs.265827	interferon, alpha-inducible protein (clone IFI-6-16)	14.9
	435354	AA678267	Hs.117115	ESTs	14.8
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	14.8
25	416109	AI420311	Hs.126550	suppressor of K transport defect 1	14.8
	417933	X02308	Hs.82962	thymidylate synthetase	14.7
	438970	AA837782	Hs.321058	ESTs	14.7
	409680	W31092	Hs.55847	mitochondrial ribosomal protein 64	14.7
	432401	NM_013330	Hs.274479	NME7	14.6
30	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.5
	420734	AW972872	Hs.293736	ESTs	14.5
	434256	AI378817	Hs.191847	ESTs	14.5
	418269	AA806113	Hs.189025	ESTs	14.3
	427372	AW960673	Hs.177530	ATP synthase, H transporting, mitochondrial F1 comple	14.3
35	427081	AI474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN !!!! ALU CLASS	14.2
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	14.2
	429966	BE081342	Hs.283037	HSPC039 protein	14.2
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-inducible, 67	14.1
	443957	AA521049	Hs.34487	hypothetical protein FLJ23412	14.0
40	418803	U50079	Hs.88556	histone deacetylase 1	14.0
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	14.0
	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	13.9
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin binding pr	13.9
	433255	AI274270	Hs.96840	KIAA1527 protein	13.9
45	431838	AI097229	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	13.8
	449801	AA477355	Hs.288300	hypothetical protein FLJ23231	13.8
	447078	AW885727	Hs.301570	ESTs	13.8
	441240	AA923749	Hs.132442	ESTs	13.8
	439398	AA284267	Hs.221504	ESTs	13.6
50	404630			Target Exon	13.6
	408321	AW405882	Hs.44205	cortistatin	13.6
	426427	M86699	Hs.169840	TTK protein kinase	13.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	13.5
	403055			C2002219:gi112737280 ref XP_006682.2 keratin 18 [Ho	13.5
55	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	13.5
	425261	BE385099	Hs.334727	hypothetical protein MGC3017	13.3
	439926	AW014875	Hs.137007	ESTs	13.3
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated kinesin	13.2
	451141	AW772713	Hs.247186	ESTs	13.2
60	447390	X95384	Hs.18426	translational inhibitor protein p14.5	13.2
	419828	T81422	Hs.14922	ESTs	13.2
	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109260A B cell growth factor	13.2
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	13.1
	407595	BE350012	Hs.248365	ESTs	13.1
65	432721	AL121478	Hs.180532	glucose phosphate isomerase	13.1
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associ	13.0
	413314	BE081585		gb:QV2-BT0635-210400-156-b07 BT0635 Homo sapiens cDNA	13.0
	430929	AA489166	Hs.156933	ESTs	12.9
	449571	AW016812	Hs.200266	ESTs	12.9
70	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the prostate	12.8
	417105	X60992	Hs.81226	CD6 antigen	12.6
	434263	N34895	Hs.44648	ESTs	12.6
	412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferritin associate	12.6
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	12.5
75	437056	AI147061		gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	12.5
	438768	AI307416	Hs.184675	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY	12.5
	444478	W07318	Hs.240	M-phase phosphoprotein 1	12.5
	450738	AA010907	Hs.184456	hypothetical protein	12.4
	418205	L21715	Hs.83760	troponin I, skeletal, fast	12.4
80	442994	AI026718	Hs.16954	ESTs	12.4
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone HEP20977	12.4
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	12.4
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3)-glycoprotein beta-1,4-N-acetylgl	12.3
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (survivin)	12.3

	410245	C17908	Hs.194125	ESTs	12.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	12.3
	418941	AA452970	Hs.155218	E1B-55kDa-associated protein 5	12.3
5	432325	AW973209	Hs.261782	ESTs	12.3
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	12.3
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dystonia)	12.2
	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone LNG00818	12.2
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501	12.2
10	427295	AW291212	Hs.293943	hypothetical protein MGC11266	12.2
	415443	T07353	Hs.7948	ESTs	12.1
	429770	AI766047	Hs.99736	ESTs	12.1
	428955	AA579297	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	12.1
	435244	N77221	Hs.187824	ESTs	12.1
15	432810	AA863400	Hs.23054	ESTs	12.1
	434423	NM_006769	Hs.3844	LIM domain only 4	12.0
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit, beta type, 9	12.0
	459273	AW608906	Hs.334767	hypothetical protein MGC5629	12.0
	419945	AW290975	Hs.118923	ESTs	11.9
20	442159	AW163390	Hs.278554	heterochromatin-like protein 1	11.9
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MAMMA1002566	11.9
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	11.8
	401557			Target Exon	11.8
	434408	AI031771	Hs.132586	ESTs	11.8
25	406747	AI925153	Hs.217493	annexin A2	11.8
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein (EGP) (KSA)	11.8
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor 1	11.8
	445655	AA873830	Hs.167746	B cell linker protein	11.7
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	11.7
30	427527	AI809057	Hs.302063	immunoglobulin heavy constant mu	11.7
	432287	AK001057	Hs.274268	Homo sapiens cDNA FLJ10195 fis, clone HEMBA1004771	11.6
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!! ALU CLASS C W	11.6
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 kD)	11.6
	447082	T85314	Hs.42644	thioredoxin-like	11.5
35	409931	BE293233	Hs.129771	ESTs	11.4
	426172	AA371307	Hs.125056	ESTs	11.4
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(hnRNP methyltr	11.4
	456880	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcriptional enha	11.4
	433849	BE465884	Hs.280728	ESTs	11.4
40	430519	AF129534	Hs.49210	F-box only protein 4	11.4
	434442	AA737415	Hs.152826	ESTs	11.3
	457205	AI905780	Hs.198272	Target CAT	11.3
	422713	AA902780	Hs.119325	Huntingtin-interacting protein A	11.3
	443491	AW499665	Hs.9456	SWI/SNF related, matrix associated, actin dependent r	11.3
45	424339	BE257148	Hs.145416	endoglycan	11.3
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	11.3
	450208	AI686945	Hs.272062	ESTs	11.2
	446849	AU076617	Hs.16251	cleavage and polyadenylation specific factor 3, 73kD	11.2
	424965	AW956282	Hs.144609	Homo sapiens, Similar to RIKEN cDNA 5730578N08 gene,	11.2
50	442737	AB002319	Hs.8663	KIAA0321 protein	11.2
	409113	AA074897		gb:zm85a05.r1 Stratagene ovarian cancer (937219) Homo	11.2
	415782	AA169345	Hs.123177	ESTs	11.1
	417958	AA767382	Hs.193417	ESTs	11.1
	402539	AW502761	Hs.30909	KIAA0430 gene product	11.0
55	413677	AW503116	Hs.301819	zinc finger protein 146	11.0
	414706	AW340125	Hs.76989	KIAA0097 gene product	11.0
	421632	AA825426	Hs.238832	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	11.0
	438995	AI277986	Hs.164875	ESTs	11.0
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	10.9
60	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 3'	10.9
	451655	H85689	Hs.225560	ESTs	10.9
	429237	AA448417	Hs.104990	ESTs	10.9
	427719	AI393122	Hs.134726	ESTs	10.9
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	10.8
65	410093	AW589558	Hs.296120	ESTs, Weakly similar to KIAA0970 protein [H.sapiens]	10.8
	400080			Eos Control	10.8
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643	10.8
	401539			NM_002675:Homo sapiens promyelocytic leukemia (PML),	10.8
	446099	T93096	Hs.17126	hypothetical protein MGC15912	10.7
70	451066	AI758660	Hs.206132	ESTs	10.7
	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypothetical protein [10.7
	451730	AF095687	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	10.7
	428054	AI948688	Hs.266619	ESTs	10.6
	441636	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (from clone DKFZ	10.6
75	438654	AI005270	Hs.123543	ESTs	10.6
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kinase	10.6
	449035	AI815728	Hs.19980	DNA polymerase epsilon p12 subunit	10.6
	436137	AI056769	Hs.133512	ESTs	10.6
	417863	AB000450	Hs.82771	vaccinia related kinase 2	10.6
80	439975	AW328081	Hs.6817	inosine triphosphatase (nucleoside triphosphate pyrop	10.6
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen inducible gene	10.6
	454355	AW812535		gb:CM4-ST0182-051099-021-c09 ST0182 Homo sapiens cDNA	10.6
	435542	AA687376	Hs.269533	ESTs	10.6
	431386	AA504359	Hs.110067	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	10.5

	416564	AW795793	Hs.179827	Homo sapiens cDNA FLJ12257 fis, clone MAMMA1001501, h	10.5
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT2RM4002390	10.5
	408329	AF155510	Hs.44227	heparanase	10.5
5	410146	AW592655		gb:hf45f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA c	10.5
	427600	AW630918	Hs.179774	proteasome (prosome, macropain) activator subunit 2 (10.4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	10.4
	407241	M34516		gb:Human omega light chain protein 14.1 (lg lambda ch	10.4
	435061	AI651474	Hs.163944	ESTs	10.4
10	409653	AW451693	Hs.220826	ESTs	10.4
	428294	AA425488		gb:zw46d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapie	10.4
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sensitivity prote	10.4
	408809	AW274673	Hs.279706	ESTs, Weakly similar to A47582 B-cell growth factor p	10.4
	410174	AA306007	Hs.59461	DKFZP434C245 protein	10.4
	424792	U92538	Hs.153138	origin recognition complex, subunit 5 (yeast homolog)	10.3
15	422406	AF025441	Hs.116206	Opa-interacting protein 5	10.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92kD gelati	10.3
	413809	L25851	Hs.851	integrin, alpha E (anligen CD103, human mucosal lymph	10.3
	413507	BE145360	Hs.190064	ESTs, Weakly similar to I38022 hypothetical protein [10.3
	448119	H38587	Hs.82295	dedicator of cyto-kinesis 1	10.2
20	457288	AA521458	Hs.192738	ESTs	10.2
	402025			NM_021624:Homo sapiens histamine H4 receptor (HRH4),	10.2
	440572	AW183778	Hs.249584	ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN	10.2
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside transporters), m	10.2
25	443780	NM_012068	Hs.9754	activating transcription factor 5	10.1
	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapiens cDNA 5' en	10.1
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	10.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	10.1
	430848	AW021726		gb:df27e02.y1 Morton Fetal Cochlea Homo sapiens cDNA	10.1
30	422470	AB017919	Hs.117232	peptidyl arginine deiminase, type V	10.1
	449501	AI652924	Hs.231942	ESTs	10.1
	420731	AL042052	Hs.104432	ESTs	10.1
	404345	AA730407	Hs.159156	protocadherin 11	10.1
	400438	AF185611		Target	10.1
35	438170	AI916685	Hs.194601	ESTs	10.1
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	10.1
	458715	AK000973	Hs.16725	hypothetical protein FLJ10111	10.1
	427766	AA412258	Hs.188817	ESTs	10.1
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	10.0
40	403038			Target Exon	10.0
	434674	AA831879	Hs.136985	ESTs	10.0
	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKHEAD BOX PROTE	10.0
	439428	AA835825	Hs.190490	ESTs	10.0
	403310			Target Exon	9.9
45	408392	U28831	Hs.44566	KIAA1641 protein	9.9
	421849	AW410872	Hs.108894	hypothetical protein FLJ20411	9.9
	433384	AI021992	Hs.124244	ESTs	9.9
	443343	BE409809	Hs.301005	purine-rich element binding protein B	9.9
	437267	AW511443	Hs.258110	ESTs	9.9
50	455978	AI310151	Hs.173524	ESTs	9.9
	435851	AA700946	Hs.191933	ESTs	9.9
	452243	AL355715	Hs.28555	programmed cell death 9	9.9
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	9.9
	414001	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY	9.9
55	436669	AA535975	Hs.174308	Homo sapiens, clone IMAGE:3453347, mRNA, partial cds	9.8
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate), member 2	9.8
	417087	AA193193	Hs.188325	Homo sapiens cDNA FLJ11484 fis, clone HEMBA1001835	9.8
	455855	BE147440		gb:RC1-HT0229-080100-015-f09 HT0229 Homo sapiens cDNA	9.8
	410390	AA876905	Hs.125286	ESTs	9.8
60	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid transpo	9.8
	442660	AW138174	Hs.130651	ESTs	9.8
	436186	BE390717	Hs.5074	similar to S. pombe dim1	9.8
	426773	NM_015556	Hs.172180	KIAA0440 protein	9.8
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	9.7
65	418347	AA216419		gb:nc16e03.s1 NCLCGAP_Pr1 Homo sapiens cDNA clone si	9.7
	448752	AA593867	Hs.300842	KIAA1608 protein	9.7
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone THYRO1001322	9.7
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	9.7
	430752	AA485330	Hs.303278	ESTs	9.7
70	436523	BE612990	Hs.5212	single-strand selective monofunctional uracil DNA gly	9.7
	415740	N80486	Hs.39911	Homo sapiens mRNA for FLJ00089 protein, partial cds	9.7
	411930	F06485	Hs.7740	oxysterol binding protein-like 1	9.7
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H	9.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical protein [9.6
75	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA1011 protein	9.6
	434957	AF283775	Hs.35380	x 001 protein	9.6
	407292	AA876638		gb:nz45e06.s1 NCLCGAP_Pr12 Homo sapiens cDNA clone s	9.6
	459109	AW292447	Hs.140821	ESTs	9.6
	457892	AA744389		gb:ny51e10.s1 NCLCGAP_Pr18 Homo sapiens cDNA clone s	9.6
80	432074	AA525248	Hs.149723	ESTs	9.6
	440463	AI733087	Hs.129994	ESTs	9.6
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	9.6
	445326	AI220072	Hs.165893	ESTs	9.6
	434953	BE049102	Hs.121573	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALI [H.sap	9.6

	420361	N92054	Hs.194718	zinc finger protein 265	9.6
	415853	H06016	Hs.100855	ESTs	9.6
	429599	AA806106	Hs.123664	ESTs	9.6
5	417037	BE083936	Hs.80976	antigen identified by monoclonal antibody Ki-67	9.6
	449317	AW293413	Hs.132906	19A24 protein	9.6
	436588	AA759233	Hs.126506	ESTs	9.6
	409261	BE315042	Hs.19210	hypothetical protein MGC11308	9.5
	401069			C11000374*:gi 10764778 gb AAG22817.1 AF302150.1 (AF30	9.5
10	414065	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PLACE1008851	9.5
	409902	AI337658	Hs.156351	ESTs	9.5
	432258	AW973078	Hs.293039	ESTs	9.5
	438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serine/threonine-s	9.5
	405536			NM_005805:Homo sapiens 26S proteasome-associated pad1	9.5
15	418216	AA662240	Hs.283099	AF15q14 protein	9.5
	434573	AW372340	Hs.159717	ESTs	9.5
	439354	AF086174		gb:Homo sapiens full length insert cDNA clone ZB94A08	9.5
	455410	AW936678		gb:PM2-DT0023-080300-004-a04 DT0023 Homo sapiens cDNA	9.5
	400736			Target Exon	9.5
20	419474	AW968619	Hs.155849	ESTs	9.4
	406464			C17000168:gi 7294725 gb AAF50062.1 (AE003544) CG7547	9.4
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	9.4
	427258	AA400091	Hs.39421	ESTs	9.4
	404680			Target Exon	9.4
25	433840	AA129782	Hs.3576	Homo sapiens mRNA full length insert cDNA clone EURO1	9.4
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	9.4
	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapiens]	9.4
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	9.4
	451846	T65840	Hs.11762	ESTs	9.4
30	419988	W39388	Hs.55336	Homo sapiens, clone MGC:17421, mRNA, complete cds	9.4
	402967			Target Exon	9.3
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.3
	441075	AA915991	Hs.179214	ets variant gene 3	9.3
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (UBE3B) mRNA, p	9.3
	404649			Target Exon	9.3
35	420897	AW139261	Hs.232280	ESTs	9.3
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	9.3
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	9.3
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypothetical protein [9.3
40	420101	AW500529	Hs.95180	KIAA0767 protein	9.3
	428166	AA423849	Hs.79530	M5-14 protein	9.3
	420022	AA256253	Hs.120817	ESTs	9.3
	444020	R92962	Hs.35052	ESTs	9.3
	454765	AW819629		gb:RC5-ST0293-140200-014-H05 ST0293 Homo sapiens cDNA	9.3
45	415021	R54409	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA, partial cds	9.3
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	9.3
	415009	C75253	Hs.220950	ESTs	9.3
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.3
	433348	AA877996	Hs.125376	ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase	9.2
50	417881	AI879117		gb:au54g09.y1 Schneider fetal brain 00004 Homo sapien	9.2
	446354	AW449650	Hs.202249	ESTs	9.2
	427018	AA397538	Hs.136280	Homo sapiens cDNA: FLJ22288 fis, clone HRC04157	9.2
	434410	AA632644		gb:np87b07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone s	9.2
	448072	AI459306	Hs.24908	ESTs	9.2
55	457322	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257	9.2
	424317	AI865032	Hs.26017	ESTs	9.2
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	9.2
	404112	BE302729	Hs.173162	neighbor of COX4	9.2
	433334	AI927208	Hs.231958	matrix metalloproteinase 28	9.1
60	434960	AW374941	Hs.72545	ESTs	9.1
	431658	BE409917	Hs.266935	tRNA selenocysteine associated protein	9.1
	439158	R60323	Hs.193888	ESTs	9.1
	443081	H86858	Hs.132909	ESTs	9.1
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	9.1
65	452706	AW449390	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN SURFEIT LOCUS	9.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	9.1
	430780	N95102	Hs.334858	hypothetical protein MGC12250	9.1
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defective, S. cere	9.1
	418379	AA218940	Hs.137516	fidgetin-like 1	9.1
70	431405	AI470895	Hs.252574	ribosomal protein L10a	9.0
	405454			C12000541:gi 5729384 ref NP_006539.1 IGF-II mRNA-bin	9.0
	438362	AA805678	Hs.12326	ESTs	9.0
	401940			Target Exon	9.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.0
75	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	9.0
	459086	AA021163	Hs.22287	ESTs	9.0
	418653	AI734064	Hs.136212	ESTs	9.0
	444152	AI125694	Hs.149305	hypothetical protein MGC2603	9.0
	437534	AA814471	Hs.291800	ESTs	9.0
	435074	AI760944	Hs.116937	ESTs	9.0
80	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA, complete cds	9.0
	442829	AW263123	Hs.127554	ESTs	9.0
	431675	AA699965	Hs.202375	ESTs	9.0
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	8.9

	420183	W92885	Hs.143408	ESTs	8.9
	421133	AA814971	Hs.257634	ESTs	8.9
	407605	W03512	Hs.6479	hypothetical protein MGC13272	8.9
5	441370	AI242433	Hs.270085	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	8.9
	437966	AW891130	Hs.38173	ESTs	8.9
	426360	AW290981	Hs.211296	ESTs, Weakly similar to 2109260A B cell growth factor	8.8
	448111	AA053486	Hs.20315	interferon-induced protein with tetralicopeptide rep	8.8
	408021	AW137133	Hs.245867	ESTs	8.8
10	429228	AI553633	Hs.337139	ESTs	8.8
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1) mRNA, partial	8.8
	431184	AW970116	Hs.310616	ESTs	8.8
	425219	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	8.8
	439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDNA clone EUROI	8.8
	432573	AA553612	Hs.324696	KIAA1594 protein	8.8
15	450881	W80462	Hs.270521	ESTs, Highly similar to ALU2_HUMAN ALU SUBFAMILY SB S	8.8
	437835	AI146771	Hs.158008	ESTs	8.8
	453204	R10799	Hs.191990	ESTs	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
20	408805	H69912	Hs.48269	vaccinia related kinase 1	8.7
	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuolar proton pu	8.7
	422583	AA410506	Hs.27973	KIAA0874 protein	8.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	8.7
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapiens]	8.7
25	454132	AW131759	Hs.248286	ESTs	8.7
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-inducing)	8.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-like	8.7
	441525	AW241867	Hs.127728	ESTs	8.7
	459539	AI279186		gb:qm24a04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone 3'	8.7
30	443148	AI034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX S	8.7
	424255	AI192657	Hs.143897	dysferlin, limb girdle muscular dystrophy 2B (autosom	8.7
	459435	AA320038		gb:EST22383 Adipose tissue, white II Homo sapiens cDN	8.7
	443117	AI248826	Hs.42029	ESTs	8.6
35	457434	AW628192	Hs.18851	hypothetical protein FLJ10875	8.6
	442505	AW003775	Hs.198248	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, p	8.6
	430901	AA488833	Hs.126711	ESTs, Weakly similar to I38588 reverse transcriptase	8.6
	439223	AW238299	Hs.250618	UL16 binding protein 2	8.6
	417739	Z43995		gb:HSC1QB121 normalized infant brain cDNA Homo sapien	8.6
40	415961	H10983	Hs.155919	ESTs	8.6
	424042	Y10601	Hs.137674	ankyrin-like with transmembrane domains 1	8.6
	4451035	AU076785	Hs.430	plastin 1 (I isoform)	8.6
	447155	AA100605	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPOSIS LOCUS PRO	8.6
	412668	AA456195	Hs.10056	hypothetical protein FLJ14621	8.6
45	458042	AW058464	Hs.6430	protein with polyglutamine repeat; calcium (ca2) home	8.6
	456530	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone DKF	8.6
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	8.6
	445006	W91903	Hs.124814	ESTs	8.6
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast homolo	8.5
	455161	BE145900		gb:MRO-HT0208-221299-204-b12 HT0208 Homo sapiens cDNA	8.5
50	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cerevisiae)	8.5
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	8.5
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interacting protein	8.5
	415018	U49395	Hs.77807	purinergic receptor P2X, ligand-gated ion channel, 5	8.5
	404534			C11001758* gij 12621132 ref NP_075243.1 MEGF1 [Rattus	8.5
55	438451	AI081972	Hs.220261	ESTs	8.5
	435176	AA744875	Hs.189413	ESTs	8.5
	443245	AI040955	Hs.151973	hypothetical protein FLJ23511	8.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	8.5
	457478	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), catalytic subuni	8.5
60	403839			Target Exon	8.5
	434932	BE613162	Hs.284135	hypothetical protein MGC3036	8.5
	420991	AW504814	Hs.121004	Homo sapiens mRNA for FLJ00111 protein, partial cds	8.4
	457854	BE547674	Hs.204169	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	8.4
	455994	BE179190		gb:RC0-HT0613-210300-032-f07 HT0613 Homo sapiens cDNA	8.4
	402796			Target Exon	8.4
65	423426	AW389579	Hs.128434	Homo sapiens ELISC-1 mRNA, partial cds	8.4
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (from clone DKF	8.4
	404110			NM_020245*:Homo sapiens tubby super-family protein (T	8.4
	424441	X14850	Hs.147097	H2A histone family, member X	8.4
70	433155	AL037035	Hs.100426	Homo sapiens cervical cancer metastasis-suppressor 1 (B	8.4
	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	8.4
	406867	AA157857	Hs.182265	keratin 19	8.4
	418278	AI088489	Hs.83937	hypothetical protein	8.4
	458696	AW375333	Hs.199890	ESTs	8.4
75	456248	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	8.4
	403152	AA576664	Hs.37078	v-crk avian sarcoma virus CT10 oncogene homolog-like	8.4
	407649	BE066724	Hs.37427	erythrocyte membrane protein band 4.1 (elliptocytosis	8.4
	448387	AI874402	Hs.170810	ESTs	8.4
	433671	AW138797	Hs.132906	19A24 protein	8.4
80	425891	AI041717	Hs.132141	ESTs	8.4
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 protein [H.sapie	8.4
	439079	AF085937	Hs.38348	ESTs	8.4
	458115	BE091587		gb:IL2-BT0731-240400-069-H04 BT0731 Homo sapiens cDNA	8.4
	428144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associated	8.4

5	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	8.3
	443056	AI457996	Hs.132578	ESTs	8.3
	410391	H17881	Hs.15043	Homo sapiens clone FLB5227 PRO1367 mRNA, complete cds	8.3
	407989	AW135208	Hs.256092	ESTs	8.3
	410536	N39533		gb:yyv27d04.s1 Soares fetal liver spleen 1NFLS Homo sa	8.3
	452273	AI870685	Hs.231022	ESTs	8.3
	454297	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	8.3
	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, calcium-indepe	8.3
10	401654			NM_007242:Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) b	8.3
	432891	AF161483	Hs.279761	HSPC134 protein	8.3
	419923	AW081455	Hs.120219	ESTs	8.2
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone KAT11914	8.2
	435452	AA831004	Hs.124874	ESTs	8.2
	418683	U90908	Hs.87241	hypothetical protein from clones 23549 and 23762	8.2
15	440065	W03476	Hs.266331	hypothetical protein MGC4595	8.2
	439752	T78968	Hs.14411	ESTs	8.2
	447983	AW612726	Hs.282113	ESTs, Weakly similar to I38022 hypothetical protein [8.2
	441966	AA568689	Hs.16131	hypothetical protein FLJ12876	8.2
20	408182	AA047854		gb:zf49g04.r1 Soares retina N2b4HR Homo sapiens cDNA	8.2
	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	8.2
	436005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 fis, clone OVARC1002143	8.2
	414962	AF273304	Hs.235376	XPMC2 protein	8.2
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), soluble	8.2
25	408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	8.2
	413940	AI633205	Hs.159914	ESTs, Weakly similar to I78885 serine/threonine-speci	8.2
	437277	AA748016	Hs.123370	ESTs	8.2
	431445	AA505135	Hs.44037	ESTs	8.1
	418927	BE349635	Hs.190284	ESTs	8.1
30	452446	AA086123	Hs.297856	ESTs	8.1
	445380	AI222019	Hs.144838	ESTs	8.1
	421174	AW969058	Hs.291974	ESTs, Moderately similar to A46010 X-linked retinopat	8.1
	444374	AA009841	Hs.11039	hypothetical protein MGC2722	8.1
	417247	N58024		gb:yy63c01.s1 Soares fetal liver spleen 1NFLS Homo sa	8.1
35	438335	AI498421	Hs.243168	ESTs	8.1
	445235	AI564022	Hs.138207	ESTs	8.1
	422585	NM_016186	Hs.118620	protein Z-dependent protease inhibitor precursor	8.1
	442522	AI087038	Hs.146592	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	8.1
	430684	AI808979	Hs.293193	ESTs	8.1
40	446442	BE221533	Hs.257858	ESTs	8.1
	441410	AA932689	Hs.233304	ESTs, Weakly similar to I38022 hypothetical protein [8.0
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein product [H.sa	8.0
	449539	W80363	Hs.58446	ESTs	8.0
	406663	U24683	Hs.302063	immunoglobulin heavy constant mu	8.0
45	423767	H18283	Hs.132753	F-box only protein 2	8.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protein 1	8.0
	430977	AA490069	Hs.306676	Homo sapiens cDNA FLJ14302 fis, clone PLACE2000003	8.0
	455677	BE066061	Hs.8867	cysteine-rich, angiogenic inducer, 61	8.0
	436706	AA725808	Hs.194609	ESTs	8.0
50	459407	N92114		gb:za22h11.r1 Soares fetal liver spleen 1NFLS Homo sa	8.0
	444132	AK000452	Hs.10340	hypothetical protein FLJ20445	8.0
	437149	AI686651	Hs.202234	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2	8.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	8.0
	411298	AW835858		gb:PM0-LT0017-031299-001-h07 LT0017 Homo sapiens cDNA	8.0
55	432571	AF151054	Hs.278429	hepatocellular carcinoma-associated antigen 59	8.0
	416295	AI064824	Hs.193385	ESTs	8.0
	427485	AF039652	Hs.178655	ribonuclease H1	8.0
	409857	AW501908		gb:UI-HF-BR0p-ajp-c-12-0-UI.r1 NIH_MGC_52 Homo sapien	7.9
	433854	AA610649	Hs.333239	ESTs	7.9
60	458080	BE142728		gb:MR0-HT0157-021299-004-d08 HT0157 Homo sapiens cDNA	7.9
	423573	AA328504		gb:EST31993 Embryo, 12 week I Homo sapiens cDNA 5' en	7.9
	404495			C8001441*gi 8923061 ref NP_060114.1 hypothetical pr	7.9
	443135	AI376331	Hs.156103	ESTs	7.9
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	7.9
65	413283	R78669	Hs.23756	hypothetical protein similar to swine acylneuraminat	7.9
	443987	AW163123	Hs.10071	seven transmembrane protein TM7SF3	7.9
	434197	AA627223		gb:nq63b04.s1 NCL_CGAP_Ov6 Homo sapiens cDNA clone si	7.9
	436882	AW016722	Hs.194976	SH2 domain-containing phosphatase anchor protein 1	7.9
	434502	AW974915	Hs.116550	ESTs	7.9
70	435507	AI143579	Hs.26510	vacuolar protein sorting 33B (yeast homolog)	7.9
	444896	AI201480	Hs.144856	ESTs	7.9
	419320	H96666	Hs.6137	ESTs	7.9
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	7.9
	425569	AA369597	Hs.301701	Homo sapiens cDNA FLJ12073 fis, clone HEMBB1002387	7.9
75	445209	AW294230	Hs.80988	collagen, type VI, alpha 3	7.9
	449193	AI637997	Hs.195653	ESTs	7.9
	447397	BE247676	Hs.18442	E-1 enzyme	7.9
	455037	BE144549		gb:MR0-HT0167-081199-001-a02 HT0167 Homo sapiens cDNA	7.9
	453367	AW732847	Hs.70573	PKC1-1-related HIT protein	7.8
80	439317	AF086127	Hs.50600	ESTs, Weakly similar to T47156 hypothetical protein D	7.8
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	7.8
	406562			NM_004520*:Homo sapiens kinesin heavy chain member 2	7.8
	435192	AK000739	Hs.4835	eukaryotic translation initiation factor 3, subunit 8	7.8
	413500	BE144914		gb:CM3-HT0183-181099-023-b05 HT0183 Homo sapiens cDNA	7.8

	436216	AA380887	Hs.5085	dolichyl-phosphate mannosyltransferase polypeptide 1,	7.8
	418623	AW194757	Hs.266804	ESTs	7.8
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapiens cDNA	7.8
5	430146	AW815330		gb:QV0-ST0215-060100-083-a09 ST0215 Homo sapiens cDNA	7.8
	441841	AA971819	Hs.176083	ESTs	7.8
	457677	AA628890	Hs.158701	ESTs	7.8
	421090	BE301870	Hs.101813	solute carrier family 9 (sodium/hydrogen exchanger),	7.8
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzy	7.8
10	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo sapiens cDNA	7.8
	406410			C5000010*:gij10440464[dbj]BAB15765.1 (AK024475) FLJ0	7.8
	453579	AI204463	Hs.61857	ESTs	7.8
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogene homolog-lik	7.7
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone COL05135	7.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa protein.	7.7
15	440777	AA994020	Hs.128553	ESTs	7.7
	446424	AW134529	Hs.244647	ESTs	7.7
	448004	AW451477	Hs.257456	ESTs	7.7
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP S	7.7
20	427080	AW068287	Hs.173466	ras-related C3 botulinum toxin substrate 2 (rho famil	7.7
	451693	BE220445	Hs.279635	ESTs	7.7
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	7.7
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	7.7
	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (polypyrimidin	7.7
25	425423	NM_005897	Hs.157180	intracisternal A particle-promoted polypeptide	7.7
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	7.7
	432585	AA705591	Hs.190209	ESTs	7.7
	402682			Target Exon	7.7
	400247			Eos Control	7.7
30	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	7.7
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (from clone DKF	7.7
	405514			ENSP00000241075:TRRAP PROTEIN.	7.7
	412406	AW948172		gb:RC0-MT0013-280300-021-b06 MT0013 Homo sapiens cDNA	7.7
	440226	AA873387	Hs.207330	ESTs	7.7
35	435625	H50654	Hs.113999	ESTs	7.7
	418529	AW005695	Hs.250897	TRK-fused gene	7.6
	407758	D50915	Hs.38365	KIAA0125 gene product	7.6
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	7.6
	449938	AW970612	Hs.172635	Homo sapiens cDNA: FLJ21367 fis, clone COL03051	7.6
40	422893	X98411	Hs.121555	myosin IF	7.6
	451593	AF151879	Hs.26706	CGI-121 protein	7.6
	424148	BE242274	Hs.1741	integrin, beta 7	7.6
	447519	U46258	Hs.339665	ESTs	7.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog 1	7.6
45	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	7.6
	426523	S68616	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger),	7.6
	456926	AB018284	Hs.158688	KIAA0741 gene product	7.6
	416294	D86980	Hs.79170	KIAA0227 protein	7.6
	409206	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo sapiens cDNA	7.6
50	417086	AA194446	Hs.73451	ESTs, Weakly similar to S55024 nebulin, skeletal musc	7.6
	418181	U37012	Hs.83727	cleavage and polyadenylation specific factor 1, 160kD	7.5
	436910	AA926944		gb:om68g01.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone 3'	7.5
	401008			Target Exon	7.5
	413245	BE244334	Hs.75249	ADP-ribosylation factor-like 6 interacting protein	7.5
55	446820	AW295037	Hs.254986	ESTs	7.5
	439279	AI039473	Hs.130636	ESTs	7.5
	426116	AA868729	Hs.144694	ESTs	7.5
	410098	BE326839	Hs.17433	hypothetical protein FLJ20967	7.5
	422326	AI114875	Hs.78592	eukaryotic translation initiation factor 2B, subunit	7.5
60	435513	AW404075	Hs.42785	DC11 protein	7.5
	421629	N80121	Hs.4983	ESTs	7.4
	434663	AA641972	Hs.130058	ESTs	7.4
	452461	N78223	Hs.108106	transcription factor	7.4
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	7.4
65	405417			CX001144*:gij7242973[dbj]BAA92547.1 (AB037730) KIAA1	7.4
	414076	AA467736		gb:nc74e05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone, m	7.4
	435014	BE560898	Hs.10026	mitochondrial ribosomal protein L17	7.4
	449610	AI242042	Hs.14044	ESTs	7.4
	403397			Target Exon	7.4
70	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant; spastin)	7.4
	404914			NM_004046*:Homo sapiens ATP synthase, H+ transporting	7.4
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-activating fact	7.4
	432820	AI554057	Hs.152477	ESTs	7.4
75	418978	T85295	Hs.268606	ESTs	7.4
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonine kinase 21)	7.4
	454639	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo sapiens cDNA	7.4
	434522	AF189259	Hs.283081	gamma-aminobutyric acid (GABA) receptor, theta	7.4
	458236	AW297043	Hs.255604	ESTs, Weakly similar to A47234 homeobox protein H6 [H	7.4
80	441043	AA913422	Hs.192104	ESTs	7.4
	422838	AA524065	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone HSI08202	7.3
	455096	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapiens cDNA	7.3
	442307	AW027690	Hs.90037	ESTs	7.3
	425453	AW374284	Hs.297215	Homo sapiens chromosome 19, cosmid R26894	7.3

	455327	AW896238	Hs.334805	Homo sapiens cDNA FLJ14604 fis, clone NT2RP1000363, m	7.3
	420982	AW576160	Hs.100729	KIAA0692 protein	7.3
	424563	AA446932	Hs.151428	ret finger protein 2	7.3
5	417125	AW181998	Hs.81248	CUG triplet repeat, RNA-binding protein 1	7.3
	453902	BE502341	Hs.3402	ESTs	7.3
	446842	AI343510	Hs.176992	ESTs	7.3
	454128	AL031259	Hs.41639	programmed cell death 2	7.3
	427011	BE302729	Hs.173162	neighbor of COX4	7.3
10	450872	AI742594		gb:wg55h05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	7.3
	451512	AI800236	Hs.207080	ESTs	7.3
	405708	AI282759		gb:ql84a01.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone l	7.3
	432576	AW157424	Hs.165954	ESTs, Weakly similar to I38022 hypothetical protein l	7.3
	459304	AW005809	Hs.281076	ESTs, Weakly similar to CHD4_HUMAN CHROMODOMAIN HELIC	7.3
15	401375			NM_020999*:Homo sapiens neurogenin 3 (NEUROG3), mRNA.	7.3
	413258	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapiens cDNA	7.3
	406016			Target Exon	7.3
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	7.3
	422742	AA316117	Hs.337128	ESTs	7.3
20	440031	BE045970	Hs.244746	ESTs	7.3
	429389	AA454779	Hs.201441	Homo sapiens cDNA FLJ11079 fis, clone PLACE1005111	7.3
	449656	AA002008	Hs.188633	ESTs	7.3
	444310	AI140432	Hs.175936	ESTs	7.3
	459274	AA382590	Hs.170980	KIAA0948 protein	7.3
25	425404	BE048060	Hs.133494	Homo sapiens clone TCCCA00164 mRNA sequence	7.3
	431150	T63857		gb:yc16e01.s1 Stratagene lung (937210) Homo sapiens c	7.3
	443217	NM_001545	Hs.9078	immature colon carcinoma transcript 1	7.2
	413405	AW022253	Hs.215976	ESTs	7.2
	447653	BE327277	Hs.161145	ESTs	7.2
30	414704	NM_014757	Hs.76986	mastermind (Drosophila), homolog of	7.2
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, clade B (o	7.2
	409188	AW363284	Hs.32553	ESTs	7.2
	453493	AL039478	Hs.304447	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	456111	AK000150	Hs.78185	MAX-like bHLHZIP protein	7.2
35	400297	AI127076	Hs.334473	hypothetical protein DKFP564O1278	7.2
	446364	AB006624	Hs.14912	KIAA0286 protein	7.2
	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	7.2
	436943	AA773838	Hs.5353	caspase 10, apoptosis-related cysteine protease	7.2
	446336	AW815036	Hs.151251	ESTs	7.2
40	418469	U34879	Hs.85279	hydroxysteroid (17-beta) dehydrogenase 1	7.2
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	7.2
	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP3002304	7.2
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polypeptide 1	7.2
	416450	AA180467		gb:zp14g08.s1 Stratagene fetal retina 937202 Homo sap	7.2
45	449714	AB033015	Hs.23941	KIAA1189 protein	7.2
	455447	AW947507		gb:RCO-MT0002-140300-011-a12 MT0002 Homo sapiens cDNA	7.2
	437154	AI023133	Hs.10739	ESTs	7.2
	423059	AW378445	Hs.123080	Homo sapiens unknown protein mRNA, partial cds	7.2
	419092	J05581	Hs.89603	mucin 1, transmembrane	7.2
50	426736	AA431615	Hs.130722	ESTs	7.2
	417748	Z43011	Hs.21169	ESTs	7.2
	434748	AI862604	Hs.211884	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	438929	AW195515	Hs.253177	ESTs	7.2
	452061	AI074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	7.1
55	446416	AV658299	Hs.163959	ESTs	7.1
	415023	AA932146	Hs.133494	Homo sapiens clone TCCCA00164 mRNA sequence	7.1
	434766	AA742222	Hs.120634	ESTs	7.1
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell growth factor	7.1
	420252	AW270404	Hs.193161	ESTs	7.1
60	435403	AA779987	Hs.269658	ESTs	7.1
	430151	AW968203		gb:EST380398 MAGE resequences, MAGJ Homo sapiens cDNA	7.1
	427908	AA417272	Hs.24122	ESTs	7.1
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitter transporter	7.1
	400098			Eos Control	7.1
65	412647	AW975090		gb:EST387196 MAGE resequences, MAGN Homo sapiens cDNA	7.1
	437234	AI472213	Hs.247711	hypothetical protein FLJ20557	7.1
	453366	AW958751	Hs.28921	zinc finger protein	7.1
	425803	AI825204	Hs.211408	ESTs	7.1
	447383	N24231		gb:yx22a11.r1 Soares melanocyte 2NbHM Homo sapiens cD	7.1
70	423864	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (gamma)	7.1
	450799	AW407504		gb:UI-HF-BMO-adj-g-12-0-UI.r1 NIH_MGC_38 Homo sapiens	7.1
	409592	BE280951	Hs.55058	EH-domain containing 4	7.1
	453945	NM_005171	Hs.36908	activating transcription factor 1	7.1
	425196	AL037915	Hs.155097	carbonic anhydrase II	7.0
75	439778	AL109729	Hs.99364	putative transmembrane protein	7.0
	417662	R07478	Hs.268845	ESTs	7.0
	438087	AI863770	Hs.190422	ESTs	7.0
	452724	R84810	Hs.30464	cyclin E2	7.0
	448633	AA311426	Hs.21635	tubulin, gamma 1	7.0
80	433154	AA578526	Hs.160994	ESTs	7.0
	440094	AI651558	Hs.270372	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.0
	409253	H91200	Hs.52002	CD5 antigen-like (scavenger receptor cysteine rich fa	7.0
	431270	BE046609		gb:hn41e11.x1 NCL_CGAP_RDF2 Homo sapiens cDNA clone 3	7.0
	407629	AA649242	Hs.62632	ESTs	7.0

5	408296	AL117452	Hs.44155	DKFZP586G1517 protein	7.0
	445439	BE243084	Hs.12719	regulator of nonsense transcripts 1	7.0
	427106	AA398193	Hs.97584	ESTs	7.0
	408623	AW811978	Hs.254037	ESTs	7.0
	426561	AA381437		gb:EST94514 Activated T-cells I Homo sapiens cDNA 5'	7.0
10	408492	AA555217	Hs.183684	eukaryotic translation initiation factor 4 gamma, 2	7.0
	428894	AA437066	Hs.271736	ESTs	7.0
	419102	AA234098	Hs.42424	ESTs, Weakly similar to 2004399A chromosomal protein	7.0
	429067	AA446019	Hs.104967	ESTs	7.0
	422684	BE561617	Hs.119192	H2A histone family, member Z	7.0
15	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase 5	7.0
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H.	7.0
	443599	AI079559	Hs.134125	ESTs	7.0
	400715			ENSP00000237081*KIAA1217 PROTEIN (FRAGMENT).	7.0
	446514	AW449233	Hs.150847	ESTs	7.0
20	413992	W26276	Hs.136075	RNA, U2 small nuclear	7.0
	402442			Target Exon	7.0
	419497	NM_006410	Hs.90753	Tat-interacting protein (30kD)	7.0
	439575	W79259		gb:zd75c06.r1 Soares_fetal_heart_NbHH19W Homo sapiens	7.0
	407027	U63312		gb:Human cosmid LL12NC01-242E1, ETV6 gene, exons 1B a	7.0

Table 15B

25	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
30	Pkey	CAT Number	Accessions	
	408182	104479_1	AA047854 AA057506 AA053841	
	409113	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204	
35			AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070	
			AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209	
			AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053	
40			AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA065051 AA079143 AA071110	
			AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200	
			AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929	
45	409206	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659	
	409857	1156298_1	AW501908 AW502959 AW502540	
	410146	1178974_1	AW592655 R05927 R06916	
50	410536	1207322_1	N39533 AW753094 AW753093	
	411298	1237955_1	AW835858 AW835836 AW835823 AW835834 AW835831 AW835832 AW835843 AW835816 AW835833 AW835815 AW835849 AW835835	
			AW835848 AW835851 AW835852 AW835862 AW835855 AW835825 AW835847 AW835838	
55	412406	1293055_1	AW948172 AW948178 AW948169 AW948176 AW948191 AW948186 AW948184 AW948187 AW948188 AW948189 AW948181	
			AW948177 AW948171 AW948183 AW948173	
	412647	1317604_1	AW975090 N44182	
60	413258	1355998_1	BE075114 BE075283 BE075118	
	413314	1360034_1	BE081585 BE081717 BE081863 BE081794 BE081659	
	413500	1373933_1	BE144914 BE394989	
65	414076	141490_1	AA467736 AA135210 AW968166 AA467804	
	416450	159551_1	AA180467 AA449184 AA464831 AA505048	
	417247	1660859_1	N58024 T58194 T11693 N64222 T05848	
70	417739	1696198_1	Z43995 R12357 R34740	
	417881	170544_1	AI879117 AW161351 Z45755 BE003661 AA206949 AA476541	
	418347	174149_1	AA216419 F03238 AA229517	
75	422429	216469_1	AA310527 AW962295 Z44865 H06641	
	423573	229714_1	AA328504 AA327783 AW962370	
	426561	269158_1	AA381437 AA628833 AW407275	
80	428294	289365_1	AA425488 AA496895 F23221	
	430146	313562_1	AW815330 AW968170 AI732587 AI732725 AA468343 AA467817 AW063961	
	430151	313668_1	AW968203 AI732757 AA470353 AA468025 AA468479 AI734151	
85	430709	322338_1	R34356 AW969880 AA484613	
	430848	324621_1	AW021726 AA487752 AA488085	
	431150	328626_1	T63857 AW971220 AA493469 T63699	
90	431270	330676_1	BE046609 BE046118 AA501504	
	432363	345469_1	AA534489 AW970240 AW970323	
	434197	381655_1	AA627223 AA643443 AA650619 AA643463 AA643453 AA643439 AA643438 AW802964 AW821595 AW821594 AA643431 AA643432	
95			AW827513	
	434407	385744_1	AW815333 AW815409 AA632563	
	434410	385798_1	AA632644 AA635376 AA664188	
100	436910	429182_1	AA926944 AA767974 AA737237	
	437056	432262_1	AI147061 AA743380 AA765223 AW976398 AI803927	
	439354	47146_1	AF086174 W31796 W04694	
105	439575	47400_1	W79259 AF086396 W73927	
	444314	600667_1	AI140497 AW749625 AW749626 AW749644	
	447197	711623_1	R36075 AI366546 R36167	
110	447383	71990_1	N24231 BE617964 N36313	
	450799	847242_1	AW407504 W31274 AI738877	
	450872	849959_1	AI742594 AI761397 R31198 AI819332 R31257	
115	454355	1130264_1	AW812535 AW812536 AW390307	
	454639	1227728_1	AW811633 AW811652 AW811898	
	454765	1233905_1	AW819629 AW854320	

455037	1249783_1	BE144549 AW851677 AW851643 AW851711 AW851719
455096	1253078_1	AW855718 AW855740 AW855748
455161	1256167_1	BE145900 AW859906 BE145895 BE145831 BE145914 BE145820 BE145817 BE145890 BE145908
455410	1288380_1	AW936678 AW936637 AW936682 AW936685 AW936817 AW936811 AW936762 AW936653 AW936815 AW936812 AW936683 AW936822
5		AW936823 AW936821 AW936732 AW936730 AW936781
455447	1292444_1	AW947507 AW947509 AW947791 BE008335
455855	1375834_1	BE147440 BE147708 BE147563 BE147456
455994	1398737_1	BE179190 BE179206 BE179182 BE179185 BE179186 BE179194
457892	432926_1	AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847698
10	458080	BE142728 AA834047 AW937124
458115	47705_29	BE091587 BE091730 BE091577 BE091655 BE091729 BE091640 BE091578 BE091727 BE091803 BE091660 BE091721 BE088255 BE076582
		AW992312 BE008791 BE082385 BE083504 BE083466 AW997967 AW997991 BE166595 AW843686 AW844334 BE079091 AW603391 BE081427
		BE079514 BE184580 BE009962 BE008722 AW579912 AW860551 AW890184 AW795276 AW860410 AW860411 AW610330 AW860564 AW860578
15		AW862519 BE073924 BE086687 BE073857 BE073921 AW274106 BE011060 AW268120 AI335067 AW793748 AW997736 BE080117 AW867987
		AI547161 AW844767 AW939596 AW579444 BE083334 AI547158 AW799863 AA585179 AW992792 AW882215 BE011913 AW997894 AI547159
		AW992772 AW581178 AA092247 AW843916 BE079190 AW878478 BE083648 BE066454 AI469937 AW393594 AW579899 AW939276 BE173265
		AW878631 AW878638 AW992802 BE079913 AA633638 AW369008 BE076590 AW843456 AW992791 BE173247 AW843921 AW843333 AW878334
		BE090235 BE078240 BE066325 AW603276 BE169310 AW817299 BE091641 BE000160 AW898164 AW994624 AW999391 AW862279 AW899438
20		AW750667 AW939685 AW940017 AI200402 BE167391 AW939318 AW799837 AW939953 AW939681 BE078188 AA449059 BE076595 AW279451
		BE076544 AW803372 BE081223 AW939237 BE084239 AI174202 BE077804 BE078028 AA512912 AI124808 AI147524 AI884882 AW939962
		AW939254 BE171687 AW998400 AW998348 AW998353 AW998288 AW998303 AW998302 AW998299 AA502748 BE077882 AW998295 BE090238
25		AW604665 AI423051 BE093093 AW579913 AW606384 BE006143 BE170415 AW998054 BE084608 AW992779 BE088111 AW610555 AW844153
		AW939423 BE085404 AW579905 BE080994 AW648482 AW876865 BE0091581 BE080940 AI811189 AW868008 AW893127 BE080064 BE184254
		AW998350 AW884228 AW992315 AW992364 BE091569 AW750680 BE066386 AA578227 BE091735 AW939830 BE078710 BE087253 BE084182
		AW800859 AW801017 AW581371 BE088300 AW995341 BE090233 AW663786 BE091739 BE080113 AW578162 AW797999 AW992366 AW994673
		BE185170 AW792778 AW663225 BE075590 BE080111 AA682934 BE090227 AI475441 BE085684 BE090223 AW581366 BE010705 AW898740
		BE088170 AW992375 BE077833 BE083557 BE010688 AW998450 AW803434 BE083280 AW892655 AA506666 BE088288 BE005859 BE173856
		BE001319 AA610814 BE011965 BE005855 BE005869 AA973929 BE185729 AW884298 BE185743 BE001342 BE005876 AI002988 AW799056
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		AW603114 BE085757 AI460195 AA491145 AA772914 AA632730 AA508388 BE080196 BE185442 BE093446 AW946433 BE080119 BE001352
		AW839003 BE006145 BE085405 BE008680 BE081428 AW581373 AW607246 BE094328 BE001336 AW868170 BE074119 AW884149 BE091734
		BE008744 AI540867 BE185806 BE080193 BE185858 AA476398 BE081040 BE074724 BE085426 BE074725 AW998297 AW867606 BE185798
		AW898734 BE076369 BE081672 BE088178 AA610264 BE088118 AA284217 AW578085 BE074518 BE001359 BE001328 AW820227 AW868196
35		AW868190 AW904548 BE008526 BE012037 BE079061 BE005870 AW867804 AW878433 BE008751 BE005875 BE008748 BE093440 BE183050
		AA506676 BE001329 BE008803 BE080123 BE008041 AW994688 AW994675 AW994760 AW994691 AW994681 BE080189 BE080112 AW868173
		AI768000 AW883094 AW868179 BE080201 AW665449 BE067473 BE008746 BE184053 BE076437 BE076376 BE076402 AA480395 BE082436
		BE184134 BE185224 BE085428 BE008682 AW868181 AW998358 AW866102 BE083507 BE077974 BE008835 BE093439 BE076108 AI416987
		BE008788 BE069909 BE093441 BE185502 BE183053 AW750669 BE011812 BE008672 BE081684 BE093445 AW868184 BE081839 BE008797
40		AW842067 BE008678 BE008670 BE551820 AW838974 BE081637 BE046696 BE008673 BE010328 BE083250 BE089614 BE082052 BE081424
		BE001678 AW581368 AA503194 AW883721 AW883522 BE085564 AW868717 BE171078 BE078249 BE078194 AA565255 BE083486 AW842081
		AW842080 AW868204 BE008717 AA484369 AI831719 AW997365 BE0799327 AA503956 BE091999 AW793852 BE080251 BE078086 BE092515
		BE170364 AW866193 AW067958 BE008042 BE008761 BE081681 BE081671 AW867400 BE082003 BE082253 BE081439 BE081486 BE081692
45		AW606020 AA501778 AW996417 BE045756 BE088394 AA491068 AW893099 AW578695 BE150440 BE0086150 AW84684 AW992796 BE086891
		AW866792 AW753605 BE082045 BE081106 BE008373 BE075399 AW996628 AW578707 BE084309 AW753604 BE185916 AW842220 BE185222
		BE006152 BE008795 AW578706 BE080256 BE183984 AI934532 AA449648 AW578699 BE150514 AW883580 AA493568 BE085748 AW753601
		BE150562 AW882677 BE091797 AW899123 BE081679 BE080121 AW606787 AW603410 BE001317 AW905799 BE150513 BE092206 AW996343
		BE086922 BE008806 AW844759 AW606009 BE150487 AW750728 BE150491 BE150515 AW606010 BE150508 BE008718 AW578702 BE150509
		AA436751 AW883918 BE183883 AW753607 BE008669 BE150446 AA533458 BE079219 AW838884 AW063806 AW063837 AW878479 AW878815
50		BE008802 AW992789 BE007925 AW802204 BE011825 BE092130 BE184059 BE079087 BE150558 BE185497 BE078808 AW883761 AW842295
		BE161523 AA484796 AA480390 AW994667 BE073205 AW607316 BE083201 AW802265 AW578700 BE078715 AW860403 AW897456 AW996558
		AW896062 AW860413 AA425412 BE008364 BE150438 AW602606 AI436236 AA574285 AI823745 AA501773 AI002987 AW832749 BE185491
		AW996489 BE001442 AW946425 BE001586 AI524864 BE085556 AW867549 AW604038 BE079832 AI752160 AW999398 AW883904 AW882376
		AW647098 BE080116 AW883984 AW883995 AA424095 BE074091 AW996348 AW860625 AW860633 AW946513 BE083485 AW860412 AW602207
55		BE075407 AW838972 AW607023 AW602201 AW799772 AW862452 AW862451 BE505041 BE161537 AW602206 AW860404 AW860555 BE007843
		AW860632 AW862457 AW998019 AW860405 BE092062 AW603921 BE183386 AW868194 BE075664 BE078184 AI541202 AI204949 BE092451
		AW603111 AA484587 AA484402 AW998675 AW896064 BE069923 AW867965 BE069919 BE092069 AA807842 AW605500 AW605501 BE085409
		AA506738 BE080080 AW749523 AA493134 AW370137 AA491844 AA504425 AW605473 BE092456 BE010682 AW602608 BE079093 AA484911
		BE010942 AI205087 AW794933 BE081848 BE011792 AW799897 BE174618 AW838848 AW821741 AW842724 BE008764 BE183962 AA501765
60		BE092513 BE183342 AW799806 AA442935 BE092268 AA580022 AW843221 BE093308 BE092275 BE087111 BE183392 AW842678 BE185597
		BE183895 BE185278 BE082343 AW946219 BE079199 BE092272 AA586687 AW946109 AW946175 AW946184 BE008365 BE078172 BE085673
		BE076240 BE083194 BE010604 BE079196 AW878636 AW799803 BE001348 BE077883 BE081835 AW992309 BE081012 BE078106 AW881899
		BE008407 BE008410 AW842670 AW603738 BE088661 AA484571 AI799184 BE174545 BE001405 AA436967 AW995884 AW995785 AW896598
		AW883999 BE075967 AA503938 BE092281 BE092279 BE087460 BE087569 BE081542 AI375386 AW843886 BE080115 BE171517 BE079898
65		AW882382 BE001450 BE076430 AW579377 BE008412 BE008790 BE182296 BE182297 BE078805 AW899132 BE078810 BE185867 BE087790
		AA484928 AW578985 BE008400 BE074080 AW605101 BE076110 AW799904 AI205094 BE008370 BE182345 BE182373 BE008401 AA984441
		BE182362 BE182372 BE008414 BE078186 BE009165 BE010266 BE009162 BE009167 BE011006 BE073335 BE182370 AW750566 BE182347
		BE011000 AA484576 BE092982 BE183897 BE092973 AA573037 AW882317 BE081832 AA478471 AA551613 BE182366 AW838886 AW026827
		BE008413 AW896605 AA503558 AA776622 BE084825 AA502971 BE081842 BE010628 AW802218 AI888924 AW867986 AW881775 BE079220
70		AI241060 AW802041 AW802005 BE001244 BE087051 AA984758 AA452997 AW992786 AW797500 BE077829 BE008402 AW881760 BE093516
		AW802084 AW369007 BE185123 BE087775 AW801018 BE093443 AW867978 AW843271 BE173850 AW997859 BE010620 AW992561 AW843908
		BE083200 BE164675 BE074340 AW880289 BE075433 BE008456 AW946438 BE066570 BE093547 AA508107 AW867992 BE076239 BE183881
		AW817422 BE087717 AW899147 BE010608 AW992295 AA436737 BE075412 BE093011 AW581656 BE089529 BE008756 BE150494 AW903020
		AW883102 BE076370 BE000625 BE166095 AW867979 BE182159 AW577501 AW577488 AW577491 BE010637 BE069910 BE093295 BE005243
75		AI620783 AW992550 AW890590 AW577496 AW577504 AW842725 AW842666 AW864691 AW997722 AW842662 BE009233 BE087809 BE083196
		AA287768 AW939691 AW815631 BE001453 AW841903 BE077613 AW577500 BE081479 AW992558 BE011065 AW843187 AW867990 AW898296
		BE074339 AA501697 AW749997 BE076249 AW867991 BE085718 AW994607 BE010678 BE075436 AW368825 AA484647 AW881144 AW577492
		AW997932 AW899089 AW842706 AW890727 AW843175 BE075428 AW843155 AW842679 AW842708 BE009915 AW842721 AW438792 AI251478
		BE069911 BE067054 BE079889 BE075453 BE069927 AA491920 BE170606 BE182305 BE080052 AW843406 BE011075 BE075969 AA525621
80		AW391518 BE079202 AA658195 BE076138 AW799901 AA493859 AW992510 BE011810 AA508724 BE075488 BE075661 AA258982 BE078726
		BE069914 AA213698 BE075376 AA484600 AW580999 BE077872 AA503571 AW884724 AW880124 AW868454 AW577502 AW577489 AW799829
		AW992545 BE075806 AW994606 BE350368 AA557836 BE077682 AW844660 AW883431 BE085872 AW838887 AW868404 AA578417
		BE074115 AW842680 AW277193 AW890728 AW605111 BE093940 AW890710 BE085560 AW868180 AW896778 BE069925 BE011054 BE075965
		AW842668 AW868310 BE011071 BE075429 AW843152 AW905848 BE075397 AW842762 BE075402 BE077950 AW837810 BE079998 BE183965

BE075431 AW815917 AW998359 AW799883 AW603782 AA557480 AW841444 BE075915 AA548034 AW843393 AW391559 BE083265 AW939721
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 BE182443 BE010296 AW577806 BE008415 BE184036 BE076597 AI817413 AW795053 AW896761 AW841433 BE182458 AW603796 AW842676
 BE085455 AW884879 BE075414 AW838836 AW878273 AW998088 AW799778 AW899125 BE082247 AA774870 BE001401 BE001485 AW817297
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 AW605626 AW939398 AA507280 AA506317 AW841230 AW992519 AA465332 AA425246 BE090234 BE090236 AA483259 AA451961 AA535566
 AA506406 AA888571 AA503568 AA507130 AA532944 AA501672 BE168634 AA492022 AA507662 AW842286 AA494226 AA776038 AA442419
 AW579900 BE171816 AA863065 AA491916 AA447490 AA461423 AA434543 AA243279 AW997466 AW603740 BE000295 AA658571

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400715	8118885	Minus	80151-80297
400736	8118985	Plus	143447-143851
401008	8117391	Minus	81421-81551,82364-82512,82862-82938
401069	3927852	Minus	45682-45831
401375	7417809	Minus	6121-6766
401405	7768126	Minus	69276-69452,69548-69958
401539	8072433	Minus	62028-62608
401557	8099866	Minus	112785-112924
401654	9097132	Minus	64695-64797
401940	3738108	Plus	153460-153592
402025	7547159	Plus	173835-173998
402442	9796503	Plus	141714-141842,142010-142122
402682	8138477	Minus	147522-147795
402796	3646083	Minus	6126-6265,6416-6689
402967	5360987	Minus	33518-34546
403038	7717439	Minus	290021-290284
403055	8748904	Minus	109532-110225
403310	8139936	Minus	183883-184026
403397	9438368	Minus	84481-84655
403839	4176355	Plus	21201-22223
404110	9212839	Minus	18344-18510
404495	8151634	Minus	59449-60477
404534	8247909	Minus	147853-148086
404630	9796665	Plus	74495-74715
404649	9796926	Minus	100027-100399
404680	9797204	Minus	159810-159979,160213-160321,161023-161304,162862-163140,164490-164644,166404-166530,166936-167083,167392-167522
404914	7341760	Plus	92603-92827
405417	4753290	Minus	50704-51499
405454	7656675	Plus	133807-134053
405510	7630909	Minus	101028-101174
405514	9454624	Plus	35953-36151
405536	9795661	Plus	164091-164162,164397-164516,166720-166790,167785-167935
406016	8272661	Plus	41341-41940
406410	9256394	Minus	115806-116104
406464	9789674	Plus	72161-72562
406562	7711584	Plus	37316-37426

TABLE 16A: 200 GENES DOWN-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

Table 16A shows 200 genes down-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 15A, except that the numerator and denominator were switched, the median value amongst normal cervixes was greater than or equal 40 units, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal cervix).

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of cervical cancer to normal cervix

Pkey	ExAccn	UnigenelD	Unigene Title	R1
453596	AA441838	Hs.62905	hypothetical protein FLJ14834	18.1
443912	R37257	Hs.184780	ESTs	16.8
420923	AF097021	Hs.273321	differentially expressed in hematopoietic lineages	13.6
414422	AA147224	Hs.337232	Homeo box A13	13.1
420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT2RP2002672	12.9
412639	AW961284	Hs.296235	ESTs	12.4

	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	12.4
	407938	AA905097	Hs.85050	phospholamban	11.3
	410544	AI446543	Hs.95511	ESTs	11.3
5	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	11.1
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 protein [H.sapiens]	11.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	10.9
	453060	AW294092	Hs.21594	hypothetical protein MGC15754	10.6
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia induci	10.5
10	452106	AI141031	Hs.21342	ESTs	9.5
	428780	AI478578	Hs.50636	ESTs	9.5
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	9.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PLACE1002968	9.0
	430468	NM_004673	Hs.241519	angiopoietin-like 1	9.0
15	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	8.7
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activin receptor inte	8.6
	401486	NA		C4000647*:gij4758508[ref NP_004253.1] airway trypsin-li	8.4
	417511	AL049176	Hs.82223	chordin-like	8.3
	429900	AA460421	Hs.30875	ESTs	8.2
20	411908	L27943	Hs.72924	cytidine deaminase	8.0
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiesterase	8.0
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone DKFZp	8.0
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	8.0
	421666	AL035250	Hs.1408	endothelin 3	7.9
25	450164	AI239923	Hs.30098	ESTs	7.9
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A; scatter factor	7.7
	425608	AA360486	Hs.92448	ESTs	7.6
	442748	AI016713	Hs.135787	ESTs	7.3
	415672	N53097	Hs.193579	ESTs	7.2
30	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	7.2
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	7.0
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nucleotide pyroph	6.7
	414214	D49958	Hs.75819	glycoprotein M6a	6.5
35	436637	AI783629	Hs.26766	ESTs	6.5
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	6.5
	432101	AI918950	Hs.123642	EphA3	6.3
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA, complete cds	6.3
	424153	AA451737	Hs.141496	MAGE-like 2	6.3
40	420228	R25023	Hs.12369	ESTs	6.2
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myotilin)	6.1
	444931	AV652066	Hs.75113	general transcription factor IIIA	6.1
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HEMBA1002970	6.1
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	6.1
	410425	BE278367	Hs.63510	KIAA0141 gene product	6.0
45	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	6.0
	424973	X92521	Hs.154057	matrix metalloproteinase 19	6.0
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like 1	5.9
	429414	AI783656	Hs.202095	empty spiracles (Drosophila) homolog 2	5.9
	440594	AW445167	Hs.126036	ESTs	5.9
50	452768	AW069459	Hs.61539	ESTs	5.9
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 protein [H.sapiens	5.9
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	5.9
	425010	T16837	Hs.4241	ESTs	5.9
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.8
55	437980	R50393	Hs.278436	KIAA1474 protein	5.8
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	5.7
	404097	NA		C5000242*:gij9369379[gb]AAF87128.1 AC006434_24 (AC00643	5.7
	422546	AB007969	Hs.301478	KIAA0500 protein	5.7
	445872	AI681573	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HEMBB1001458	5.7
60	429999	AI761902	Hs.99597	ESTs	5.6
	453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB1002492	5.6
	442082	R41823	Hs.7413	ESTs	5.5
	452073	AA625150	Hs.82098	ESTs	5.4
	430032	AW936136	Hs.99610	ESTs	5.4
65	408767	AA057279	Hs.211928	ESTs	5.4
	433234	AB040928	Hs.65366	KIAA1495 protein	5.3
	431708	AI698136	Hs.108873	ESTs	5.3
	421200	AA284811	Hs.264433	ESTs	5.2
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HEMBA1001008	5.2
70	409643	AW450866	Hs.257359	ESTs	5.1
	416676	AW392022	Hs.79507	KIAA0582 protein	5.1
	420357	U94333	Hs.97199	complement component C1q receptor	5.0
	417355	D13168	Hs.82002	endothelin receptor type B	5.0
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL06674	5.0
75	430965	AA489732	Hs.154918	ESTs	4.9
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	4.9
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	4.8
	404485	NA		Target Exon	4.8
80	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fis, clone HEMBB1001024	4.8
	417692	R09338	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OVARC1000640	4.8
	432304	AA932186	Hs.69297	ESTs	4.7
	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.7
	448851	AI582207	Hs.177166	ESTs	4.7
	405523			C8001409*:gij7441226[pir]S31212 collagen alpha 1(XIV)	4.7

	450656	AA010539	Hs.18912	ESTs	4.6
	422942	AF054839	Hs.122540	tetraspan 2	4.6
	401479	T49304	Hs.110950	Rag C protein	4.6
5	444192	AW469413	Hs.151145	ESTs	4.6
	439648	AW780192	Hs.267596	ESTs	4.5
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, member 4	4.5
	444702	AI220122	Hs.326560	hypothetical protein MGC2780	4.5
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX	4.5
10	452249	BE394412	Hs.202095	empty spiracles (Drosophila) homolog 2	4.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	4.5
	411037	BE145915	Hs.99472	ESTs	4.4
	442803	AI675298	Hs.199917	ESTs	4.4
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulatory, type II, be	4.4
	400628	NA		C10001871*:gij1705533[sp]P32018[CA1E_CHICK COLLAGEN ALP	4.3
15	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage serine esterase	4.3
	437110	AL049240	Hs.144995	ESTs	4.2
	410646	W79408	Hs.50745	ESTs	4.2
	456304	AI820973		gb:nc21c02.y5 NCL_CGAP_Pr1 Homo sapiens cDNA clone, mRNA	4.2
20	401270			Target Exon	4.2
	419447	BE092696	Hs.75928	ESTs	4.2
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	4.2
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	4.2
	434469	AA634806		gb:ab28c02.r1 Stratagene lung (937210) Homo sapiens cDN	4.1
25	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR	4.1
	418947	W52990	Hs.22860	ESTs	4.1
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.0
	454736	BE184348		gb:CM0-HT0676-010500-355-e11 HT0676 Homo sapiens cDNA,	4.0
	407945	X69208	Hs.606	ATPase, Cu transporting, alpha polypeptide (Menkes synd	4.0
30	447499	AW262580	Hs.147674	protocadherin beta 16	4.0
	430686	NM_001942	Hs.2633	desmoglein 1	4.0
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (cardiovascula	3.9
	419047	AW952771	Hs.90043	ESTs	3.9
	414272	AI651603	Hs.46988	ESTs	3.9
35	443808	AW377736	Hs.12420	ESTs	3.9
	426883	H21520	Hs.35088	ESTs	3.9
	410659	AI080175	Hs.68826	ESTs	3.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.9
	432181	AA527650	Hs.156037	ESTs	3.9
40	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.8
	453296	AA034413	Hs.62560	ESTs	3.8
	400878	NA		Target Exon	3.8
	401103	NA		C12001233:gij7305361[ref]NP_038652.1 otogelin [Mus mus	3.8
	436670	AI690021	Hs.201536	ESTs	3.7
45	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface receptor	3.7
	408793	BE258371	Hs.254660	ESTs	3.7
	419093	AI804054	Hs.112885	spinal cord-derived growth factor-B	3.7
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	3.7
	450776	NM_007250	Hs.320861	Kruppel-like factor 8	3.7
50	437140	AA312799	Hs.283689	activator of CREM in testis	3.6
	418421	R58620	Hs.85050	phospholamban	3.6
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOTHETICAL PROTEIN	3.6
	417194	N53793		gb:yz07a01.r1 Soares_multiple_sclerosis_2NbHMSP Homo sa	3.6
	443567	AI077540	Hs.134090	ESTs	3.6
55	451879	AI821030		gb:yb52f11.y5 Stratagene ovary (937217) Homo sapiens cD	3.6
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.5
	451896	AF196304	Hs.27197	SUMO-1-specific protease	3.5
	413237	AI468574	Hs.171965	ESTs	3.5
	424636	AA453734	Hs.10198	ESTs	3.5
60	432660	AI288430	Hs.64004	ESTs	3.5
	414681	AL079440	Hs.74002	nuclear receptor coactivator 1	3.5
	400802	NA		Target Exon	3.5
	430015	AW768399	Hs.112157	ESTs	3.5
	451978	AW813747	Hs.27371	Homo sapiens mRNA; cDNA DKFZp566J123 (from clone DKFZp5	3.5
65	449088	AI654048	Hs.196556	ESTs	3.5
	425113	AI936992	Hs.154658	pleckstrin and Sec7 domain protein	3.5
	458459	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone COL09609	3.5
	420249	BE262895	Hs.276916	nuclear receptor subfamily 1, group D, member 1	3.5
	401159	NA		Target Exon	3.5
70	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQ	3.5
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5 [H.sapiens]	3.4
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC FINGER PROTEIN	3.4
	423587	AA328074	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia induci	3.4
	443178	AI631241	Hs.47312	ESTs	3.4
75	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTONE H2B H [H.sap	3.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Drosophila) homol	3.4
	437950	U79244	Hs.112642	ESTs	3.3
	419368	AI753518	Hs.209464	KIAA1604 protein	3.3
	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	3.3
80	451398	AI793124	Hs.144479	ESTs	3.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	3.3
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, expressed in pro	3.3
	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	3.3
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	3.3

444216	D25303	Hs.222	integrin, alpha 9	3.3
418771	AA807881	Hs.25329	ESTs	3.3
433036	AA574091	Hs.105964	ESTs	3.2
404584			Target Exon	3.2
404195			NM_015718*:Homo sapiens NADPH oxidase 3 (NOX3), mRNA. V	3.2
428819	AL135623	Hs.193914	KIAA0575 gene product	3.2
425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
420833	R47948	Hs.188732	ESTs	3.1
413156	AA127133		gb:zl87e03.r1 Stratagene colon (937204) Homo sapiens cD	3.1
413607	T64741		gb:yc48f11.r1 Stratagene liver (937224) Homo sapiens cD	3.1
443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.1
428790	AF023456	Hs.193558	protein phosphatase, EF hand calcium-binding domain 2	3.1
434520	AA205273	Hs.177011	hypothetical protein	3.1
432247	AA531287	Hs.105805	ESTs	3.1
429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	3.1
439734	AC005013	Hs.149	cAMP response element-binding protein CRE-BPa	3.1
433546	AI075877	Hs.125461	hypothetical protein FLJ11539	3.0
430317	AB020645	Hs.239189	glutaminase	3.0
425130	AA448208	Hs.99163	ESTs	3.0
444195	AB002351	Hs.10587	KIAA0353 protein	3.0
409007	AL122107	Hs.49599	Homo sapiens mRNA; cDNA DKFZp434G0827 (from clone DKFZp	3.0
453773	AL133761		gb:DKFZp761C1413_r1 761 (synonym: hamy2) Homo sapiens c	3.0
442974	AI025670	Hs.109308	ESTs, Weakly similar to leucine-rich glioma-inactivated	3.0
446936	H10207	Hs.47314	ESTs	3.0
454086	AW885909	Hs.6975	PRO1073 protein	3.0
420271	AI954365	Hs.42892	ESTs	3.0
435545	AA687415	Hs.28107	ESTs	3.0
445175	AV652851	Hs.20255	ESTs	3.0

TABLE 16B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
413156	135116_1	AA127133 AA384396 AW958912 T72119
413607	1379911_1	T64741 BE158393 BE152805
417194	1657323_1	N53793 N53716 N53739
434469	387447_1	AA634806 C18732 AA729161 AA729860
451879	888642_1	AI821030 T47126 AI821318
453773	980699_1	AL133761 AL133767
454736	1232235_1	BE184348 AW817453 BE011068
456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101

TABLE 16C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400628	3818355	Plus	41851-41984
400802	8567867	Minus	174571-174856
400878	9864757	Plus	31493-32842
401103	8568122	Minus	98330-98449
401159	6067118	Minus	3180-3953
401270	9797168	Minus	141659-141813
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
404097	7770701	Plus	55512-55781
404195	3805917	Minus	39186-39332
404485	8096921	Plus	75166-75264,124036-124232
404584	9857511	Plus	138651-139153
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

TABLE 17A: 605 genes upregulated in testicular cancer relative to normal body tissues

Table 17A lists about 605 genes upregulated in cervical cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.ProT.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M,

UniGene Title: likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 R1 UniGene gene title
 95th percentile of cervical cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prot.Domains; R1

408522; AI541214; Hs.46320; Small proline-rich protein SPRK [human; ; none,Cornifin; 33.942
 422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psorias; ehand,S_100;TM=M;SS=N; 33.05
 424098; AF077374; Hs.139322; small proline-rich protein 3; Cornifin;TM=M;SS=N; 32.856
 422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap;TM=M;SS=Y; 29.604
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_recpt;TM=M;SS=Y; 27.95054945
 421948; L42583; Hs.334309; keratin 6A; filament,RhoGAP,DUF286,bZIP,Tropomyosin,tubulin,DUF164,TBCA,Collagen;TM=M;SS=N; 26.778
 446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium_transp,FecCD;TM=Y;SS=M; 26.1133829
 407242; M18728; ; gb:Human nonspecific crossreacting antig; ig;TM=M;SS=M; 23.382
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2,hemopexin,Peptidase_M10; ; 22.522
 412719; AW016610; Hs.816; ESTs; none,none; 21.198
 406690; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; ig;TM=M;SS=M; 20.028
 402075; ; ENSP00000251056*:Plasma membrane calcium; none; ; 19.038
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin,Cadherin_C_term;TM=Y;SS=M; 17.92061281
 412471; M63193; Hs.73946; endothelial cell growth factor 1 (platelet; Glycos_transf_3,Glycos_trans_3N;TM=M;SS=M; 17.8978979
 417308; H60720; Hs.81892; KIAA0101 gene product; none;TM=M;SS=N; 17.08333333
 429259; AA420450; Hs.380088; Plakophilin; none,none; 17.08235294
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; ; 16.91568628
 439926; AW014875; Hs.137007; ESTs; none,none; 16.69
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 16.365
 413753; U17760; Hs.75517; laminin, beta 3 (nicein (125kD), kalinin; laminin_EGF,laminin_Nterm; ; 15.75294118
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; ; 15.48600509
 401781; ; Target Exon; filament;TM=M;SS=N; 15.43668831
 420440; NM_002407; Hs.97644; mammaglobin 2; Uteroglobin; ; 15.394
 441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none;TM=M;SS=M; 15.12264151
 452240; AI591147; Hs.61232; ESTs; none,none; 14.63
 428957; NM_003881; Hs.194679; WNT1 inducible signaling pathway protein; tsp_1,vwc,IGFBP;TM=M;SS=M; 14.49772727
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;SS=N; 14.4389313
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis, clone PL; none,none; 14.00909091
 400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin,Peptidase_M10,Astacin; ; 13.824
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 13.7754386
 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR; ; 13.74595843
 400284; ; NM_000125*:Homo sapiens estrogen recepto; hormone_rec,zf-C4,Oest_recep;TM=M;SS=M; 13.31578947
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 13.05294118
 411274; NM_002776; Hs.69423; kallikrein 10; trypsin;TM=M;SS=N; 13.038
 406687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase_M10; ; 13.00311527
 427666; AI791495; Hs.180142; calmodulin-like skin protein (CLSP); ehand;TM=M;SS=N; 12.79
 400301; X03635; Hs.1657; estrogen receptor 1; F-box,hormone_rec,zf-C4,Oest_recep,adh_zinc,ketoacyl-synt,pp-binding,Acyl_transf,Thioesterase,ketoacyl-synt_C,AAA,E7,RFX_DNA_binding;TM=M;SS=N; 12.472
 410001; AB041036; Hs.57771; kallikrein 11; trypsin;TM=M;SS=M; 12.47
 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none,pkinase,fn3,lg; 12.28597122
 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M;SS=N; 12.13379205
 437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none;TM=M;SS=M; 12.04945055
 418462; BE001596; Hs.85266; integrin, beta 4; fn3,integrin_B,Ca1x-beta,EGF;TM=M;SS=M; 11.95538462
 443859; NM_013409; Hs.9914; follistatin; kazal; ; 11.95467422
 426350; NM_003245; Hs.2022; transglutaminase 3 (E polypeptide, prote; Transglutamin_N,Transglutamin_C,Transglut_core;TM=M;SS=N; 11.61
 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;SS=N; 11.564
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associated prote; UPAR_LY6,lactamase_B; 11.55285714
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ;
 aa_pemases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_Pi4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 11.47956989
 418663; AK001100; Hs.41690; desmocollin 3; cadherin,Cadherin_C_term,none; 11.456
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none; ; 11.45352113
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolys; Kunitz_BPTI,fn3,vwa,Collagen,beta-lactamase;TM=M;SS=M; 11.32234432
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7trn_3;TM=Y;SS=M; 11.28686327
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none,none; 11.076
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg;TM=M;SS=N; 11.0381579
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 11
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin,Peptidase_M10;TM=M;SS=M; 11
 425071; NM_013989; Hs.154424; deiodinase, iodothyronine, type II; T4_deiodinase;TM=M;SS=Y; 10.93859649
 437938; AI950097; Hs.369628; gb:wg05c02.x1 NCI_CGAP_Kid12 Homo sapien; none,none; 10.78064516
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 10.74825175
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH; none,none; 10.542
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC,none; 10.49538462
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none;TM=M;SS=Y; 10.48210736
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A recepto; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 10.26714286
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 10.142
 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M;SS=N; 10.1
 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin,Repolyisin,Pep_M12B_propep,EGF;TM=Y;SS=M; 10.072
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisolV,HATPase_cc; 9.996363636
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor; serpin; ; 9.896825397
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M;SS=N; 9.888888889
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 9.876056338
 424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF; ; 9.851635514
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 9.840720222
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT,none; 9.823170732
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); ehand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AIP3;TM=M;SS=N; 9.812

- 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S.; MCM,aldo_ket_red;TM=M;SS=N; 9.787878788
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;SS=N; 9.637037037
 425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin;TM=M;SS=M; 9.596
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevi; WD40;TM=M;SS=N; 9.558
 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase_2;TM=Y;SS=M; 9.55
 421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 9.529085873
 408591; AF015224; Hs.46452; mammaglobin 1; Uteroglobulin;TM=M;SS=M; 9.506
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 9.477961433
 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; ldl_recept_a,PKD,MHC_I;TM=M;SS=Y; 9.415151515
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; 9.408
 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 atrophin-; ras;TM=M;SS=N; 9.36
 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg;TM=M;SS=N; 9.315693431
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 9.31
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 9.29
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh; 9.264
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 9.241561181
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 9.207272727
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 9.195167286
 439223; AW238299; Hs.250618; UL16 binding protein 2; ldl_recept_a,PKD,MHC_I;TM=M;SS=Y; 9.108
 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA;TM=Y;SS=N; 9.028
 421777; BE562088; Hs.108196; HSPC037 protein; none;TM=M;SS=N; 9.004
 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 9.001096491
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;SS=N; 8.942
 455601; A1368680; Hs.816; SRY (sex determining region Y)-box 2; HMG_box; 8.87
 429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin;TM=Y;SS=M; 8.77131783
 456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4,Cbl_N,Cbl_N3;TM=M;SS=N; 8.738
 430397; A1924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;SS=N; 8.736
 417034; NM_006183; Hs.80962; neurotensin; none; 8.592
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 8.536
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3,none; 8.49
 439285; A1133916; Hs.47860; hypothetical protein FLJ20093; ig,ptkinase,LRR,LRRNT,LRRCT,none; 8.460655738
 409420; Z15008; Hs.54451; laminin, gamma 2 (nicotin (100kD), kalini; laminin_B,laminin_EGF; 8.414
 438746; A185815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanylate_kin,PDZ,SH3; 8.376205788
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1;TM=Y;SS=M; 8.37
 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 8.364
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;SS=N; 8.266
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 8.248314607
 431620; AA126109; Hs.264981; 2'-5'-oligoadenylate synthetase 2 (69-71; NTP_transf_2;TM=M;SS=N; 8.156
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M;SS=N; 8.142857143
 448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitte; SNF;TM=Y;SS=N; 8.137559809
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_inh; 8.043478261
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; DNA_ligase; 8.038194444
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M;SS=N; 8.024752475
 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none;TM=Y;SS=M; 8
 424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibitor; serpin;TM=M;SS=N; 7.982
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.973684211
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 7.892
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 7.824
 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 7.823874755
 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP,Rhabd_glycop,integrin_A;TM=Y;SS=M; 7.758985201
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3;TM=M;SS=Y; 7.75887574
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M;SS=N; 7.757751938
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd_glycop;TM=Y;SS=M; 7.624
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 7.605660377
 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M;SS=N; 7.578
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 7.476
 429299; A1620463; Hs.347408; hypothetical protein MGC13102; none;TM=Y;SS=N; 7.442528736
 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 7.442495127
 446163; AA026880; Hs.25252; prolactin receptor; none;NA;NA; 7.436781609
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant_thionins; 7.435897436
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,pkinase,Recep_L_domain,YLP,none; 7.398360656
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 7.394039735
 431890; X17033; Hs.271986; Integrin, alpha 2 (CD49B, alpha 2 subuni; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 7.383419689
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none,none; 7.382
 436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin;TM=Y;SS=M; 7.327160494
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 7.316
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;SS=N; 7.315412186
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;SS=N; 7.2984375
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 7.28
 451253; H48299; Hs.26126; claudin 10; PMP22_Claudin,Peptidase_M1,K_tetra;TM=Y;SS=M; 7.256802721
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase; 7.234455959
 421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 7.162534435
 451035; AU076785; Hs.430; plastin 1 (I isoform); ehfand,CH,Adaptin_N; 7.145454546
 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1;TM=Y;SS=M; 7.126
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 7.122413793
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX; Troponin,Exo_endo_phos,IQ;TM=M;SS=N; 7.106719368
 430890; X54232; Hs.2699; glypican 1; Glypican;TM=M;SS=M; 7.088937093
 407792; A1077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 7.052
 426514; BE616633; Hs.170195; bone morphogenetic protein 7 (osteogenic; TGF-beta,TGFB_propeptide; 7.042
 431241; AA496799; Hs.36958; ESTs; SH2,RasGEF,none; 7.03
 437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm_1;TM=Y;SS=M; 7.03
 420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-530115; none,none; 7.026
 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none;TM=M;SS=N; 7.008

- 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3,PX;TM=M;SS=N; 6.991626794
 416250; AA581386; Hs.73452; Kremen 2; kringle,CUB,WSC;; 6.972
 430770; AA765694; Hs.123296; ESTs; none,none; 6.95
 5 418869; AW516565; ; gb:qx01d05.x1 Soares_NHCCc_cervical_tumo; none,RasGAP,WW,IQ; 6.948
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfam; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD;; 6.914
 418283; S79895; Hs.83942; cathepsin K (pseudosclerosis); Peptidase_C1;; 6.876190476
 419667; AU077005; Hs.92208; a disintegrin and metalloproteinase doma; disintegrin,Repolyisin,Pep_M12B_propep;TM=M;SS=M; 6.862970711
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing le; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 6.849056604
 56181; L36463; Hs.1030; ras inhibitor; RA,SH2,VPS9;TM=M;SS=N; 6.762
 10 436856; A166355; Hs.127310; ESTs; pkinase,rrm;TM=M;SS=N; 6.721428571
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 6.720348837
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 6.717307692
 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2;TM=Y;SS=M; 6.715240642
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg,UQ_con,none; 6.688194444
 15 439738; BE246502; Hs.9588; sema domain, immunoglobulin domain (ig); Sema,PSI,integrin_B;TM=Y;SS=N; 6.670553936
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;; 6.662921348
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM,PDZ,pkinase;; 6.653713299
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;; 6.652671756
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M;SS=N; 6.639555172
 20 438113; A1467908; Hs.8882; ESTs; 7tm_1,none; 6.6
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH,none; 6.6
 408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1;TM=Y;SS=M; 6.548148148
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 6.532763533
 414809; A1434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=N; 6.526951673
 25 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 6.512704174
 420039; NM_004605; Hs.376147; sulfotransferase family, cytosolic, 2B;; Sulfotransfer; 6.496
 423031; A1278995; Hs.374579; ESTs; none,none; 6.447658402
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans,K_tetra,asp; 6.426666667
 30 433933; A1754389; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none,NA;NA; 6.4
 435094; A1560129; Hs.289008; EST; none,none; 6.312
 432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3,PDZ,Guanylate_kin,none; 6.276556777
 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rrm,PAP_assoc;TM=Y;SS=M; 6.272727273
 35 435232; NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank;TM=M;SS=N; 6.269720102
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 6.219081272
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin;TM=M;SS=N; 6.19
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD,helicase_C,CARD;TM=M;SS=N; 6.188888889
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; ig,Isodh,Ribosomal_L6,F-box;TM=Y;SS=M; 6.188046647
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-Ii; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 6.15503876
 40 450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta,TGFb_propeptide;; 6.152
 432314; AA533447; Hs.285173; ESTs; Xlink,none; 6.123040752
 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase,PLAT;TM=M;SS=N; 6.12
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; ig,pkinase;TM=Y;SS=M; 6.095758355
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial; mito_carr;TM=M;SS=N; 6.089164786
 45 452683; A1089575; Hs.374574; progesterone membrane binding protein; homeobox,none; 6.06284153
 445537; AJ245671; Hs.12844; EGF-like domain, multiple 6; EGF,MAM;; 6.05513308
 444309; U83236; Hs.10803; calcium and integrin binding protein (DN; ehand;; 6.04015544
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPC,isp_1,Ribosomal_S21,rvp;TM=M;SS=N; 6.009562842
 50 438108; A1471795; Hs.287776; vanilloid receptor-related osmotically a; ank,ion_trans;TM=Y;SS=N; 6.004
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 5.984536083
 405484; ; ; C3002124;gil12737280[ref]XP_006682.2] k; none;; 5.978964401
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,tRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M;; 5.978431373
 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8;; 5.976
 55 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y_phosphatase;TM=M;SS=N; 5.969387755
 411756; BE294350; Hs.71891; discoidin domain receptor family, member; pkinase,F5_F8_type_C;TM=Y;SS=M; 5.95184136
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 5.951550388
 453459; BE047032; Hs.257789; ESTs; none,none; 5.95
 60 456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=N; 5.938
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-in; hemopexin,Peptidase_M10;TM=M;SS=M; 5.917857143
 414703; BE243877; Hs.380063; ATPase, Na? transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 5.910455487
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moi; NUDIX;TM=M;SS=M; 5.901886793
 452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none,none; 5.868362832
 418345; AJ001696; Hs.241407; serine (or cysteine) proteinase inhibitor; serpin;TM=Y;SS=M; 5.842
 65 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 11; Euk_porin;TM=M;SS=M; 5.816363636
 439625; AF086453; Hs.58611; ESTs; Fork_head,glycolytic_enzy,Na_sulph_symp; 5.811594203
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 5.81
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR;TM=M;SS=N; 5.806
 415198; AW009480; Hs.943; natural killer cell transcript 4; none;TM=M;SS=N; 5.804137931
 70 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase,Furin-like,Recep_L_domain,none; 5.8
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;SS=N; 5.794
 439335; AA742697; Hs.62492; NM_052863;Homo sapiens secretogloblin, fa; none;; 5.778588808
 439246; A1498072; Hs.351474; membrane-associated tyrosine- and threon; ank,pkinase,UPF0073;; 5.763492064
 452461; N78223; Hs.108106; transcription factor; zf-C3HC4,ubiquitin,PHD,YDG_SRA;TM=M;SS=N; 5.728
 75 414883; AA928660; Hs.348669; CDC28 protein kinase 1; CKS;; 5.714634146
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2,STAT,STAT_bind,STAT_prot,none; 5.701666667
 419056; M89957; Hs.89575; CD79B antigen (immunoglobulin-associated; ig,ITAM;TM=Y;SS=M; 5.692
 432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase,Sema,PSI,TIG,A4_EXTRA;TM=M;SS=M; 5.686
 452696; A1826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate_kin,PDZ,SH3; 5.683673469
 80 411030; BE387193; Hs.67896; 7-60 protein; none;TM=M;SS=N; 5.676767677
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazaro; none;TM=Y;SS=N; 5.672977625
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1;TM=Y;SS=M; 5.666
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; ptkB;TM=M;SS=N; 5.655616943

427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M; SS=N; 5.6485623
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threonine; ank, pkinase, UPF0073; 5.648
 452690; AI536070; Hs.15085; ESTs; pou, homeobox, lig_chan, ANF_receptor; 5.646
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2, SH3, pkinase; TM=M; SS=N; 5.642405063
 418703; NM_014448; Hs.87435; Rho guanine exchange factor (GEF) 16; SH3, PH, RhoGEF, Bim_VP3; TM=M; SS=N; 5.636
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122; TM=M; SS=N; 5.635087719
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M; SS=N; 5.620930233
 432065; AA01039; Hs.2903; protein phosphatase 4 (formerly X), cata; Metallophos; TM=M; SS=N; 5.608352145
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related; SH2, SH3, pkinase; TM=M; SS=N; 5.596052632
 430696; AA531276; Hs.59509; ESTs; pkinase, PP2C, none; 5.575112108
 435017; AA336522; Hs.12854; angiotensin II, type I receptor-associat; none; TM=Y; SS=M; 5.556910569
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH, Lipase_GDSL; TM=M; SS=N; 5.556195965
 415012; NM_004383; Hs.77793; c-src tyrosine kinase; SH2, SH3, pkinase; TM=M; SS=N; 5.555421687
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; 5.549751244
 413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidyl); SH2, SH3, C2, PH, PI-PLC-Y, PI-PLC-X, PDGF; 5.541366907
 406621; X57809; Hs.181125; immunoglobulin lambda locus; ig, HSP70, Ppx-GppA; TM=M; SS=N; 5.54076087
 417700; M36542; Hs.1101; POU domain, class 2, transcription factor; homeobox, pou; TM=M; SS=N; 5.536
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M; SS=N; 5.52661597
 436576; AI458213; Hs.77542; ESTs; 7tm_1, DnaJ; 5.52638191
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase, DAG_PE-bind, pkinase_C, OPR; TM=M; SS=N; 5.519672131
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (f; MIF, sugar, Ir, none; 5.516453382
 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR, LRRNT, LRRCT; TM=Y; SS=M; 5.514964789
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; fn3, Ig_Y, phosphatase, MAM; TM=Y; SS=M; 5.494202899
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC, tran, ABC, membrane; TM=Y; SS=M; 5.471947195
 410608; AI538438; Hs.159087; ESTs; ubiquitin, integrin_B, UBA, none; 5.465384615
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin; TM=M; SS=N; 5.460076046
 408716; AI567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein, ; UvrD-helicase, RNB, Runt; TM=M; SS=N; 5.450413223
 426410; BE298446; Hs.305890; BCL2-like 1; Bcl-2, BH4, none; 5.444805195
 457819; AA057484; Hs.35400; FLJ20522 Hypothetical protein FLJ20522; none, none; 5.444281525
 422597; BE245909; Hs.118634; ATP-binding cassette, sub-family B (MDR; ABC, tran, ABC, membrane, PRK; TM=Y; SS=N; 5.437931035
 429191; AF065215; Hs.198161; phospholipase A2, group IVB (cytosolic); C2, PLA2_B, jmjC; TM=M; SS=N; 5.4375
 449961; AW265634; Hs.133100; ESTs; pkinase, Furin-like, Recep_L_domain, none; 5.435211268
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH, RhoGEF; TM=M; SS=M; 5.433333333
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible Ik; pkinase, RIO1; TM=M; SS=N; 5.429657795
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C, none; 5.423322684
 423189; M59371; Hs.171595; EphA2; fn3, pkinase, SAM, EPH, lbd; TM=Y; SS=M; 5.421621622
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae); pkinase; TM=M; SS=N; 5.412
 432527; AW975028; Hs.102754; ESTs; none, none; 5.40625
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz, Frizzled, 7tm_2; TM=Y; SS=M; 5.405504587
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M; SS=N; 5.396
 434467; BE552368; Hs.231853; Homo sapiens cDNA FLJ13445 fis, clone PL; 7tm_1, none; 5.391472868
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ; 5.389250814
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC004358 3 U1 sm; none, none; 5.382
 437016; AU076916; Hs.5398; guanine monophosphate synthetase; PHD, SET, zf-
 CXXC, EGF, ank, notch, WW, FCH, GATase, GMP_synth_C, Occludin, YEATS, metalthio, EB, heme_1, RCC1, ZZ, FeThRed_A, ENTH, Band_41, HECT; TM=M; SS=N; 5.373937677
 424848; AI263231; Hs.327090; EST; SH3, PDZ, Guanylate_kin, none; 5.36
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate; MORN, sugar, Ir; TM=Y; SS=M; 5.35971223
 405932; ; C15000305; gi3806122[gb]AAC69198.1 (AF0); ras; TM=M; SS=N; 5.349226804
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated); ig, ITAM, Zn_clus; TM=Y; SS=M; 5.346153846
 453143; AA382234; Hs.356289; protein tyrosine phosphatase, receptor t; serpin; 5.333667335
 423973; AF038461; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase, PLAT; TM=M; SS=N; 5.33
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none, none; 5.328
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 5.316
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 5.309638554
 410165; BE560228; Hs.71869; apoptosis-associated speck-like protein; PAAD, DAPI, CARD; TM=M; SS=N; 5.293560606
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-t; fn3, Y_phosphatase, carb_anhydase; TM=Y; SS=M; 5.28
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none, spectrin, SH3, PH, CH; 5.278947368
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y; SS=N; 5.274746193
 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, comp; none; TM=Y; SS=M; 5.272222222
 415117; AF120499; Hs.78016; polynucleotide kinase 3-phosphatase; Viral_helicase1; TM=M; SS=N; 5.27
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3, RhoGAP, FCH; TM=M; SS=N; 5.251865672
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc, Rhodanese, none; 5.248
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 5.232
 422017; NM_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2; 5.212418301
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; 5.209259259
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphate; Ribosomal_L20, Na_Pi_cotrans; TM=Y; SS=N; 5.202
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos, SH2; TM=M; SS=N; 5.19979716
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC, tran, GTP_EFTU, ABC, membrane, none; 5.199074074
 416802; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF, vwc, TSPN; 5.198224852
 429556; AW139399; Hs.314807; ESTs; none; TM=M; SS=N; 5.192439863
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin_head, IQ, zf-MYND; TM=M; SS=M; 5.190251572
 400517; ; lengsin; none; TM=M; SS=N; 5.18
 413438; AF238083; Hs.68061; sphingosine kinase 1; DAGKc; TM=M; SS=N; 5.172881356
 423527; AI206965; Hs.105861; hypothetical protein FLJ13824; none; TM=M; SS=N; 5.165060241
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion_trans, SPRY, RYDR, ITPR, RyR, MIR; TM=Y; SS=N; 5.156976744
 437809; AL137723; Hs.5855; Homo sapiens mRNA; cDNA DKFZp434D0818 (f; none, none; 5.154676259
 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos; TM=M; SS=N; 5.152360515
 409340; BE174629; Hs.321130; hypothetical protein MGC2771;
 aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_PI4_kinase, FAT, FATC, BoA, RUN; TM=M; SS=N; 5.144859813
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra, DUF51, none; 5.142
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3, PH, WW, RhoGAP; 5.141534392
 434808; AF155108; Hs.256150; NY-REN-41 antigen; none; TM=M; SS=N; 5.14
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M; SS=N; 5.13968254

- 431685; AW296135; Hs.267659; vav 3 oncogene; CH,DAG_PE-bind,PH,RhoGEF,SH2,SH3,DC1;TM=M;SS=N; 5.129476584
 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase, pkinase_C,HR1;TM=M;SS=N; 5.121527778
 433573; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G-type rece; 7tm_2,EGF,cadherin,laminin_EGF,laminin_G,Trypan_glycop,GPS,HRM;TM=Y;SS=M; 5.107438017
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC_tran,arf;TM=M;SS=M; 5.10251046
 419493; AF001212; Hs.90744; proteasome (prosome, macropain) 26S subu; CDK5_activator,PCI,none; 5.095194085
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor; ; inositol_P,ig;TM=M;SS=N; 5.092
 435243; AW292886; Hs.348932; hypothetical protein dJ434O14.3; IRF,none; 5.092
 434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp586F2224 (f; DSPc,none; 5.091922006
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 5.088932806
 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA; 5.082840237
 420030; BE503994; Hs.146233; KIAA0418 gene product; SH3,none; 5.080645161
 440665; AW449415; Hs.10260; Homo sapiens cDNA FLJ11341 fis, clone PL; SH3; 5.063953488
 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 5.056
 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase; 5.054133858
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 5.054
 423883; AF250238; Hs.134514; ATP-binding cassette, sub-family A (ABC1; ABC_tran,photoRC,SRP54,Ca_channel_B,Pterin_4a;TM=Y;SS=M; 5.051724138
 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P14_kinase,PI3Ka;TM=M;SS=N; 5.051282051
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;SS=N; 5.047311828
 410026; AJ912061; Hs.55016; hypothetical protein FLJ21935; none,none; 5.04674221
 426395; BE151985; Hs.355669; hypothetical protein FLJ23316; pkinase,none; 5.040298508
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 5.039039039
 444895; AI674383; Hs.22891; solute carrier family 7 (cationic amino; ASC,death,TNFR_c6; 5.037151703
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF;TM=Y;SS=M; 5.034
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep;TM=M;SS=N; 5.03030303
 410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Topoisom_bac,Toprim; 5.027985075
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase; pkinase,CNH;TM=M;SS=N; 5.014652015
 415166; NM_003652; Hs.78068; carboxypeptidase Z; Zn_carbOpept,Dioxygenase,Fz; 5.012269939
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 5.001811594
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; 4.997983871
 430024; AI808780; Hs.227730; integrin, alpha 6; integrin_A,FG-GAP;TM=Y;SS=M; 4.994871795
 409220; BE243323; Hs.51233; tumor necrosis factor receptor superfam; TNFR_c6,death,Lipoprotein_5,TIL;TM=Y;SS=M; 4.987135506
 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 4.985185185
 423011; NM_000683; Hs.123022; adrenergic, alpha-2C-, receptor; 7tm_1;TM=Y;SS=M; 4.984
 419577; L36531; Hs.91296; integrin, alpha 8; integrin_A,FG-GAP;TM=Y;SS=N; 4.968
 402328; ; Target Exon; pkinase;TM=M;SS=N; 4.96728972
 421242; AW161386; Hs.13561; hypothetical protein MGC4692; none;NA;NA; 4.966334165
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 4.964491363
 414203; BE262170; Hs.78629; ATPase, Na? transporting, beta 1 polypep; none,none; 4.961956522
 409582; R27430; Hs.271565; ESTs; none,Neur_chan_LBD,Neur_chan_memb; 4.946
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;SS=N; 4.943181818
 453449; W16752; Hs.32981; sema domain, immunoglobulin domain (Ig); Ig,Sema,PSI; 4.930508475
 425233; Z17861; Hs.155218; E1B-55kDa-associated protein 5; SPRY,SAP,pkinase,fn3,ig; 4.925347222
 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase_M10; 4.92
 422282; AF019225; Hs.114309; apolipoprotein L; MoA_ExbB;TM=Y;SS=M; 4.912181303
 442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 4.910224439
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.909972299
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 4.904
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M;SS=N; 4.897338403
 411770; NM_014278; Hs.71992; heat shock protein (hsp110 family); HSP70;TM=M;SS=N; 4.894
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm_1;TM=Y;SS=M; 4.886
 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese,none; 4.884
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none; 4.876379691
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevi; NusG; 4.876117497
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfam; SRP14,TNFR_c6; 4.873684211
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,ig,Neuregulin;TM=M;SS=N; 4.872641509
 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 4.869318182
 429619; AL120751; Hs.211568; eukaryotic translation initiation factor; none,none; 4.868073879
 458873; AW150717; Hs.345728; STAT induced STAT inhibitor 3; none,none; 4.861538462
 437669; AI358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA; none,pkinase,pkinase_C; 4.854651163
 405545; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 4.85
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 4.848387097
 424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus; fn3,ig,IRK;TM=Y;SS=M; 4.846153846
 425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar_tr;TM=Y;SS=M; 4.843694494
 421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 4.842532468
 418736; T18979; Hs.87908; Snf2-related CBP activator protein; helicase_C,AT_hook,SNF2_N;TM=M;SS=N; 4.842
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2,none; 4.841071429
 417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2,PID,zf-C2H2,SCAN,AMP-binding,KRAB;TM=M;SS=N; 4.839464883
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar_tr; 4.837837838
 434521; NM_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg,IBB;TM=M;SS=N; 4.833333333
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 4.821666667
 453082; H18835; Hs.31608; hypothetical protein FLJ20041; ion_trans;TM=Y;SS=M; 4.820936639
 417949; AL049795; Hs.83004; interleukin 14; none,Armadillo_seg,IBB,WD40; 4.81443299
 439569; AW602166; Hs.222399; CEP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 4.81
 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 4.805063291
 432194; AL040801; Hs.273219; breast cancer anti-estrogen resistance 1; SH3; 4.803191489
 431472; AK001023; Hs.256549; nucleotide binding protein 2 (E.coli Min; fer4_NiH,ParA,APS_kinase,ArsA_ATPase;TM=M;SS=N; 4.800990099
 406690; AA296696; Hs.333418; FYXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 4.795480881
 448950; AF288687; Hs.9275; CGI-152 protein; E1-E2_ATPase,Hydrolase;TM=Y;SS=N; 4.776923077
 427681; AB018263; Hs.284232; tumor necrosis factor receptor superfam; death,TNFR_c6,PH,Xlink,RhoGEF,Metallothio_5;TM=M;SS=M; 4.772196262
 432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH,RhoGAP,SH3;TM=M;SS=N; 4.760115607
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 4.751162791
 419981; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.748
 431657; AI345227; Hs.105448; ESTs, Weakly similar to B34087 hypotheti; pkinase,PA28_alpha,PA28_beta,Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3; 4.746

412958; BE391579; Hs.75087; Fas-activated serine/threonine kinase; none;; 4.736781609
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor;; ig, pkinase; TM=Y; SS=N; 4.733
 419250; AW770185; Hs.356066; U5 snRNP-specific protein, 116 kD; 7tm_1, BAH, zf-CXXC, DNA_methylase; 4.725454546
 417903; NM_002342; Hs.1116; lymphotoxin beta receptor (TNFR superfam; TNFR_c6; TM=M; SS=M; 4.718858132
 5 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK_CoaE;; 4.718836565
 426059; BE292842; Hs.166120; interferon regulatory factor 7; IRF;; 4.718543046
 414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase; TM=M; SS=N; 4.708
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC; TM=Y; SS=M; 4.707920792
 10 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase, DCX; TM=M; SS=N; 4.707671958
 407143; C14076; Hs.332329; EST; none; TM=Y; SS=M; 4.682675815
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 4.681818182
 408806; AW847814; Hs.75608; Homo sapiens cDNA: FLJ21532 fis, clone C; SH3, PDZ, Guanylate_kin, none; 4.680440771
 448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec, MIP; TM=M; SS=M; 4.679841897
 15 418936; AI655499; Hs.161712; ESTs; pkinase, Activin_rec, PDZ, ZU5, death; 4.679180887
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; ig, kringle, pkinase, Fz; TM=Y; SS=M; 4.675342466
 414665; AA160873; Hs.356307; serum amyloid A1; zf-C2H2, BTB, K_tetra, none; 4.674474796
 449843; R85337; Hs.24030; solute carrier family 31 (copper transp; none; TM=Y; SS=M; 4.673701299
 428245; AF151048; Hs.183180; anaphase promoting complex subunit 11 (y; none;; 4.656756757
 20 417088; M54915; Hs.81170; pim-1 oncogene; pkinase; TM=M; SS=N; 4.656190476
 420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TIT3 com; ITAM; TM=M; SS=M; 4.65
 425966; NM_001761; Hs.1973; cyclin F; cyclin, F-box, cyclin_C; TM=M; SS=N; 4.644
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; ig, abhydrolase; 4.640384615
 430603; AA148164; Hs.247280; HBV associated factor; zf-C3HC4, zf-RanBP, pkinase; 4.630653266
 25 419273; BE271180; Hs.293490; ESTs, Weakly similar to I38022 hypotheti; none, none; 4.628
 453880; AI803166; Hs.135121; ESTs, Weakly similar to I38022 hypotheti; HSP70, none; 4.619047619
 459399; BE407712; Hs.153998; creatine kinase, mitochondrial 1 (ubiqui; none, none; 4.618577075
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese, DSPC;; 4.616
 433577; AW007080; Hs.284192; ESTs; none, none; 4.614
 444838; AV651680; Hs.208558; ESTs; Integrin_A, FG-GAP, none; 4.612149533
 30 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/pep; PTR2; TM=Y; SS=N; 4.602
 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ, Guanylate_kin;; 4.596875
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22, Claudin, none; 4.587931035
 433083; AL042759; Hs.191762; ESTs; SH3, PX; TM=M; SS=N; 4.586
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, ; ig; TM=Y; SS=M; 4.58557047
 35 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS;; 4.579087049
 422009; AI742845; Hs.110713; DEK oncogene (DNA binding); SAP;; 4.576347305
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none, lectin_c; 4.57312253
 414561; AI064813; Hs.195155; Homo sapiens amino acid transport system; Aa_trans; TM=Y; SS=N; 4.573015873
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 4.570526316
 40 459053; AI807052; Hs.97792; ESTs; none, 7tm_2, GPS; 4.569230769
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, ig, FAD_Synth, Idh, Idh_C, pkinase;; 4.566195373
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p_like; TM=M; SS=N; 4.56056338
 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.558
 408051; AI623351; Hs.172148; ESTs; PH, RhoGAP, none; 4.552307692
 45 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; eftand, Idl_recept_a;; 4.547761194
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7tm_1, LRR; TM=Y; SS=N; 4.547169811
 426201; AW182614; Hs.128499; ESTs; SH3, none; 4.541666667
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; SS=N; 4.536
 445229; BE276013; Hs.343828; Homo sapiens mRNA for FLJ00086 protein, ; G-alpha; TM=M; SS=N; 4.530588235
 50 413109; AW389845; Hs.110855; ESTs; PHO4, none; 4.529761905
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolo; EGF, cadherin, laminin_G; TM=Y; SS=M; 4.529710145
 402330; ; Target Exon; pkinase, none; 4.528070175
 439238; N47305; Hs.302161; EDG-8 (endothelial differentiation, sph; 7tm_1; TM=Y; SS=M; 4.524
 55 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10, ICE_p20;; 4.523715415
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenas; CBS, IMPDH_C, IMPDH_N, NPD; TM=M; SS=N; 4.522900763
 431429; AF072813; Hs.252831; reticulon 3; Reticulon, Fz, ig, kringle, pkinase; TM=Y; SS=N; 4.512
 424078; AB006625; Hs.139033; paternally expressed 3; zf-C2H2, KRAB, none; 4.512
 420602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS; TM=M; SS=N; 4.51
 60 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1; TM=Y; SS=M; 4.506
 408157; AA047685; Hs.62946; ESTs; none, pkinase; 4.504
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M; SS=Y; 4.50215208
 431326; AW970580; Hs.198689; KIAA0728 protein; none, none; 4.501
 428072; BE258602; Hs.182366; heat shock protein 75; HATPase_c, HSP90; TM=M; SS=N; 4.48828125
 65 415149; X12451; Hs.78056; cathepsin L; Peptidase_C1;; 4.484375
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypept; p450; TM=Y; SS=M; 4.48
 445143; U29171; Hs.378918; casein kinase 1, delta; zf-C3HC4, Filamin, zf-B_box, NHL, pkinase, zf-MIZ; TM=M; SS=N; 4.478092784
 421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen; none; TM=Y; SS=M; 4.477337111
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none; TM=M; SS=N; 4.476
 70 438774; AA431620; Hs.379034; hypothetical protein MGC2745; none, none; 4.474874372
 410726; AI623859; Hs.15936; ESTs; pkinase, pro_isomerase, none; 4.47
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory su; CDK5_activator, none; 4.468
 426485; NM_008207; Hs.170040; platelet-derived growth factor receptor-; ig;; 4.464944649
 433646; AA603319; Hs.155195; ESTs; pou, homeobox, lig_chan, ANF_receptor; 4.458
 75 410293; AK000047; Hs.61960; hypothetical protein; K_tetra; TM=M; SS=N; 4.453020134
 453464; AI884911; Hs.32889; receptor (calcitonin) activity modifying; none; TM=Y; SS=N; 4.448198198
 410593; AW770280; Hs.36258; ESTs, Moderately similar to JC5238 galac; SH3, PDZ, Guanylate_kin, none; 4.446927374
 441455; AJ271671; Hs.7854; zinc/iron regulated transporter-like; Zip; TM=Y; SS=M; 4.445010183
 453054; R40334; Hs.89463; potassium large conductance calcium-acti; none, none; 4.436480187
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 4.433411215
 80 411825; AK000334; Hs.352415; solute carrier family 39 (zinc transport; SNF, Zip; TM=Y; SS=N; 4.432765152
 428376; AF119665; Hs.184011; pyrophosphatase (inorganic); Pyrophosphatase; TM=M; SS=N; 4.428571429
 429592; AB029041; Hs.209646; KIAA1118 protein; Troponin_Exo_endo_phos, IQ; TM=M; SS=N; 4.428
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); ank, DAGKa, DAGKc, DAG_PE-bind; TM=M; SS=N; 4.426229508

- 427138; N77624; Hs.173717; phosphatidic acid phosphatase type 2B; PAP2,none; 4.4234375
 414496; W73853; Hs.355424; ESTs; pkinase,F5_F8_type_C,adh_short,none; 4.42114094
 429432; A1678059; Hs.202676; synaptonemal complex protein 2; none;TM=M;SS=N; 4.42
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone;TM=M;SS=N; 4.419207317
 5 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L2; none;TM=M;SS=N; 4.418181818
 435411; AW444619; Hs.138211; ESTs; none,pkinase; 4.414
 414581; AA256213; Hs.72010; ESTs; none,Carn_acyltransf,Choline_kinase,SCO1-SenC,Glycos_transf_3,Glycos_trans_3N; 4.41
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domain; death,DED;; 4.408523909
 10 442259; A1690269; Hs.201345; ESTs; Acetyltransf,RhoGAP,FCH,SH3,Kelch,fn3; 4.406
 415860; D56051; Hs.78888; diazepam binding inhibitor (GABA receptor; ACBP;TM=M;SS=N; 4.404678363
 434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPC;TM=M;SS=N; 4.404
 404440; ; NM_021048;Homo sapiens melanoma antigen; MAGE;TM=M;SS=N; 4.4
 435542; AA687376; Hs.351226; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 4.394
 15 413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;SS=N; 4.39028777
 435732; AF229178; Hs.123136; leucine rich repeat and death domain con; none,none; 4.38490566
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm_1,none; 4.382129278
 425749; AW328587; Hs.159448; surfeit 2; none;; 4.382
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=Y;SS=N; 4.381422925
 10 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 4.380681818
 431837; T79326; Hs.331967; olfactory receptor, family 2, subfamily ; none,7tm_3,sushi,ANF_receptor; 4.376
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm,pkinase;; 4.370247934
 434876; AF160477; Hs.61460; Ig superfamily receptor LNIR; ig,Rhbd_glycop;TM=Y;SS=M; 4.37
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans;TM=Y;SS=M; 4.367777778
 25 403912; ; C5000394*:gij12737280[ref]XP_006682.2] k; none;TM=M;SS=N; 4.367684478
 426268; AF083420; Hs.168913; serine/threonine kinase 24 (Ste20, yeast; pkinase;; 4.366348449
 434263; N34895; Hs.79187; ESTs; ig,none; 4.358527132
 404760; ; Target Exon; cadherin;TM=M;SS=M; 4.356
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M;SS=N; 4.35472973
 20 420757; X78592; Hs.99915; androgen receptor (dihydrotestosterone r; hormone_rec,zf-C4,Androgen_recep;TM=M;SS=N; 4.354
 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chlo; none;TM=Y;SS=N; 4.353244838
 431674; AA088901; Hs.301642; G-protein coupled receptor; none,GCV_H; 4.35
 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M;SS=N; 4.347893916
 447719; BE387402; Hs.19333; hypothetical protein FLJ10349; adenylatekinase,ATP-bind;TM=M;SS=N; 4.346007605
 35 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerev; Acetyltransf;TM=M;SS=N; 4.344
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone K; none,none; 4.334722222
 411768; NM_013371; Hs.71979; interleukin 19; IL10;; 4.322
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2;TM=M;SS=N; 4.320359281
 425964; AW889928; Hs.9071; progesterone membrane binding protein; homeobox,none; 4.318867925
 40 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; rrm;TM=M;SS=N; 4.316573557
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;; 4.316
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; none,Cys_knot; 4.314728682
 438899; AF085833; Hs.135624; ESTs; none,PI3_P14_Kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B; 4.314084507
 418883; BE387036; Hs.12111; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 4.312121212
 45 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; IMP4;TM=M;SS=N; 4.304407714
 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg,HEAT;TM=M;SS=N; 4.304
 430017; AA263172; Hs.35; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=M;SS=M; 4.302
 447224; BE617125; Hs.142076; gb:601441664F1 NIH_MGC_65 Homo sapiens c; none;NA;NA; 4.302
 425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;SS=N; 4.301639344
 50 454042; H22570; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 4.30141844
 446143; BE245342; Hs.306079; sec61 homolog; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 4.300872093
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_HUMAN ALU S; none,rm; 4.292620865
 432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2;TM=M;SS=N; 4.290258449
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 4.288405797
 55 421921; H83363; Hs.355993; translocase of inner mitochondrial membr; zf-Tim10,DDP,ethand,CH,spectrin,serpin;TM=M;SS=N; 4.284
 448564; AL044962; Hs.21453; inositol 1,4,5-trisphosphate 3-kinase C; IPK;; 4.28057554
 453941; U39817; Hs.36820; Bloom syndrome; DEAD,helicase_C,HRDC;TM=M;SS=N; 4.28
 437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor ; Tropomyosin,pkinase,LRR,LRRCT,Hydantoinase_B,Hydantoinase_A;TM=M;SS=N; 4.277477478
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,Integrin_B; 4.276162791
 60 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none,none; 4.273927393
 438012; AA393254; Hs.43619; ESTs; Armadillo_seg,none; 4.273134328
 409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG;TM=M;SS=N; 4.273109244
 418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;SS=N; 4.272123894
 65 415214; A1445236; Hs.125124; EphB2; fn3,pkinase,SAM,EPH_Ibd;TM=Y;SS=M; 4.268
 438233; W52448; Hs.56147; ESTs; Neur_chan_LBD,Neur_chan_memb,MAGE; 4.26284585
 429019; AA443280; Hs.279907; myosin IIIA; myosin_head,pkinase,PRK,IQ;TM=M;SS=N; 4.262
 424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; ldn,ldh_C,SH3,pkinase,UBA;TM=M;SS=N; 4.258695652
 453655; AW960427; Hs.342874; transforming growth factor, beta recepto; zona_pellucida,none; 4.257208766
 70 417414; AA434589; Hs.367676; dUTP pyrophosphatase; dUTPase,KRAB; 4.251785714
 453905; NM_002314; Hs.36566; LIM domain kinase 1; pkinase,LIM,PDZ,zf-PARP;TM=M;SS=N; 4.249116608
 424232; AB015982; Hs.143460; protein kinase C, nu; pkinase,DAG_PE-bind,PH;TM=M;SS=N; 4.247692308
 404883; ; ENSP00000216009:Sodium-glucose cotranspo; SSF;TM=Y;SS=M; 4.242424242
 412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH_Ibd;TM=Y;SS=M; 4.239285714
 75 411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none,none; 4.237313433
 436957; AA902488; Hs.122952; ESTs; none,DAGKc,DAGKa,RA,DAG_PE-bind; 4.236
 452568; AA805634; Hs.300870; Homo sapiens mRNA; cDNA DKFZp547M072 (fr; PI3_P14_kinase;TM=M;SS=M; 4.23537415
 433535; AF111106; Hs.3382; protein phosphatase 4, regulatory subuni; HEAT;TM=M;SS=N; 4.234793187
 432728; NM_006979; Hs.278721; HLA class II region expressed gene KE4; Zip,lig_chan;TM=Y;SS=M; 4.234545455
 80 416350; AF188625; Hs.189507; phospholipase A2, group IID; phoslip;TM=M;SS=Y; 4.234
 409533; AW969543; Hs.144609; mitogen-activated protein kinase kinase ; Peptidase_C48,none; 4.230666667
 427127; AW802254; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 4.228009259
 403362; ; NM_001615*:Homo sapiens actin, gamma 2 ; actin;; 4.22688478
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;; 4.226388889

428897; AJ245719; Hs.194385; hypothetical protein FLJ20234; SH2; TM=M; SS=N; 4.224731183
 425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinase; SH2, SH3, pkinase, PH, BTK; TM=M; SS=N; 4.223684211
 418566; C21220; Hs.321717; hypothetical protein FLJ10875; zf-C2H2, BTB, K_tetra, 7tm_1; 4.222807018
 454098; W27953; Hs.217493; Plakophilin; none, none; 4.22
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); pkinase, FHA, DnaJ; TM=M; SS=N; 4.21875
 419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4; TM=Y; SS=M; 4.217130215
 436756; Z18364; Hs.198298; v-src avian sarcoma (Schmidt-Ruppin A-2); none, none; 4.216
 450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2; TM=M; SS=N; 4.215163934
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand; 4.212041885
 432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; none, DS, UPF0139, Glyco_hydro_38; 4.207407407
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain, rrm; TM=M; SS=N; 4.206
 432284; AA532807; Hs.287740; ESTs; pkinase, none; 4.205454546
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase, RIO1; TM=M; SS=N; 4.204142012
 450056; BE047394; Hs.502; ESTs; Weakly similar to S71512 hypothetl; ABC_tran, ABC_membrane, Ig, MHC_II_beta, SRP54, proteasome, ABC_membrane, ABC_tran; 4.202572347
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subu; PC_rep; TM=M; SS=N; 4.202061856
 425394; AA356730; Hs.323949; kangai 1 (suppression of tumorigenicity); transmembrane4, none; 4.195014663
 449335; AW150717; Hs.345728; STAT induced STAT inhibitor 3; SH2; TM=M; SS=N; 4.192248062
 415023; AA932146; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none, NA; NA; 4.192
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none; TM=M; SS=Y; 4.191878981
 445330; R52656; Hs.21691; ESTs; 7tm_1, none; 4.189922481
 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX, EXS; TM=Y; SS=N; 4.188333333
 434633; AI189587; Hs.120915; ESTs; SH3, PH, RhoGAP, none; 4.187106918
 452908; AB001451; Hs.30965; neuronal Shc adaptor homolog; SH2, PID, Zn_carbOpept; TM=M; SS=N; 4.186885246
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2, CytC_asm, GPS; TM=Y; SS=M; 3.930957684
 432201; AI538613; Hs.298241; Transmembrane protease, serine 3; ldl_receptL_a, trypsin; TM=Y; SS=M; 3.893103448
 428969; AF120274; Hs.194689; artemin; TGF-beta; 3.884030418
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ig; TM=Y; SS=M; 3.831669044
 432305; M62402; Hs.274313; insulin-like growth factor binding prole; thyroglobulin_1, IGFBP, A2M_N; TM=M; SS=N; 3.742996346
 405547; ; NM_018833; Homo sapiens transporter 2, A; ABC_tran, SRP54, ABC_membrane; TM=Y; SS=M; 3.676
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none; TM=M; SS=Y; 3.634
 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 3.562
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q, Collagen; 3.49
 405546; ; NM_018833; Homo sapiens transporter 2, A; ABC_tran, SRP54, ABC_membrane; TM=Y; SS=M; 3.422661871
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length insert cDN; none, none; 3.402
 404210; ; NM_005936; Homo sapiens myeloid/lymphoid; FHA, PDZ, RA, DIL; TM=M; SS=N; 3.368807339
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase, pkinase_C; 3.213402062
 418678; NM_001327; Hs.87225; cancer/testis antigen (NY-ESO-1); none; TM=M; SS=N; 3.084
 451106; BE382701; Hs.25960; N-MYC oncogene; HLH, Myc_N_term; TM=M; SS=N; 1.55

TABLE 17B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
418869	12789_14	AA229762 AA230035

TABLE 17C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035, 122804-122921, 124019-12416
401781	7249190	Minus	83215-83435, 83531-83656, 83740-83901, 8423
405484	5922025	Plus	199214-199579, 199672-199920, 200262-20049
405932	7767812	Minus	123525-123713
400517	9796686	Minus	49996-50346
402328	4464283	Minus	13758-13922, 14558-14752
405545	1054740	Plus	118677-118807, 119091-119296, 121626-12182
402330	4464283	Minus	15325-15380, 15484-15588, 15842-15915
404440	7528051	Plus	80430-81581
403912	7710730	Minus	72000-72290, 72431-72700, 72929-73199
404760	7767724	Plus	223266-223352, 224472-224585
404883	5101762	Minus	94626-94730, 96998-97069
403362	8571772	Plus	64099-64260
405547	1054740	Plus	124361-124520, 124914-125050
405546	1054740	Plus	124010-124183
404210	5006246	Plus	169926-170121

Table 18A: 194 Up-Regulated Genes in Uterine Cancer Versus Normal Adult Tissues

Table 18A lists about 194 genes up-regulated in uterine cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" uterine cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" uterine cancer level was set to the 2nd highest amongst uterine cancers. The "average" normal adult tissue level was set to the 90th percentile value amongst non-malignant tissues. In order to remove gene-specific background

levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor vs. normal tissue			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
15	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	55.7
	435094	AI560129	Hs.277523	EST	45.2
	438817	AI023799	Hs.163242	ESTs	42.6
	421478	AI683243	Hs.97258	ESTs	35.2
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	27.3
20	450451	AW591528	Hs.202072	ESTs	26.0
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252	24.8
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49) (HG38)	24.2
	438993	AA828995	Hs.52620	integrin; beta 8	16.7
	436775	AA731111	Hs.291891	ESTs	14.3
25	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDNA clo	13.5
	441377	BE218239	Hs.202656	ESTs	13.5
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	12.3
	400292	AA250737	Hs.72472	BMPR-Ib; bone morphogenetic protein receptor Ib	10.7
	403899			predicted exon	10.1
30	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA	10.0
	447350	AI375572	Hs.1939	HER4 (c-erb-B4)	9.8
	453964	AI961486	Hs.12744	ESTs	9.7
	443830	AI142095	Hs.143273	ESTs	9.1
	459325	AW088369	Hs.282184	ESTs	9.0
35	415245	N59650	Hs.27252	ESTs	8.9
	446608	N75217	Hs.257846	ESTs	8.9
	426635	BE395109	Hs.129327	ESTs	8.8
	433426	H69125	Hs.133525	ESTs	8.7
	437960	AI669586	Hs.222194	ESTs	8.5
40	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b [H	8.3
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.s	7.3
	447835	AW591623	Hs.164129	ESTs	7.2
	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone THYRO10	7.1
	412925	AI089319	Hs.179243	ESTs	7.0
45	408562	AI436323	Hs.31141	Roundabout homolog 2 transmembrane receptor (robo2)	7.0
	429272	W25140	Hs.110667	ESTs	6.9
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAM	6.3
	437938	AI950087		ESTs; Weakly similar to Gag-Pol polyprotein	6.2
	420610	AI683183	Hs.99348	distal-less homeo box 5	6.2
50	448672	AI955511	Hs.225106	ESTs	6.1
	452461	N78223	Hs.108106	transcription factor	6.1
	413335	AI613318	Hs.48442	ESTs	6.1
	449611	AI970394	Hs.197075	ESTs	6.0
	449260	AA741180	Hs.29879	ESTs	6.0
55	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	6.0
	443715	AI583187	Hs.9700	cyclin E1	6.0
	432113	AA935065	Hs.152385	ESTs	5.9
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.7
	410658	AW105231	Hs.192035	ESTs	5.7
60	426465	AI758948		gb:ty16f07.x1 NCI_CGAP_U13 Homo sapiens cDNA	5.7
	446704	AI337228	Hs.197083	ESTs	5.5
	419503	AA243642	Hs.137422	ESTs	5.5
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	5.4
	436076	AI193277	Hs.120954	ESTs	5.4
65	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.3
	445258	AI635931	Hs.147613	ESTs	5.3
	440901	AA909358	Hs.128612	ESTs	5.3
	434636	AA083764	Hs.241334	ESTs	5.3
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone LNG020	5.2
70	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.2
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapiens cDN	5.2
	436787	AA908554	Hs.192756	ESTs	5.2
	400301	X03635	Hs.1657	Estrogen receptor 1	5.1
	428771	AB028992	Hs.193143	KIAA1069 protein	5.1
75	444929	AI685841	Hs.161354	ESTs	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
	405609			predicted exon	5.0
	410102	AW248508	Hs.279727	ESTs;	5.0
	433283	BE041135	Hs.175622	ESTs	4.8
80	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	4.8
	410247	AF181721	Hs.61345	RU2S	4.7
	422589	AA312735	Hs.179725	ESTs	4.7
	452771	T05477		gb:EST03366 Fetal brain, Stratagene (cat93620	4.7
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens cDNA	4.7
	420440	NM_002407	Hs.97644	mammaglobin 2	4.6
	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	4.6

	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypept	4.6
	424115	AA335497	Hs.293965	ESTs	4.6
	414245	BE148072	Hs.75850	WAS protein family, member 1	4.6
5	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	4.5
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	4.5
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone LNG076	4.4
	458861	AI630223		PHD finger DNA binding protein isoform 1 (int	4.4
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	4.3
10	420149	AA255920	Hs.88095	ESTs	4.3
	433479	AW511459	Hs.249972	ESTs	4.3
	449416	AI651016	Hs.246311	ESTs	4.3
	457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone HEP106	4.3
	450109	AI539295	Hs.17967	ESTs	4.3
	436954	AA740151	Hs.130425	ESTs	4.3
15	415511	AI732617	Hs.182362	ESTs	4.3
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT2RM40	4.3
	406411			predicted exon	4.2
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog	4.2
20	416456	H57052	Hs.176626	hypothetical protein EDAG-1	4.2
	454692	AW813350		gb:MR3-ST0192-100100-024-g07	4.1
	452249	BE394412	Hs.61252	ESTs	4.1
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	4.1
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN ALU SUB	4.1
25	434988	AI418055	Hs.161160	ESTs	4.1
	423515	AA327017	Hs.162204	ESTs	4.0
	435407	AI149774	Hs.117178	ESTs	4.0
	440886	AW511032	Hs.190516	ESTs	4.0
	444783	AK001468	Hs.62180	ESTs	4.0
	452039	AI922988	Hs.172510	ESTs	4.0
30	407300	AA102616	Hs.120769	Homo sapiens cDNA FLJ20463 fis, clone KAT0614	4.0
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	4.0
	449433	AI672096	Hs.9012	ESTs	3.9
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone NT2RP20	3.9
35	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFp586i1518	3.9
	453096	AW294631	Hs.11325	ESTs	3.9
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP010	3.9
	445034	AW293376	Hs.160323	ESTs	3.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	3.8
40	422219	AW976073		gb:EST390182 MAGE resequences	3.8
	440304	BE159984	Hs.125395	ESTs	3.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFp434P228	3.8
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK	3.8
	400250			predicted exon	3.8
45	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN	3.8
	420092	AA814043	Hs.88045	ESTs	3.8
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	3.8
	437212	AI765021	Hs.210775	ESTs	3.8
	409867	AW502161		gb:UI-HF-BR0p-ajr-g-12-0-UI.r1 NIH_MGC_52	3.7
50	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	3.7
	427119	AW880562	Hs.114574	ESTs	3.7
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234	3.7
	434539	AW748078	Hs.214410	ESTs	3.7
	424717	H03754	Hs.152213	wingless-type MMTV integration site family	3.7
55	412078	X69699	Hs.73149	paired box gene 8 (PAX-8)	3.7
	447342	AI199268	Hs.19322	ESTs; Weakly similar to !!! ALU SUBFAMILY J	3.7
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.7
	446619	AI076643	Hs.313	secreted phosphoprotein 1 (osteopontin)	3.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDNA clo	3.7
60	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapiens c	3.6
	441285	NM_002374	Hs.167	microtubule-associated protein 2	3.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	3.6
	417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC052	3.6
	441484	AA935481	Hs.58972	ESTs	3.6
	415802	AA169515	Hs.6006	ESTs	3.6
65	448112	AW245919	Hs.301018	ESTs	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	3.6
	402606			predicted exon	3.6
	407905	AW103655	Hs.252905	ESTs	3.6
70	424917	AI636208	Hs.96901	Homo sapiens cDNA: FLJ23049 fis, clone LNG025	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	3.6
	451842	AI820539	Hs.267087	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.6
	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	3.6
	431731	BE266322	Hs.211374	ESTs, Weakly similar to SP49_HUMAN SPLICEOSOM	3.6
75	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retinal sh	3.6
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	3.6
	406030			predicted exon	3.5
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA Libr	3.5
	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.5
80	437641	AA811452	Hs.291911	ESTs	3.5
	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN	3.4
	443450	N66045	Hs.133529	ESTs	3.4
	457438	NM_014053	Hs.270594	FLVCR protein	3.4
	451254	AI571016	Hs.172967	ESTs	3.4

5	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.4
	427778	AA412323	Hs.105323	ESTs	3.3
	435031	AI632091	Hs.116877	ESTs	3.3
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	3.3
	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-187J11 on c	3.3
	431548	AI834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP30	3.2
	432415	T16971	Hs.289014	ESTs	3.2
	423126	AA322245	Hs.290165	ESTs	3.2
10	433420	AI674093	Hs.293961	ESTs	3.2
	435174	AA687378	Hs.194624	ESTs	3.2
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moiety X	3.2
	452588	AA889120	Hs.110637	Homeo box A10	3.2
	427304	AA761526	Hs.163853	ESTs	3.2
15	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (from cl	3.1
	417728	AW138437	Hs.24790	KIAA1573 protein	3.1
	419356	AI656166	Hs.7331	ESTs	3.1
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [3.1
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrolase 1	3.1
20	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone COL064	3.1
	405174			predicted exon	3.1
	403776			predicted exon	3.1
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily, m	3.1
	431255	AA497043	Hs.115685	ESTs	3.1
25	442353	BE379594	Hs.49136	ESTs	3.1
	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (formerl	3.1
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	3.1
	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens cDNA c	3.1
	406400			kallikrein 8 (neuropsin/ovasin)	3.0
30	439949	AW979197	Hs.292073	ESTs	3.0
	430704	AW813091		gb:RC3-ST0186-240400-111-d07 ST0186 Homo sapi	3.0
	401517			predicted exon	3.0
	417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncog	3.0
	435267	N23797	Hs.110114	ESTs	3.0
35	426384	AI472078		ESTs	3.0
	422797	AB033064	Hs.120908	KIAA1238 protein	3.0
	428832	AA578229		gb:n122b12.s1 NCI_CGAP_HSC1 Homo sapiens cDNA	3.0
	449722	BE280074	Hs.23960	cyclin B1	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A	3.0
40	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	3.0

TABLE 18B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
50	409745	115237_1 AA077391 AI347618 AI361453 AI088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
	409867	1156530_1 AW502161 AW502587 AW502345
	422219	213547_1 AW978073 AW978072 AA807550 AA306567
	422689	219896_1 AW856665 AA315006 AW954733
	426384	266211_1 AI472078 AA377209 AA865807
55	426465	267664_1 AI758948 AA379527 AA379948 AA379262 AW963933
	428832	296144_1 AA578229 AA436432 AA481375 AA481363
	430704	322217_1 AW813091 AW206655 AA484440
	431322	331543_1 AW970622 AA503009 AA502998 AA502989 AA502805 T92188
60	437938	44573_2 AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598
		AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328517 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
		AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915
		AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975
		AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669
		AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628
65		N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056
		AI002839 R67840 AA300207 AW959581 T63226 F04005
	438993	467651_1 AA828995 AA834879 AI926361
	442438	542469_1 AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
	443613	575391_1 AI079356 W23287
70	449034	794817_1 AI624049 AW117770 AI858360
	451105	859083_1 AI761324 AW880941 AW880937
	452771	930983_1 T05477 T07855 AI917711
	454392	115882_1 BE260893 AA078319 R85057 AW803024 H85811 AA078293
	454692	1229118_1 AW813350 AW816082 AW813476 AW813383
75	455666	1349545_1 BE065813 BE065788 BE065889 BE065832
	458154	491768_1 AW816379 AA888282 AA879046 AA879195
	458861	798085_1 AI630223 AI630470

TABLE 18C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

5	Pkey	Ref	Strand	Nt_position
	401517	7677912	Plus	29278-29770
	402606	9909429	Minus	81747-82094
	403776	7770611	Minus	1414-1513,1624-1756
10	403899	7381715	Minus	9144-9350
	405174	7108030	Minus	102814-103063
	405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
	406030	8312328	Minus	96123-96547
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
15	406411	9256407	Plus	7400-7527

Table 19A: 225 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, UTERINE Cancer Versus Normal Adult Tissues

Table 19A lists about 225 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. Ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor vs. normal tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	PSDomain	R1
35	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	TM	27.3
	438993	AA828995	Hs.52620	integrin; beta 8	SS,TM,integrin_B	16.7
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stroma	SS,hemopexin	12.3
	446608	N75217	Hs.257846	ESTs	TM	8.9
	433426	H69125	Hs.133525	ESTs	TM	8.7
40	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clo	TM,PAX	7.1
	408562	AI436323	Hs.31141	Roundabout homolog 2 transmembrane	SS,TM,ig,fn3	7.0
	420610	AI683183	Hs.99348	distal-less homeo box 5	TM,homeobox	6.2
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rab	TM,kinesin	6.0
	443715	AI583187	Hs.9700	cyclin E1	TM,cyclin	6.0
45	432113	AA935065	Hs.152385	ESTs	TM	5.9
	419503	AA243642	Hs.137422	ESTs	TM	5.5
	444342	NM_014398	Hs.10887	similar to lysosome-associated memb	TM,Lamp	5.4
	436076	AI193277	Hs.120954	ESTs	TM	5.4
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	TM,hemopexin	5.3
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.2
50	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo s	TM	5.2
	400301	X03635	Hs.1657	Estrogen receptor 1	TM,hormone_rec,zf-C4	5.1
	405609			predicted exon	TM,Myosin_tail,myosin_head	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazol	TM	5.0
55	410102	AW248508	Hs.279727	ESTs;	SS,TM,	5.0
	433283	BE041135	Hs.175622	ESTs	TM	4.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gen	TM	4.8
	410247	AF181721	Hs.61345	RU2S	TM	4.7
	422589	AA312735	Hs.179725	ESTs	TM	4.7
60	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sap	TM	4.7
	420440	NM_002407	Hs.97644	mammaglobin 2	TM,Uteroglobin	4.6
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediat	TM,Ribosomal_S27e	4.6
	424115	AA335497	Hs.293965	ESTs	TM	4.6
	414245	BE148072	Hs.75850	WAS protein family, member 1	TM,WH2	4.6
65	458861	AI630223		PHD finger DNA binding protein isof	TM,PHD	4.4
	449416	AI651016	Hs.246311	ESTs	SS,TM,	4.3
	420149	AA255920	Hs.88095	ESTs	TM	4.3
	433479	AW511459	Hs.249972	ESTs	TM	4.3
	457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, cl	TM	4.3
70	406411			predicted exon	TM,vwa,FG-GAP	4.2
	416456	H57052	Hs.176626	hypothetical protein EDAG-1	TM	4.2
	454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192	TM	4.1
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	TM	4.1
	434988	AI418055	Hs.161160	ESTs	TM	4.1
75	444783	AK001468	Hs.62180	ESTs	TM,PH	4.0
	440886	AW511032	Hs.190516	ESTs	TM,FG-GAP	4.0
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HU	TM,Glyco_transf_29,TEA	4.0
	445034	AW293376	Hs.160323	ESTs	TM	3.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box	TM,HMG_box	3.8
80	400250			predicted exon	TM,Hist_deacetyl	3.8
	428227	AA321649	Hs.2248	interferon-gamma induced protein	TM,IL8	3.8
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 T	TM,Kunitz_BPTI,G-gamma	3.8
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234	TM,WW	3.7
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	TM	3.7

	413472	BE242870	Hs.75379	solute carrier family 1 (glial high	TM,SDF	3.7
	447342	AI199268	Hs.19322	ESTs; Weakly similar to !!! ALU SU	TM	3.7
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopon	TM,Osteopontin	3.7
5	453891	AB037751	Hs.36353	Homo sapiens mRNA full length inser	TM	3.7
	441285	NM_002374	Hs.167	microtubule-associated protein 2	TM,tubulin-binding	3.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuro	TM,Thymosin	3.6
	441484	AA935481	Hs.58972	ESTs	TM,fn3,ig,Y_phosphatase	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matril	SS,Peptidase_M10	3.6
10	407905	AW103655	Hs.252905	ESTs	SS,TM,Ephrin	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellula	SS,TM,	3.6
	402606			predicted exon	TM	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1	TM	3.6
	437641	AA811452	Hs.291911	ESTs	TM	3.5
15	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFA	TM,IQ,Rlla	3.4
	443450	N66045	Hs.133529	ESTs	TM	3.4
	457438	NM_014053	Hs.270594	FLVCR protein	TM	3.4
	435031	AI632091	Hs.116877	ESTs	TM,RhoGEF,PH	3.3
	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-1	TM	3.3
20	435174	AA687378	Hs.194624	ESTs	TM,SPRY	3.2
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linke	TM,mulT	3.2
	433420	AI674093	Hs.293961	ESTs	TM	3.2
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E23	TM	3.1
	417728	AW138437	Hs.24790	KIAA1573 protein	TM	3.1
25	403776			predicted exon	SS,TM,IL8	3.1
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) supe	TM,TNF	3.1
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, cl	TM,Ets	3.1
	405174			predicted exon	TM	3.1
30	431255	AA497043	Hs.115685	ESTs	TM	3.1
	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog	TM,homeobox	3.1
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	TM,trypsin,pro_isomerase	3.1
	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapi	TM	3.1
	406400			kallikrein 8 (neuropsin/ovasin)	TM,trypsin	3.0
	401517			predicted exon	TM,HMG14_17	3.0
35	417830	AW504786	Hs.132808	epithelial cell transforming sequen	TM	3.0
	435267	N23797	Hs.110114	ESTs	TM	3.0
	449722	BE280074	Hs.23960	cyclin B1	TM,cyclin	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2	TM,ank	3.0
40	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297	TM,SNF2_N	3.0
	441794	AW197794	Hs.253338	ESTs	TM,ank	2.9
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractura	TM,EGF,TB	2.9
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic pr	SS,wap	2.9
	418113	AI272141	Hs.83484	ESTs	TM,HMG_box	2.9
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome	TM,TEA	2.9
45	431989	AW972870	Hs.291069	ESTs	SS	2.9
	400284			Estrogen receptor 1	TM,hormone_rec,zf-C4	2.9
	438578	AA811244	Hs.164168	ESTs	TM,formyl_transf,AIRS,GARS	2.9
	423513	AF035960	Hs.129719	transglutaminase 5	TM,Transglutamin_N	2.8
	448966	AW372914	Hs.287462	Homo sapiens cDNA FLJ11875 fis, clo	TM	2.8
50	431870	AW449902	Hs.105500	ESTs	TM,MHC_I,ig	2.8
	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276	TM	2.8
	438777	AA825487	Hs.142179	ESTs, Weakly similar to ORF2 [M.mus	TM	2.8
	451807	W52854	Hs.27099	DKFZP564J0863 protein	TM	2.8
	433326	AI379486	Hs.159430	ESTs	TM	2.8
55	448221	BE622615		gb:601440775T1 NIH_MGC_72 Homo sapi	TM	2.8
	448141	AI471598	Hs.197531	ESTs	TM,bZIP	2.8
	456311	AA225632	Hs.190016	ESTs	TM,Sec7	2.8
	405454			predicted exon	TM	2.8
60	459287	AL079369		gb:DKFZp564G2378_r1 564 (synonym: h	TM	2.8
	438935	H40665	Hs.31564	ESTs	TM	2.7
	421312	AA824627	Hs.291670	ESTs	TM,G-patch	2.7
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	TM,ABC_membrane,ABC_tran	2.7
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clo	TM	2.7
	417956	AA210704	Hs.190465	ESTs	SS,sushi	2.7
65	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,EGF	2.7
	448089	AI467945	Hs.173696	ESTs	SS,TM,	2.6
	446643	AA194417	Hs.282060	ESTs	TM,Clat_adaptor_s	2.6
	456671	AB011142	Hs.114293	KIAA0570 gene product	TM	2.6
	457256	AA459443	Hs.231816	ESTs	SS	2.6
70	438986	AF085888	Hs.269307	ESTs	TM,Spin-Ssty	2.5
	435313	AI769400	Hs.189729	ESTs	TM,MBD	2.5
	417351	T90278	Hs.15049	ESTs	TM,CH	2.5
	412198	AA937111	Hs.69165	ESTs	TM	2.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 k	TM,ubiquitin	2.5
75	421502	AF111856	Hs.105039	solute carrier family 34 (sodium ph	TM,Na_Pi_cotrans	2.5
	418092	R45154	Hs.106604	ESTs	TM,pkinase	2.5
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (TM,FG-GAP	2.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	TM,ENTH,LWEEQ	2.5
80	431974	AW972689	Hs.200934	ESTs	TM,bZIP	2.5
	438209	AL120659	Hs.6111	KIAA0307 gene product	TM,HLH,PAS	2.5
	447578	AA912347	Hs.136585	ESTs	TM	2.5
	414812	X72755	Hs.77367	monokine induced by gamma interfero	SS,IL8	2.5
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase	TM,Glyco_transf_29	2.4
	416402	NM_000715	Hs.1012	complement component 4-binding prot	TM,sushi	2.4

5	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HU	TM	2.4
	428242	H55709	Hs.2250	leukemia inhibitory factor (choline	SS,LIF_OSM	2.4
	417693	AW959741	Hs.40368	adaptor-related protein complex 1,	TM,ClaI_adaptor_s	2.4
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Hom	TM,HECT	2.4
	436311	AA708958	Hs.168732	ESTs	TM	2.4
	426920	AA393351	Hs.132121	ESTs	TM	2.4
	426698	AA394104	Hs.97489	ESTs	TM	2.4
	443426	AF098158	Hs.9329	Homo sapiens mRNA for fls353, compl	TM	2.4
10	406815	AA833930	Hs.288036	IRNA isopentenylpyrophosphate trans	TM,IPPT	2.4
	434808	AF155108	Hs.256150	ESTs, Highly similar to NY-REN-41 a	TM	2.3
	432441	AW292425	Hs.163484	EST	TM,Fork_head	2.3
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQ	TM	2.3
	402298			predicted exon	TM,zf-C2H2,KRAB	2.3
15	435542	AA687376	Hs.269533	ESTs	TM	2.3
	442952	AI743261	Hs.131860	ESTs	TM	2.3
	418203	X54942	Hs.83758	CDC28 protein kinase 2	TM,CKS	2.3
	429228	AI553633	Hs.104985	ESTs	TM	2.3
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	TM,SH3	2.3
20	447570	AI868315	Hs.99669	ESTs	TM,PHD	2.3
	405032			predicted exon	TM,FMO-like	2.3
	416566	NM_003914	Hs.79378	cyclin A1	TM,cyclin	2.3
	420900	AL045633	Hs.44269	ESTs	TM,FAD_binding_5	2.3
	430563	AA481269	Hs.178381	ESTs	TM,ABC_membrane,p450	2.3
25	417372	T99755	Hs.290814	ESTs	TM	2.3
	449083	AI948808	Hs.191144	ESTs	TM	2.3
	410361	BE391804	Hs.62661	guanylate binding protein 1, interf	TM,GBP	2.3
	434131	AI858275	Hs.143659	ESTs	TM	2.3
	431846	BE019924	Hs.271580	Uroplakin 1B	TM,transmembrane4	2.3
30	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific	TM	2.3
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	TM	2.3
	445870	AW410053	Hs.13406	syntaxin 18	TM	2.3
	430639	AW025427	Hs.233552	ESTs	TM,pkinase	2.3
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfam	SS,TM,	2.3
35	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	SS,TM,Cu-oxidase	2.2
	411558	AA102670	Hs.70725	*Human GABA-A receptor pi subunit m	TM,neur_chan	2.2
	408380	AF123050	Hs.44532	diubiquitin	TM,7tm_3,ANF_receptor	2.2
	403721			predicted exon	TM	2.2
	440711	AA904389	Hs.143511	ESTs	TM,rrm	2.2
40	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1	TM,efhand	2.2
	422956	BE545072	Hs.122579	ESTs	TM	2.2
	433482	AI953499	Hs.152617	ESTs	TM	2.2
	431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fis, cl	TM	2.2
	420777	AA280223	Hs.130865	ESTs	TM	2.2
45	446659	AI335361	Hs.226376	ESTs	TM	2.2
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	TM	2.2
	422282	AF019225	Hs.114309	apolipoprotein L	TM	2.2
	431701	AW935490	Hs.14658	ESTs	TM,Occludin	2.2
	426910	AA470023	Hs.190089	ESTs	TM,MMR_HSR1	2.2
50	405636		Hs.153595	predicted exon	SS,TM,EGF_idl_recept_a	2.2
	401933			predicted exon	TM,ion_trans	2.1
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed pro	TM	2.1
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 pr	TM	2.1
	410664	NM_006033	Hs.65370	lipase, endothelial	SS,TM,Ribosomal_L22,lipase	2.1
55	449378	AW664026	Hs.59892	ESTs	TM	2.1
	433345	AI681545	Hs.152982	EST cluster (not in UniGene)	TM	2.1
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase	SS,TM,Branch	2.1
	431832	AW276866	Hs.192715	ESTs	TM,Ets,SAM_PNT	2.1
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating prot	TM,kinesin_abhydrolase_2	2.1
60	423049	X59373	Hs.188023	ESTs	TM,homeobox	2.1
	427510	Z47542	Hs.179312	small nuclear RNA activating comple	TM	2.1
	418076	R61388	Hs.6724	ESTs	TM	2.1
	413670	AB000115	Hs.75470	hypothetical protein, expressed in	TM	2.1
	429183	AB014604	Hs.197955	KIAA0704 protein	TM	2.1
65	439031	AF075079		gb:Homo sapiens full length insert	TM	2.1
	431060	AF039307	Hs.249171	homeo box A11	TM,homeobox	2.1
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HU	TM	2.1
	419978	NM_001454	Hs.93974	forkhead box J1	TM,Fork_head	2.1
	404535	Z25884	Hs.121483	chloride channel 1, skeletal muscl	SS	2.1
70	445181	AW338972	Hs.147471	ESTs	TM	2.1
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	TM,Hydrolase	2.1
	443591	AI078281	Hs.179240	ESTs	TM	2.1
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN	TM,trypsin	2.1
	424310	AA338648	Hs.50334	ESTs	TM	2.0
75	450193	AI916071	Hs.224623	ESTs	TM,pkinase	2.0
	436009	H57130	Hs.120925	ESTs	SS,TM,Ephrin	2.0
	453313	BE005771	Hs.153746	Homo sapiens cDNA: FLJ22490 fis, cl	TM	2.0
	419833	AA251131	Hs.220697	ESTs	TM,WHEP-TRS	2.0
	437555	AA759263	Hs.14041	ESTs	TM,Nramp	2.0
80	411828	AW161449	Hs.72290	wingless-type MMTV integration site	TM,wnt	2.0
	440052	AI633744	Hs.195648	ESTs	TM,PAC	2.0
	410718	AI920783	Hs.191435	ESTs	TM,SQS_PSY	2.0
	404767			predicted exon	TM	2.0
	447462	AW337214	Hs.158973	ESTs	TM	2.0

442255	AI701857	Hs.202388	ESTs	TM	2.0
410292	AA843087	Hs.124194	ESTs	TM	2.0
442748	AI016713	Hs.135787	ESTs	TM	2.0
458760	AI498631	Hs.111334	ferritin, light polypeptide	TM,HCO3_cotransp	2.0
409799	D11928	Hs.76845	phosphoserine phosphatase-like	TM,Hydrolase	2.0
401324			predicted exon	TM,myosin_head	2.0
432140	AK000404	Hs.272688	hypothetical protein FLJ20397	SS	2.0
447541	AK000288	Hs.18800	hypothetical protein FLJ20281	TM,zf-CCHC	2.0
421379	Y15221	Hs.103982	small inducible cytokine subfamily	SS,TM,IL8	2.0

TABLE 19B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
409457	1132521_1	AW818081 AW392887 AW514700 AW392881
410008	116812_1	AA079552 BE142525 BE142527
422689	219896_1	AW856665 AA315006 AW954733
428679	294049_1	AA431765 AA432015
438993	467651_1	AA828995 AA834879 AI926361
439031	46798_1	AF075079 H48601 H48795
448221	75534_1	BE622615
454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
454692	1229118_1	AW813350 AW816082 AW813476 AW813383
458154	491768_1	AW816379 AA888282 AA879046 AA879195
458861	798085_1	AI630223 AI630470
459287	977129_1	AL079369 D81804

TABLE 19C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NT_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
401324	9863791	Plus	234057-234174
401517	7677912	Plus	29278-29770
401933	3810668	Minus	48725-49057,51864-51955,52424-52589
402298	6598824	Plus	36758-37953
402606	9909429	Minus	81747-82094
403721	7528046	Minus	156647-157366
403776	7770611	Minus	1414-1513,1624-1756
404767	7882827	Minus	23244-23759
405032	7107731	Minus	131945-132224
405174	7108030	Minus	102814-103063
405454	7656675	Plus	133807-134053
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
405636	5123990	Plus	56384-56587
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406411	9256407	Plus	7400-7527

Table 20A: 56 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, Uterine Cancer Versus Normal Adult Tissues

Table 20A lists about 56 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulated by small molecules (e.g. pkinase, peptidase, isomerase, transporters). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
PSDomain: Protein Structural Domain
R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigenelD	Unigene Title	PSDomain	R1
428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	7tm_1	24.2
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromely	hemopexin	12.3
447350	AI375572	Hs.172634	HER4 (c-erb-B4)	kinase	9.8
420610	AI683183	Hs.99348	distal-less homeo box 5	homeobox	6.2
405609			predicted exon	Myosin_tail,myosin_head	5.0
458861	NM_007358	Hs.31016	PHD finger DNA binding protein	PHD	4.4
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone	NA	4.3

5	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	NA	4.1
	444783	AK001468	Hs.62180	ESTs	PH	4.0
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	HMG_box	3.8
	413472	BE242870	Hs.75379	solute carrier family 1	SDF	3.7
	443613	AI079356	Hs.21807	gb:oz39b09.s1 Soares_NhHMPu_S1 Homo s	zf-C2H2	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	Peptidase_M10	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 re	NA	3.6
	435031	AI632091	Hs.116877	ESTs	RhoGEF,PH	3.3
10	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-187	NA	3.3
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrola	NA	3.1
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	trypsin,pro_isomerase	3.1
	406400	AA343629	Hs.104570	kallikrein 8 (neurosin/ovasin)	trypsin	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A	ank	3.0
15	441794	AW197794	Hs.253338	ESTs	ank	2.9
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome de	TEA	2.9
	423513	AF035960	Hs.129719	transglutaminase 5	Transglutamin_N	2.8
	448141	AI471598	Hs.197531	ESTs	bZIP	2.8
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	guanylate_cyc	2.7
20	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	ABC_membrane,ABC_tran	2.7
	448435	BE293439	Hs.182278	calmodulin 2	NA	2.6
	417351	T90278	Hs.15049	ESTs	CH	2.5
	430372	AI206173	Hs.211375	ESTs	SH3,efhand,C2,PH	2.5
	431974	AW972689	Hs.200934	ESTs	bZIP	2.5
25	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hy	ank	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I	Glyco_transf_29	2.4
	403095			predicted exon	homeobox,PAX	2.4
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transfe	IPPT	2.4
	435615	Y15065	Hs.4975	potassium voltage-gated channel	ion_channel	2.3
30	402298			predicted exon	zf-C2H2,KRAB	2.3
	418203	X54942	Hs.83758	CDC28 protein kinase 2	CKS	2.3
	430563	AA481269	Hs.178381	ESTs	ABC_membrane,p450	2.3
	447570	AI868315	Hs.99669	ESTs	PHD	2.3
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily	NA	2.3
35	415539	AI733881	Hs.72472	BMPRIIb;	bone morphogenetic protein NA	2.2
	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	Cu-oxidase	2.2
	408380	AF123050	Hs.44532	diubiquitin	ANF_receptor,sushi,7tm_1	2.2
	440711	AA904389	Hs.143511	ESTs	rm	2.2
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-	efhand	2.2
40	418506	AA084248	Hs.85339	G protein-coupled receptor 39	NA	2.2
	410664	NM_006033	Hs.65370	lipase, endothelial	Ribosomal_L22,lipase,PLAT	2.1
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1	Branch	2.1
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein	kinesin,PHD,abhydrolase_2	2.1
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-dom	rm,NTF2	2.1
45	404535	Z25884	Hs.121483	chloride channel 1, skeletal muscle	NA	2.1
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2	trypsin	2.1
	446342	BE298665	Hs.14846	Cationic amino acid transporter (ecto	NA	2.0
	458760	AI498631	Hs.111334	ferritin, light polypeptide	HCO3_cotransp,zf-C3HC4	2.0
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	Hydrolase	2.0
50	401324			predicted exon	myosin_head	2.0

TABLE 20B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
443613	575391_1	AI079356 W23287
458861	798085_1	AI630223 AI630470

TABLE 20C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401324	9863791	Plus	234057-234174
402298	6598824	Plus	36758-37953
403095	8954339	Plus	150025-150240,151564-151690
75 405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
80 406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 21A: 270 Up-Regulated Genes, Uterine Cancer Versus Normal Uterus

Table 21A lists about 270 genes up-regulated in uterine cancer compared to normal uterus. These were selected as for Table 18A, except that the ratio was greater than or equal to 5.0, and the denominator was the median value for six non-malignant uterine specimens.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens	55.7
435094	AI560129	Hs.277523	EST	45.2
438461	AW075485	Hs.286049	phosphoserine aminotransferase	19.5
434779	AF153815	Hs.50151	potassium inwardly-rectifying channel	15.6
441633	AW958544	Hs.112242	ESTs	15.2
429183	AB014604	Hs.197955	KIAA0704 protein	14.6
436775	AA731111	Hs.291891	ESTs	14.3
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	14.0
446921	AB012113	Hs.16530	CC chemokine SCYA18 (MIP-4) (PARC)	13.0
413753	U17760	Hs.301103	Laminin, beta 3 (nicein (125kD), kalinin	12.9
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, 1	12.2
414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	12.0
453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	11.7
425196	AL037915	Hs.155097	carbonic anhydrase II	11.4
444863	AW384082	Hs.301323	ESTs	11.3
449785	AI225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	11.1
446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	10.9
449801	AA477355	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	10.3
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	10.3
414812	X72755	Hs.77367	monokine induced by gamma interferon	10.2
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	10.1
423645	AI215632	Hs.147487	ESTs	10.1
442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens	10.0
415786	AW419196	Hs.257924	ESTs	10.0
458017	AA813426	Hs.192034	ESTs, Weakly similar to KIAA0705 protein	10.0
435525	AI831297	Hs.123310	ESTs	9.9
413335	AI613318	Hs.48442	ESTs	9.7
420297	AI628272	Hs.88323	ESTs	9.6
452799	AI948829	Hs.213786	ESTs	9.6
434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	9.4
408243	Y00787	Hs.624	interleukin 8	9.3
430713	AA351647	Hs.2642	eukaryotic translation elongation factor	9.3
452092	BE245374	Hs.27842	hypothetical protein FLJ11210	9.2
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	9.2
443830	AI142095	Hs.143273	ESTs	9.1
442547	AA306997	Hs.268362	ESTs, Weakly similar to hypothetical pro	9.0
421633	AF121860	Hs.106260	sorting nexin 10	9.0
403381			0	8.9
426635	BE395109	Hs.129327	ESTs	8.8
440500	AA972165	Hs.150308	ESTs	8.7
436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulati	8.7
431668	AW969610	Hs.151179	ESTs	8.7
439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	8.7
424966	AI077312	Hs.153985	solute carrier family 7 (cationic amino	8.6
425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	8.6
428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9	8.5
438986	AF085888	Hs.269307	ESTs	8.4
422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	8.4
441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin	8.3
415992	C05837	Hs.145807	Homo sapiens cDNA FLJ13593 fis, clone PL	8.2
431211	M86849	Hs.5566	Homo sapiens connexin 26 (GJB2) mRNA, co	8.2
409865	AW502208		gb:U1-HF-BR0p-aju-e-09-0-U1.r1 NIH_MGC_5	8.0
448158	AI627292	Hs.190877	ESTs	8.0
401519			0	7.9
441730	AI243276	Hs.149017	ESTs	7.9
432441	AW292425	Hs.163484	EST	7.8
448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	7.8
438424	AI912498	Hs.25895	ESTs, Weakly similar to PI-3 kinase [H.s	7.8
447342	AI199268	Hs.19322	ESTs; Weakly similar to !!! ALU SUBFAM1	7.7
408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	7.7
423081	AF262992	Hs.123159	sperm associated antigen 4	7.6
414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	7.6
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	7.6
459142	AI903396		gb:RC-BT029-120199-219_1 BT029 Homo sapi	7.5
411094	BE066142		gb:CM4-BT0320-221199-047-g10 BT0320 Homo	7.5
436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	7.5
452607	AI160029	Hs.61438	ESTs	7.5
443171	BE281128	Hs.9030	TONDU	7.4
459081	W07808		gb:zb03a12.r1 Soares_fetal_lung_NbHL19W	7.4
431195	AA503083	Hs.79742	ESTs	7.4
444459	AI680624	Hs.148676	ESTs	7.4

5	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	7.3
	414918	AI219207	Hs.72222	Hypothetical protein FLJ13459	7.3
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	7.3
	448865	R35027		gb:yg60g02.r1 Soares infant brain 1NIB H	7.3
	409219	AA393383	Hs.133331	ESTs	7.3
10	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	7.2
	403485			0	7.2
	408350	AW183350	Hs.250127	ESTs	7.2
	445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fis, clone L	7.1
	400995			0	7.1
15	406086			0	7.1
	403378			0	7.0
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	7.0
	422038	R39098	Hs.192028	ESTs	7.0
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	6.9
20	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.9
	427494	AI628365	Hs.130412	ESTs, Weakly similar to sre-2 [C.elegans	6.9
	429272	W25140	Hs.110667	ESTs	6.9
	427258	AA400091	Hs.39421	ESTs	6.9
	449309	AW59823	Hs.224189	ESTs	6.9
25	400104			0	6.9
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	6.8
	404767			0	6.8
	406690	M29540	Hs.220529	CEA (carcinoembryonic antigen-related ce	6.8
	439750	AL359053	Hs.57664	ESTs	6.8
30	403127	AI904493	Hs.99890	polymerase (DNA directed), delta 1, cata	6.8
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.8
	425858	AA364923		gb:EST75602 Pineal gland II Homo sapiens	6.8
	421712	AK000140	Hs.107139	hypothetical protein	6.7
	456903	D49441	Hs.155981	mesothelin	6.7
35	414564	AA164803	Hs.71994	ESTs	6.7
	457942	AW665665	Hs.153034	ESTs	6.7
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	6.7
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	6.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	6.7
40	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	6.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.6
	410664	NM_006033	Hs.65370	lipase, endothelial	6.6
	428575	M19684	Hs.184929	serine (or cysteine) proteinase inhibito	6.6
	406400			kallikrein 8 (neuropsin/ovasin)	6.6
45	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	6.5
	441460	AI962478	Hs.226804	ESTs, Moderately similar to ALUC_HUMAN!	6.5
	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, beta pol	6.5
	424349	AF141289	Hs.145550	solute carrier family 7 (cationic amino	6.5
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.4
50	445258	AI635931	Hs.147613	ESTs	6.4
	456032	AW957446	Hs.301711	ESTs	6.4
	404727			0	6.4
	422810	AA317400		gb:EST19374 Retina II Homo sapiens cDNA	6.4
	440044	AW665167	Hs.259563	EST	6.4
55	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	6.4
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	6.4
	422170	AI791949	Hs.112432	anti-Mullerian hormone	6.4
	449611	AI970394	Hs.197075	ESTs	6.4
	402539	AW502761	Hs.30909	KIAA0430 gene product	6.3
60	456983	AI081687	Hs.170225	thymopoietin	6.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	6.3
	457887	AI240007	Hs.148812	ESTs	6.3
	431765	AF124249	Hs.268541	novel SH2-containing protein 1	6.3
	420344	BE463721	Hs.97101	Putative G protein-coupled receptor GPCR	6.2
65	443494	T99719	Hs.270404	Homo sapiens cDNA: FLJ22389 fis, clone H	6.2
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphalida	6.2
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	6.2
	413982	BE503035	Hs.279193	ESTs	6.2
	458091	AF150286		gb:AF150286 Human mRNA from cd34+ stem c	6.2
70	402104			0	6.2
	428771	AB028992	Hs.193143	KIAA1069 protein	6.1
	435313	AI769400	Hs.189729	ESTs	6.1
	441666	AI188346	Hs.301776	ESTs	6.1
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.1
75	427308	D26067	Hs.174905	KIAA0033 protein	6.1
	423069	W15613	Hs.1613	adenosine A2a receptor	6.1
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.1
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	6.1
	449409	AI650935	Hs.301694	ESTs	6.1
80	400855			0	6.1
	454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192 Homo	6.0
	414869	AA157291	Hs.72163	ESTs	6.0
	439662	H97552	Hs.269060	ESTs	6.0
	445181	AW338972	Hs.147471	ESTs	6.0
	437129	AL049327		gb:Homo sapiens mRNA; cDNA DKFZp564E016	6.0
	440128	AA962623	Hs.189144	ESTs, Weakly similar to NPT2_HUMAN RENAL	6.0
	443715	AI583187	Hs.9700	cyclin E1	6.0

	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3	5.9
	405291			0	5.9
	432113	AA935065	Hs.152385	ESTs	5.9
5	441236	AA923489	Hs.130432	ESTs	5.9
	424418	BE503432	Hs.66170	HSKM-B protein	5.9
	453028	AB006532	Hs.31442	RecQ protein-like 4	5.8
	407137	T97307	Hs.199067	EST	5.8
	443462	AI064690	Hs.171176	ESTs	5.8
10	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens c	5.8
	456311	AA225632	Hs.190016	ESTs	5.8
	446501	AI302616	Hs.150819	ESTs	5.8
	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	5.8
	409615	AW444861		gb:UI-H-BI3-ajz-a-04-0-UI.s1 NCI_CGAP_Su	5.8
15	459360	BE384526		gb:601277913F1 NIH_MGC_20 Homo sapiens c	5.8
	403824			0	5.8
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	5.8
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabbins)	5.7
	410658	AW105231	Hs.192035	ESTs	5.7
20	426465	AI758948		gb:ty16f07.x1 NCI_CGAP_UI3 Homo sapiens	5.7
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retin	5.7
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	5.7
	405392			0	5.7
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	5.7
25	449796	AA004321	Hs.194397	ESTs	5.7
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	5.7
	428987	NM_004751	Hs.194710	glucosaminyl (N-acetyl) transferase 3	5.7
	404220			0	5.6
	420973	AA743415	Hs.291368	ESTs	5.6
30	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	5.6
	442549	AI751601	Hs.8375	TNF receptor-associated factor 4	5.6
	409867	AW502161		gb:UI-HF-BR0p-ajr-g-12-0-UI.r1 NIH_MGC_5	5.6
	451110	AI955040	Hs.301584	ESTs	5.6
	418216	AA662240	Hs.283099	AF15q14 protein	5.6
35	411897	AW875066		gb:RC6-PT0001-180100-021-F04 PT0001 Homo	5.6
	456161	BE264645	Hs.282093	Homo sapiens cDNA: FLJ21918 fis, clone H	5.6
	406536			0	5.6
	432540	AI821517	Hs.105866	ESTs	5.6
	446315	NM_016293	Hs.14770	bridging integrator 2	5.6
40	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.6
	451035	AU076785	Hs.430	plastin 1 (I isoform)	5.6
	406685	M18728		gb:Human nonspecific crossreacting antig	5.5
	454590	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HE	5.5
	402430			0	5.5
45	446704	AI337228	Hs.197083	ESTs	5.5
	435282	AA677428	Hs.189731	ESTs	5.5
	426062	N57014	Hs.44013	ESTs	5.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	5.5
	456002	AI628729	Hs.191450	ESTs, Weakly similar to type II membrane	5.5
50	409613	AW444816	Hs.171537	Homo sapiens cDNA: FLJ21596 fis, clone C	5.5
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	5.5
	434609	R76593		gb:y160c11.r1 Soares placenta Nb2HP Homo	5.5
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	5.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	5.4
55	400379	NM_018432	Hs.283076	Homo sapiens ovarian cancer related prot	5.4
	436076	AI193277	Hs.120954	ESTs	5.4
	432119	T80289		gb:y03h04.r1 Soares infant brain 1NIB H	5.4
	417175	R44558	Hs.94002	ESTs	5.4
	445774	AI254165	Hs.145504	ESTs	5.4
60	455604	BE011183		gb:PM3-BN0218-100500-003-d09 BN0218 Homo	5.4
	411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	5.4
	445262	AW205650	Hs.253503	ESTs	5.4
	412517	BE271584		gb:601141065F1 NIH_MGC_9 Homo sapiens cD	5.4
	434756	AA827650	Hs.259307	ESTs	5.3
65	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	5.3
	439949	AW979197	Hs.292073	ESTs	5.3
	414995	C18200		gb:C18200 Human placenta cDNA (TFujiwara	5.3
	428071	AF212848	Hs.182339	transcription factor ESE-3B	5.3
	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	5.3
70	434283	AW235341	Hs.58715	mouse thiamin pyrophosphokinase homolog	5.3
	447798	AI425049	Hs.119629	ESTs, Moderately similar to ALU1_HUMAN A	5.3
	401723			0	5.3
	406270			0	5.3
	452194	AI694413	Hs.298262	ESTs, Weakly similar to dJ88J8.1 [H.sapi	5.3
75	415757	AA830854	Hs.187810	ESTs	5.3
	430051	AA464611	Hs.52515	transducin (beta)-like 2	5.2
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-like	5.2
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	5.2
	449009	BE044755	Hs.224812	ESTs	5.2
80	424001	W67883	Hs.137476	KIAA1051 protein	5.2
	409479	BE163800	Hs.136912	ESTs	5.2
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	5.2
	435928	H64345	Hs.183961	ESTs	5.2
	447397	BE247676	Hs.18442	E-1 enzyme	5.2

449183	AW445022	Hs.196985	Homo sapiens cDNA: FLJ21135 fis, clone C	5.2
410146	AW592655		gb:hf45f12.x1 Soares_NFL_T_GBC_S1 Homo s	5.2
458164	AI208666	Hs.192081	ESTs	5.2
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	5.1
439509	AF086332	Hs.58314	ESTs	5.1
422569	BE552132	Hs.118442	cyclin C	5.1
430664	AW969834		gb:EST381912 MAGE resequences, MAGK Homo	5.1
411231	AW833501		gb:QV4-TT0008-091199-025-e09 TT0008 Homo	5.1
412194	AW900282	Hs.115412	Homo sapiens cDNA FLJ13881 fis, clone TH	5.1
425188	AK002052	Hs.155071	hypothetical protein FLJ11190	5.1
417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	5.1
433279	AW971745		gb:EST383834 MAGE resequences, MAGL Homo	5.1
454112	NM_000885	Hs.301806	ESTs	5.1
423261	Z43509		gb:HSC1EA031 normalized infant brain cDN	5.1
434084	AI061640	Hs.192788	hypothetical protein PRO1905	5.1
446115	AI733075	Hs.292682	ESTs, Weakly similar to S69913 hypertens	5.1
416719	H79731		gb:yu81f12.r1 Soares fetal liver spleen	5.1
421462	AF016495	Hs.104624	aquaporin 9	5.1
424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	5.1
403383			0	5.1
430832	AI073913	Hs.100686	ESTs, Weakly similar to secreted cement	5.1
436070	AK000073		gb:Homo sapiens cDNA FLJ20066 fis, clone	5.0
416969	AI815443	Hs.283404	organic cation transporter	5.0
444929	AI685841	Hs.161354	ESTs	5.0
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
439031	AF075079		gb:Homo sapiens full length insert cDNA	5.0
414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	5.0
425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	5.0
449986	AW864502		gb:PM4-SN0016-120400-004-b12 SN0016 Homo	5.0
418717	AI334430	Hs.86984	ESTs	5.0
438769	AA830684	Hs.163426	ESTs	5.0
441859	AW194364	Hs.12802	ESTs, Weakly similar to FIG1 MOUSE FIG-1	5.0
446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase	5.0

TABLE 21B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
409615	1143425_1	AW444861 BE074994 BE074966 BE074992
409865	1156518_1	AW502208 AW502366 AW502148
409867	1156530_1	AW502161 AW502587 AW502345
410146	1178974_1	AW592655 R05927 R06916
411094	1231982_1	BE066142 AW817074
411231	1236356_1	AW833501 AW833506 AW833722 AW833332 AW833509 AW833511 AW833767 AW833339
411426	1245515_1	BE141714 AW845993 AW845989
411897	1264907_1	AW875066 AW875079 AW875075 AW875062 AW875061 AW875074
412323	1288770_1	AW937143 AW937150 AW937141 AW937151 AW937132 AW937160 AW937191 AW937174 AW937195 AW937173 AW937159 AW937139 AW937171 AW937142 AW937145 AW937165 AW937163 AW937164 AW937137 AW937179 AW937156 AW937140 AW937135 AW937170
412517	130281_1	BE271584 AA112511
414484	1452830_1	BE314385
414539	1460320_1	BE379046 BE395459
414995	1511736_1	C18200 D78681 T82025
416719	1611345_1	H79731 H79732
422731	220507_1	AL138411 AL138412 AA315860
422810	221630_1	AA317400 AA434584
423261	226553_1	Z43509 H09001 AA375202 AW954383
425858	257265_1	AA364923 AW963483 BE182774 C21461
426465	267664_1	AI758948 AA379527 AA379948 AA379262 AW963933
430664	321423_1	AW969834 AA528493 AA483165 AW969842
432119	34170_1	T80289 AF052168
433279	361800_1	AW971745 AA581359 AA581358
433921	377350_1	AA618174 AI114549 R36464 R36465
434609	38950_1	R76593 AF147390 R76594
436070	41426_1	AK000073 AA380183 AA380181 AW963533
437129	43343_1	AL049327 AA847105
439031	46798_1	AF075079 H48601 H48795
442438	542469_1	AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
448865	78535_1	R35027 R12034 BE407120
449034	794817_1	AI624049 AW117770 AI858360
449986	821463_1	AW864502 AW864369 AI678780
454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
454692	1229118_1	AW813350 AW816082 AW813476 AW813383
455604	1337197_1	BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
458091	472385_1	AF150286 AA835857
459081	889426_1	W07808 AI822066
459142	918906_1	AI903396 AI903361 AI903360

TABLE 21C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400855	1931571	Minus	17801-18228
400995	8099094	Plus	141186-141601
401519	6649315	Plus	157315-157950
401723	7656694	Plus	147273-147503
402104	8119072	Plus	122409-122600
402430	9796372	Minus	62382-62552
403378	9438244	Minus	44264-44443
403381	9438267	Minus	26009-26178
403383	9438267	Minus	119837-121197
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
403824	9798468	Plus	473-887
404220	6706820	Plus	46107-46439
404727	8081050	Plus	115534-115747
404767	7882827	Minus	23244-23759
405291	3845420	Plus	19999-20473,20672-21036,21147-21285,21378-21667
405392	6624069	Minus	116167-116289,118879-119030
406086	7107817	Plus	9418-9573
406270	7534217	Plus	13136-13591
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406536	7711478	Plus	25655-25782

TABLE 22A: 430 SIGNIFICANTLY DOWN-REGULATED GENES, UTERINE CANCER VERSUS NORMAL UTERUS

Table 22A lists about 430 genes significantly down-regulated in uterine cancer compared to normal uterus. These were selected as for Table 21A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 14 (i.e. 14-fold down-regulated in tumor vs. normal uterus).

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
414063	H26904	Hs.75736	apolipoprotein D	93.0
447990	BE048821	Hs.20144	small inducible cytokine subfamily A, member 14	75.7
407815	AW373860	Hs.301716	ESTs	68.7
452547	AA335295	Hs.74120	adipose specific 2	61.1
415165	AW887604	Hs.78065	complement component 7	55.1
453655	AW960427	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE	54.0
429350	AI754634	Hs.131987	ESTs	52.6
407228	M25079	Hs.155376	hemoglobin, beta	52.0
425869	AA524547	Hs.160318	FXVD domain-containing ion transport regulato	51.6
416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	51.4
408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (from c	49.7
417542	JO4129	Hs.82269	progesterone-associated endometrial protein (p	49.3
412295	AW088826	Hs.22971	ESTs	48.0
421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	47.0
452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (from c	46.7
429707	W76631	Hs.211819	matrix metalloproteinase 23B	45.7
416950	AL049798	Hs.80552	dermatopontin	45.6
408221	AA912183	Hs.47447	ESTs	44.6
406791	AI220684	Hs.272572	hemoglobin, alpha 2	43.0
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chromosome	42.6
407938	AA905097	Hs.85050	phospholamban	41.1
410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)	41.0
412524	AA417813	Hs.11177	ESTs	39.4
452426	AI904823	Hs.31297	Homo sapiens cDNA: FLJ23001 fis, clone LNG002	38.6
414290	AI568801	Hs.71721	ESTs	38.2
439627	BE621702	Hs.29076	Homo sapiens cDNA: FLJ21841 fis, clone HEP018	38.0
400258		Hs.79064	deoxyhypusine synthase	37.0
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	36.1
410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	35.4
407663	NM_016429	Hs.37482	COP22 for nonclathrin coat protein zeta-COP	34.3
410286	AI739159	Hs.61898	DKFZP586N2124 protein	33.8
418986	AI123555	Hs.81796	ESTs	33.1
409060	AI815867	Hs.50130	necdin (mouse) homolog	33.1
436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)	32.8
420674	NM_000055	Hs.1327	butyrylcholinesterase	32.6
417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, member	32.4
450810	BE207588	Hs.25511	transforming growth factor beta 1 induced tra	31.7
438150	AA037534	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE	31.6

	430468	NM_004673	Hs.130699	ESTs	31.5
	453060	AW294092	Hs.21594	ESTs	31.3
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vascular	30.8
5	422126	AW973784	Hs.112028	Missshapen/NIK-related kinase	30.5
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (isoform	30.3
	421639	NM_012082	Hs.297921	Homo sapiens mRNA full length insert cDNA clo	30.3
	402520				29.9
	418043	AW377752	Hs.83341	H.sapiens mRNA for tyrosine kinase receptor	29.7
10	443906	AA348031	Hs.7913	ESTs	29.7
	450958	AL137669	Hs.25700	Homo sapiens mRNA; cDNA DKFZp434M0435 (from c	29.4
	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-type 12-	29.4
	412828	AL133396	Hs.74621	prior protein (p27-30) (Creutzfeld-Jakob dise	29.4
	429507	NM_003102	Hs.2420	superoxide dismutase 3, extracellular	29.2
	400545				29.1
15	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	29.1
	429942	AI338993	Hs.134535	ESTs	28.9
	438303	AB028998	Hs.6147	KIAA1075 protein	28.7
	419971	AA400027	Hs.296234	ESTs, Highly similar to mitogen-activated pro	28.7
20	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	28.7
	452877	AI250789	Hs.32478	ESTs	28.6
	412442	AI983730	Hs.26530	serum deprivation response (phosphatidylserin	28.6
	424378	W28020	Hs.184367	GTPase activating protein-like	28.6
	421823	N40850	Hs.28625	ESTs	27.9
25	447786	BE620810	Hs.39619	hypothetical protein LOC57333	27.6
	400023			AFFX control: 18S ribosomal RNA	27.5
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	27.2
	414134	X60188	Hs.861	mitogen-activated protein kinase 3	27.1
	428451	AW970451	Hs.98570	ESTs	26.9
30	435520	AA297990	Hs.9315	HNOEL-iso protein	26.6
	437179	AA393508	Hs.171409	serologically defined colon cancer antigen 8	26.4
	441481	AA935303	Hs.270553	ESTs	26.0
	450227	BE388192	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone COL001	25.6
	403731				25.5
35	452814	AI092790	Hs.55016	hypothetical protein FLJ21935	25.5
	410036	R57171	Hs.57975	calsequestrin 2, cardiac muscle	25.5
	416854	H40164	Hs.80296	Purkinje cell protein 4	25.4
	418421	R58620	Hs.85050	phospholamban	25.4
	407000	U12139		gb:Human alpha1(XI) collagen (COL11A1) gene,	25.3
40	421803	NM_012205	Hs.108441	3-hydroxyanthranilate 3,4-dioxygenase	25.3
	445613	BE550889	Hs.158491	ESTs	25.1
	432302	AA345857	Hs.274307	KIAA1442 protein	24.8
	420796	L34355	Hs.99931	sarcoglycan, alpha (50kD dystrophin-associate	24.8
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone COL021	24.7
	417302	BE245812	Hs.8941	ESTs	24.6
45	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mimecan)	24.6
	440130	AI083899	Hs.157527	ESTs	24.5
	431967	AJ243653	Hs.283404	organic cation transporter	24.5
	424580	AA446539	Hs.35092	ESTs	24.4
50	406907	Z25427		gb:H.sapiens protein-serine/threonine kinase	24.2
	443745	AB039670	Hs.9728	ALEX1 protein	24.1
	429101	AW452174	Hs.173780	ESTs	23.5
	410691	AW239226	Hs.65450	reticulon 4	23.4
	408853	AW291484	Hs.254967	ESTs	23.3
	407979	AA046306	Hs.62927	ESTs	23.1
55	448619	AI867182	Hs.202255	ESTs	22.8
	424585	AA464840		gb:zx43h11.1 Soares_total_fetus_Nb2HF8_9w Ho	22.7
	407891	AA486620	Hs.41135	Endomucin 2	22.6
	407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma virus (FB	22.5
60	426990	AL044315	Hs.173094	Homo sapiens mRNA; cDNA DKFZp564H142 (from cl	22.5
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endothelial cell)	22.1
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-like	22.0
	423690	AA329648	Hs.23804	ESTs	22.0
	402865				21.9
65	417387	AW021102	Hs.21509	ESTs	21.9
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	21.9
	459722			Homo sapiens cDNA: FLJ23449 fis, clone HSI058	21.8
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	21.8
	402195				21.7
70	418213	AW978753	Hs.127327	ESTs	21.6
	440274	R24595	Hs.7122	scrapie responsive protein 1	21.6
	455818	AI733747		gb:zn86d04.y5 Stratagene lung carcinoma 93721	21.4
	420861	AI039044	Hs.88827	Homo sapiens mRNA for FLJ00033 protein, parti	21.4
	405228				21.3
75	441292	AF131218	Hs.7765	chromosome 16 open reading frame 5	21.3
	432553	AA553334	Hs.211095	ESTs	21.3
	417098	AB017365	Hs.173859	frizzled (Drosophila) homolog 7	21.2
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	21.2
	405313				21.1
80	410243	D83402	Hs.289006	ESTs, Weakly similar to alternatively spliced	21.1
	413186	AU077141	Hs.75231	solute carrier family 16 (monocarboxylic acid	21.1
	425954	AK000633	Hs.164476	hypothetical protein FLJ20626	21.0
	421770	AA374192	Hs.108124	ribosomal protein L41	21.0
	435265	AA779958	Hs.185932	ESTs	20.8

	430036	AL050284	Hs.227782	DKFZP586M1019 protein	20.7
	430233	AW367902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (from c	20.7
	436130	AA341497	Hs.31408	ESTs	20.7
5	434843	R43707	Hs.133159	ESTs, Weakly similar to PIHUSD salivary proli	20.7
	429303	AW137635	Hs.44238	ESTs	20.6
	442422	AI344415	Hs.156082	ESTs	20.5
	410399	BE068889	Hs.63236	synuclein, gamma (breast cancer-specific prot	20.5
	435869	AF255910	Hs.54650	ESTs, Weakly similar to (define not availabl	20.5
10	447384	AI377221	Hs.40528	ESTs	20.5
	440610	AI733098	Hs.130800	ESTs	20.5
	445806	AL137516	Hs.13323	hypothetical protein FLJ22059	20.4
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	20.4
	436467	AW450278	Hs.91681	ESTs	20.3
15	440191	AI990417	Hs.116107	Homo sapiens genomic DNA, chromosome 21q, sec	20.2
	417511	AL049176	Hs.82223	chordin-like	20.2
	406976	M60299		gb:Human alpha-1 collagen type II gene, exons	20.1
	443547	AW271273	Hs.23767	ESTs	20.1
	417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo sapi	20.1
20	419313	AA843387	Hs.87279	ESTs	20.1
	408322	AW181985	Hs.249986	ESTs	20.0
	448422	BE263813		gb:601194177F1 NIH_MGC_7 Homo sapiens cDNA cl	20.0
	403121				19.9
25	424198	AB029010	Hs.143026	KIAA1087 protein	19.9
	459060	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein D (AU	19.9
	457829	AI742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [H.sapiens	19.9
	445029	AF196481	Hs.12256	midline 2	19.9
	424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (from c	19.8
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal monoa	19.7
30	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYDROXY	19.6
	435891	AW249394	Hs.5002	copper chaperone for superoxide dismutase	19.6
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac muscle,	19.6
	400637				19.5
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (car	19.4
35	430310	U60115	Hs.239069	four and a half LIM domains 1	19.4
	402741				19.4
	401703				19.3
	409229	H60333	Hs.251928	nuclear pore complex interacting protein	19.3
40	453856	AA804789	Hs.19447	Homo sapiens mRNA for FLJ00106 protein, parti	19.3
	430342	NM_005938	Hs.239663	myeloid/lymphoid or mixed-lineage leukemia (t	19.3
	404033				19.2
	411939	AI365585	Hs.146246	ESTs	19.2
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	19.1
	452669	AA216363	Hs.262958	ESTs, Weakly similar to alternatively spliced	19.1
45	439698	AW779654	Hs.55876	ESTs	18.9
	416253	BE250659	Hs.15463	ESTs	18.9
	418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo sapien	18.9
	408877	AA479033	Hs.130315	ESTs	18.9
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24kD	18.9
50	417054	AF017060	Hs.174151	aldehyde oxidase 1	18.8
	404654				18.8
	420174	AI824144	Hs.23912	ESTs	18.8
	400625				18.7
	406150				18.7
55	457835	BE256338	Hs.192375	ESTs, Highly similar to dJ127B20.3 [H.sapiens	18.6
	420105	AW015571	Hs.32244	ESTs	18.6
	404619	BE514535	Hs.77171	minichromosome maintenance deficient (S. cere	18.5
	423282	AL137563	Hs.126378	putative ABC transporter	18.5
	424097	M13981	Hs.1734	inhibin, alpha	18.5
60	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from c	18.5
	427605	NM_000997	Hs.179779	ribosomal protein L37	18.4
	406535				18.4
	418947	W52990	Hs.22860	ESTs	18.4
	414323	NM_014759	Hs.239500	KIAA0273 gene product	18.3
65	457111	AA482027	Hs.142569	ESTs	18.3
	418373	AW750770	Hs.84344	CGI-135 protein	18.3
	424461	D83542	Hs.148090	cadherin 15, M-cadherin (myotubule)	18.2
	451565	NM_000897	Hs.456	leukotriene C4 synthase	18.2
	407751	BE276096	Hs.38205	from HeLa cyclin-dependent kinase 2 interacti	18.2
70	432031	AF039196	Hs.284126	hairless (mouse) homolog	18.1
	404608	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	18.1
	451962	AW078832	Hs.226806	ESTs	18.1
	424100	AI793080	Hs.123525	ESTs, Weakly similar to NGAL RAT NEUTROPHIL G	18.1
	451509	AI969529	Hs.171637	Homo sapiens cDNA: FLJ21937 fis, clone HEP044	18.1
75	453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker protein	18.0
	429924	W39693	Hs.226138	Homo sapiens mRNA; cDNA DKFZp566H2446 (from c	17.9
	423780	AA352013		gb:EST59935 Infant brain Homo sapiens cDNA 5'	17.9
	427030	AA397600	Hs.97531	ESTs	17.9
	439872	T81058		gb:yd26c08.r1 Soares fetal liver spleen 1N1LS	17.9
80	407836	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone CAE112	17.9
	451427	AI091441	Hs.26401	tumor necrosis factor (ligand) superfamily, m	17.9
	424462	AU076666	Hs.148101	serum constituent protein	17.9
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidylserin	17.8
	422319	AW403342	Hs.115232	splicing factor 3a, subunit 2, 66kD	17.8

	400489				17.8
	454421	BE409759	Hs.59563	Homo sapiens mRNA for FLJ00007 protein, parti	17.8
	449282	AL048056	Hs.23437	Homo sapiens cDNA FLJ13555 fis, clone PLACE10	17.7
5	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (from c	17.7
	429790	AK001352	Hs.221737	hypothetical protein FLJ10490	17.7
	422796	AW897265		gb:CM0-NN0057-150400-335-a04 NN0057 Homo sapi	17.7
	427980	AA418305		gb:zv96g05.s1 Soares_NhHMPu_S1 Homo sapiens c	17.6
	409543	AW410200		gb:fh05b12.x1 NIH_MGC_17 Homo sapiens cDNA cl	17.6
10	440206	AI762232	Hs.46794	ESTs	17.6
	455904	BE156173		gb:QV0-HT0367-201299-079-a02 HT0367 Homo sapi	17.5
	427707	NM_005578	Hs.180398	LIM domain-containing preferred translocation	17.5
	437140	AA312799	Hs.283689	activator of CREM in testis	17.5
	417637	AA204969	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB10	17.5
15	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor type,	17.4
	417808	AF177909	Hs.12828	tweet (Drosophila) homolog 1	17.4
	426232	Z70024	Hs.168157	nuclear transcription factor Y, gamma	17.4
	440747	AW297226	Hs.137840	ESTs, Moderately similar to SIX1_HUMAN HOMEOB	17.4
	415307	F05232	Hs.27495	prostate cancer associated protein 7	17.3
20	407049	X72632		(NONE)	17.3
	454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT2RM40	17.3
	411085	AF022991	Hs.68398	period (Drosophila) homolog 1	17.3
	443104	AA088470	Hs.83135	p53-responsive gene 6	17.2
	424106	AA412442	Hs.98132	ESTs	17.2
25	446716	AA436575	Hs.16602	ESTs	17.1
	448677	AI560769	Hs.227051	ESTs	17.0
	434919	AI821740	Hs.116531	ESTs	17.0
	401171	AA360954	Hs.27268	Homo sapiens mRNA; cDNA DKFZp564N196 (from cl	17.0
	456804	AI421645	Hs.139851	caveolin 2	17.0
30	453621	AW749983		gb:QV3-BT0537-280100-070-e04 BT0537 Homo sapi	16.9
	413419	BE093686	Hs.48938	Homo sapiens cDNA: FLJ21802 fis, clone HEP007	16.9
	426515	BE394222	Hs.231444	ESTs	16.9
	428937	T82221	Hs.56729	lymphocyte-specific protein 1	16.9
	424562	AI420859	Hs.150557	basic transcription element binding protein 1	16.9
35	444655	AF088886	Hs.11590	cathepsin F	16.9
	447424	AI681105	Hs.181641	ESTs	16.8
	425439	D38024	Hs.157425	double homeobox, 2	16.8
	446707	AI591214	Hs.156336	ESTs	16.8
	405324				16.8
40	434340	AI193043	Hs.128685	ESTs	16.8
	422942	AF054839	Hs.122540	tetraspan 2	16.8
	421820	AW662990	Hs.108675	heme-binding protein	16.8
	420037	BE299598	Hs.135569	ESTs, Weakly similar to NEUROD [H.sapiens]	16.7
	428818	AI131291	Hs.98866	ESTs	16.7
45	426485	NM_006207	Hs.170040	platelet-derived growth factor receptor-like	16.7
	404947				16.6
	412677	AW029608	Hs.17384	ESTs	16.6
	401551				16.6
50	408053	AW139474	Hs.246862	ESTs	16.6
	425016	AA376049	Hs.154162	ADP-ribosylation factor-like 2	16.6
	418179	X51630	Hs.1145	Wilms tumor 1	16.6
	418994	AA296520	Hs.89546	Selectin E (endothelial adhesion molecule 1)	16.5
	457514	AA775208	Hs.136423	ESTs	16.5
	426275	BE151551		gb:RC0-HT0297-201199-031-f12 HT0297 Homo sapi	16.5
55	457924	AL390142	Hs.288697	Homo sapiens cDNA FLJ13861 fis, clone THYRO10	16.5
	430712	AW044647	Hs.196284	ESTs	16.5
	455144	AW875942		gb:CM1-PT0013-131299-067-b10 PT0013 Homo sapi	16.4
	407524	X64985		gb:H.sapiens mRNA HTPCRX11 for olfactory rece	16.4
	426712	AW173177	Hs.197755	ESTs	16.4
60	429954	AI918130	Hs.21374	ESTs	16.4
	446208	BE258323	Hs.225795	ESTs, Highly similar to OTX1_HUMAN HOMEBOX P	16.4
	442792	AI352340	Hs.131194	ESTs	16.3
	420485	AF218586	Hs.288835	cell death-inducing DFFA-like effector b	16.3
	426767	AA384398	Hs.192491	ESTs	16.3
65	436950	L05779	Hs.113	epoxide hydrolase 2, cytoplasmic	16.3
	415186	AK000150	Hs.78185	MAX-like bHLHZIP protein	16.3
	442197	AW837912		gb:QV3-LT0048-260100-068-c02 LT0048 Homo sapi	16.3
	433457	AA830194	Hs.199417	Homo sapiens mRNA for FLJ00027 protein, parti	16.2
	402316				16.2
70	409736	AA078628		gb:7P07H07 Chromosome 7 Placental cDNA Librar	16.2
	407964	AW130334	Hs.281111	ESTs	16.2
	433677	AI791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN ALU SU	16.2
	425507	AI684745	Hs.165983	hypothetical C2H2 zinc finger protein FLJ2250	16.2
	413724	AA131466	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT2RM40	16.2
75	408922	R87388		gb:ym88g04.r1 Soares adult brain N2b4HB55Y Ho	16.1
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-induc	16.1
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	16.1
	442208	AW296984	Hs.255595	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	16.1
	402426				16.0
80	412399	N53816	Hs.14394	hypothetical protein FLJ20157	16.0
	413200	AA127395	Hs.222414	ESTs	16.0
	404597				15.9
	453143	AA382234	Hs.170121	protein tyrosine phosphatase, receptor type,	15.9
	455984	BE177442		gb:RC1-HT0595-200400-012-f01 HT0595 Homo sapi	15.9

	416193	T25400		gb:PTH069 HTCDL1 Homo sapiens cDNA 5'/3' sim	15.9
	407065	Y10141		gb:H.sapiens DAT1 gene, partial, VNTR.	15.9
	441785	AW138139	Hs.244598	ESTs	15.9
5	413784	BE165819		gb:CMO-HT0486-220300-301-d12 HT0486 Homo sapi	15.9
	429092	AI190864	Hs.178226	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.8
	408499	AW205323	Hs.253475	ESTs	15.8
	453754	AW972580	Hs.172753	ESTs	15.8
	450826	U43030	Hs.25537	cardiotrophin 1	15.8
10	428486	AW583497	Hs.184604	pancreatic polypeptide	15.7
	405895				15.7
	409108	AA339443	Hs.48793	ESTs	15.7
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	15.6
	422948	AW810824	Hs.21351	ESTs	15.6
15	447852	AW504781		gb:Ul-HF-BN0-aln-c-04-0-Ul.r1 NIH_MGC_50 Homo	15.6
	419084	AA496539	Hs.179902	transporter-like protein	15.6
	456771	AW016739	Hs.232201	ESTs	15.6
	438564	AA381553	Hs.198253	major histocompatibility complex, class II, D	15.6
	448705	H05072	Hs.124984	ESTs, Moderately similar to unnamed protein p	15.6
20	454460	X66945	Hs.748	fibroblast growth factor receptor 1 (fms-rela	15.5
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.5
	426759	AI590401	Hs.21213	ESTs	15.5
	453769	R35261	Hs.24947	ESTs	15.4
	434179	AI743448	Hs.116177	ESTs	15.4
25	404111				15.4
	402056				15.4
	458602	AI262208	Hs.276489	ESTs	15.3
	427530	AA405093	Hs.126519	ESTs	15.3
	414716	AF199598	Hs.97044	Kv channel-interacting protein 2	15.3
30	400632				15.3
	443918	AA305475	Hs.22660	Homo sapiens cDNA FLJ11658 fis, clone HEMBA10	15.3
	432037	AW450592	Hs.300459	ESTs	15.3
	412921	BE009345	Hs.128942	ESTs	15.3
	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H.sapi	15.3
35	441704	AI458766	Hs.201988	ESTs	15.3
	414272	AI651603	Hs.46988	ESTs	15.3
	448224	R48700	Hs.20733	EH-domain containing 2	15.2
	404611	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	15.2
	448391	D61580	Hs.21036	Homo sapiens mRNA; cDNA DKFZp434A1010 (from c	15.2
40	454719	BE006547		gb:RC2-BN0130-040400-011-b03 BN0130 Homo sapi	15.2
	446973	H95724	Hs.4283	ESTs	15.2
	457760	AA668123	Hs.134170	ESTs	15.2
	440144	AW082297	Hs.88523	ESTs	15.2
	407387	AB000895		gb:Homo sapiens mRNA for cadherin FIB1, parti	15.2
45	427850	AA416756	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN ALU SU	15.2
	404244				15.1
	402959				15.1
	435487	W07343	Hs.182538	phospholipid scramblase 4	15.1
50	414213	BE297765		gb:601176246F1 NIH_MGC_17 Homo sapiens cDNA c	15.0
	455916	BE156710		gb:QV0-HT0368-310300-181-d01 HT0368 Homo sapi	15.0
	448943	AI608810	Hs.193288	ESTs	15.0
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	15.0
	454082	AF283508	Hs.63168	cell death regulator aven	14.9
	453308	AW959731	Hs.32538	ESTs	14.9
55	458823	AW207574	Hs.179501	ESTs	14.9
	452532	AI905811	Hs.110757	DNA segment on chromosome 21 (unique) 2056 ex	14.9
	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB55Y Ho	14.9
	409473	AL137716	Hs.296567	Homo sapiens mRNA; cDNA DKFZp434D2030 (from c	14.8
	449779	AA004258	Hs.25218	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU C	14.8
60	457546	AA568484	Hs.153632	ESTs	14.8
	403368				14.8
	432163	AK000440	Hs.272799	hypothetical protein FLJ20433	14.8
	421531	AA713505	Hs.291769	ESTs	14.8
	428283	AI439096	Hs.25832	Homo sapiens mRNA; cDNA DKFZp564P116 (from cl	14.8
65	443528	AK001778	Hs.9547	hypothetical protein FLJ10916	14.8
	402399				14.8
	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	14.8
	450300	AL041440	Hs.58210	ESTs	14.8
	403552				14.7
70	406929	U04690		gb:Human olfactory receptor (OR17-210) gene,	14.7
	436365	AW444548	Hs.163118	ESTs	14.7
	402550				14.7
	441782	AW140126	Hs.132357	ESTs	14.7
	415672	N53097	Hs.193579	ESTs	14.7
75	430582	AI215509	Hs.143964	ESTs	14.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (sacsin	14.7
	432683	AW995441	Hs.10475	ESTs	14.7
	441871	AI306150	Hs.153450	ESTs, Weakly similar to 1909123A Na glucose c	14.6
	447481	AF052151	Hs.18686	Mouse Mammary Tumor Virus Receptor homolog	14.6
80	405114				14.6
	401082				14.6
	454316	AW366144		gb:QV0-HT0101-051099-032-b12 HT0101 Homo sapi	14.6
	421572	AA531607	Hs.125143	ESTs, Weakly similar to POL2 MOUSE RETROVIRUS	14.6
	424591	R55704	Hs.150968	hypocretin (orexin) receptor 1	14.6

	441503	AW172263	Hs.185202	ESTs	14.6
	416199	R83537		gb:yq12a08.r1 Soares fetal liver spleen 1NFLS	14.6
	420360	U83171	Hs.97203	small inducible cytokine subfamily A (Cys-Cys	14.6
5	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	14.5
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, member	14.5
	405100				14.5
	454012	M76424	Hs.37014	carbonic anhydrase VII	14.5
	402457				14.5
10	454613	AW810814		gb:MR2-ST0129-201099-004-e01 ST0129 Homo sapi	14.5
	429821	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (from cl	14.5
	431073	BE254470	Hs.249186	cone-rod homeobox	14.5
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing leucine	14.5
	401223				14.4
15	438627	AI087335	Hs.123473	ESTs	14.4
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.4
	437217	AW779241	Hs.155316	ESTs	14.4
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G protein	14.4
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-biphosp	14.4
20	413237	AI468574	Hs.171965	ESTs	14.4
	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, SP-40,	14.4
	426488	X03350	Hs.4	alcohol dehydrogenase 2 (class I), beta polyp	14.4
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	14.4
	405479				14.3
25	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	14.3
	426316	NM_002430	Hs.301852	Human DNA sequence from clone 437G10 on chrom	14.3
	412171	AW897452		gb:CMO-NN0058-150400-337-b08 NN0058 Homo sapi	14.3
	447241	BE382838	Hs.19322	ESTs	14.3
	402100				14.2
30	438286	AW139266	Hs.134807	Homo sapiens cDNA FLJ12057 fis, clone HEMBB10	14.2
	407947	AI500332	Hs.102367	ESTs, Weakly similar to hTcf-4 [H.sapiens]	14.2
	402275				14.2
	402358				14.2
	439624	AA838771	Hs.124407	ESTs	14.2
35	444455	AI149879	Hs.175024	Homo sapiens cDNA: FLJ23447 fis, clone HSI033	14.2
	455314	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	14.2
	427872	AA835058	Hs.21111	ESTs	14.2
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	14.2
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene homolo	14.2
40	442682	AI014545	Hs.231027	EST	14.1
	457033	AF029674	Hs.173422	KIAA1605 protein	14.1
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	14.1
	401007				14.1
	458274	AF149297	Hs.8087	NAG-5 protein	14.1
45	454106	D19687	Hs.245146	ESTs	14.1
	432928	AA570454	Hs.186467	ESTs, Moderately similar to ALU1_HUMAN ALU SU	14.1
	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin/ bet	14.1
	433887	AW204232	Hs.279522	ESTs	14.1
	434927	H46612	Hs.293815	ESTs, Weakly similar to PLM_HUMAN PHOSPHOLEMM	14.1
50	404282				14.1
	422581	NM_016339	Hs.118562	Link guanine nucleotide exchange factor II	14.0
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	14.0
	408107	AA806754	Hs.62835	ESTs	14.0
	401577				14.0
55	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 proline-rich p	14.0
	408104	AW972927	Hs.293968	ESTs	14.0
	404642				14.0
	400675				14.0
	406059				14.0
60	448386	AB037750	Hs.21061	KIAA1329 protein	14.0
	407287	AI678812	Hs.201658	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	14.0

TABLE 22B

65	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
	Pkey	CAT number	Accession
70	408922	109017_1	R87388 R84328 AA058916
	409543	1138723_1	AW410200 AW409705 AW411433 BE296786 BE270309
	409736	115189_1	AA078628 R09051 AA078197 AA077334 AW748808 AW748807
	412171	1280759_1	AW897452 Z20302 D55805 D52877 D60432
75	413784	1389150_1	BE165819 BE165853 W01386
	414213	1426375_1	BE297765 BE262061 BE302686 T83915
	416193	1577102_1	T25400 H26834 H44554 R73193
	416199	1577561_1	R83537 W80940 H27368
80	417998	171375_1	AW967420 AA210915 AA236991 AA210916
	418464	1759038_2	R87580
	418556	1767866_1	T02850
	422796	221500_1	AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361
			T06241 AA326794 AL138130 AW407975 AW999277
	423780	231952_1	AA352013 AA330878 AA339379 AW966303

	424585	241151_1	AA464840 AA343628
	426275	263712_1	BE151551 AA373783 BE182852 BE008826 BE008827 BE008781 BE008699
	427980	285225_1	AA418305 AI264351
5	439872	47823_1	T81058 AL357200 T70270
	442197	535550_1	AW837912 AW837934 AA984475 AW997490
	447852	73973_1	AW504781 BE620394
	448422	762770_1	BE263813 BE253504 AI500202 BE251145
	453621	974526_1	AW749983 AL045823
10	454316	1109350_1	AW366144 AW366154 AW366142 AW366151 AW366140 AW366155 BE141715 BE141718 BE141698
	454613	1226904_1	AW810814 AW810787 AW810854 AW810773 AW810735 AW810785 AW810660 AW810834 AW810874 AW810723
			AW810881 AW810791 AW810644 AW810659 AW810676
	454719	1230646_1	BE006547 AW815578 AW815311 AW856304
	455144	1254914_1	AW875942 AW858234 AW875938 AW875941 AW858235 AW875958
15	455818	137219_1	AI733747 AA129802
	455904	1382290_1	BE156173 BE156305 BE156196
	455916	1382748_1	BE156710 BE156726 BE156712
	455984	1397288_1	BE177442 BE177439 BE177445 BE177440 BE177448 BE177444 BE177433

TABLE 22C

	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
25	Strand:	Indicates DNA strand from which exons were predicted.
	NL_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
30	400489	8954013	Plus	131475-131652
	400545	9800107	Minus	124618-124881
	400625	7228177	Minus	117266-117441
	400632	3818355	Plus	72875-73447,75874-76425
	400637	8894326	Plus	68901-69507
35	400675	8118750	Plus	11223-11816
	401007	8117333	Minus	140821-141050
	401082	3242744	Plus	22937-23494,27677-27966
	401223	8099088	Plus	148940-150214
	401551	8096896	Minus	189824-190728
40	401577	9280797	Minus	139377-139674,141195-141281,142217-142340
	401703	4826475	Plus	135-1229
	402056	8084234	Plus	207002-207288
	402100	8117697	Plus	133649-133792
	402195	7689778	Minus	147901-148884
45	402275	2935596	Minus	31065-31233,33680-33771,34345-34411,38890-39125,39779-39943
	402316	7527774	Minus	10751-10919,18817-19052,22131-22328
	402358	8886976	Minus	131788-132729
	402399	1905915	Minus	24502-24666,24986-25102
	402426	9796361	Minus	73590-73824
50	402457	9796782	Minus	16513-16577,16838-16926
	402520	7596899	Minus	171761-171996
	402550	7652009	Minus	80413-80673
	402741	9212200	Minus	18603-18760,19719-19890
	402865	9716300	Plus	3197-3429,3722-3914,5795-5987,6802-6961,8653-8815,9292-9660
55	402959	9368493	Plus	36729-37084
	403121	9180223	Plus	4059-4258
	403368	4388738	Plus	70286-70429,75165-75258
	403552	6862638	Minus	117504-117662
	403731	7543752	Minus	144000-144618
60	404033	8122195	Plus	7976-8156
	404111	9408736	Plus	161506-161781
	404244	5672609	Minus	98173-98517
	404282	2276311	Plus	61503-62205
	404597	9958262	Minus	114369-114599
65	404642	9796810	Plus	102999-103145
	404654	9797010	Plus	6275-6527
	404947	7382205	Plus	29740-30105,30176-30412
	405100	8076846	Plus	144114-144234
	405114	8096938	Minus	97013-97560
70	405228	7248990	Plus	92234-95905
	405313	3638954	Plus	68924-69093
	405324	3342751	Minus	5475-5677
	405479	6453391	Plus	1668-1844
	405895	7677903	Minus	66990-67484
75	406059	9103984	Minus	13856-14004
	406150	9886026	Minus	59331-59701
	406535	7711477	Plus	83135-83362

TABLE 23A: 626 genes upregulated in uterine cancer relative to normal body tissues

Table 23A lists about 626 genes upregulated in uterine cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis

was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

5	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
	Pred.Prod.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
10	UniGene Title:	UniGene gene title
	R1	95th percentile of uterine cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator
15	Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prod.Domains; R1	
		428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase_M10; 35.11
		420440; NM_002407; Hs.97644; mammaglobin 2; Uteroglobulin; 22.80
20		439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretoglobulin, fa; none; 21.66
		425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homolog 4; none; 21.11
		421481; AW391972; Hs.104696; KIAA1324 protein; none; TM=M; SS=M; 20.20
		437938; AI950087; Hs.369628; gb:WQ5C02.X1 NCI_CGAP_Kid12 Homo sapien; none, none; 19.83
		406687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin, Peptidase_M10; 17.68
25		446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin; 17.60
		418281; U09550; Hs.1154; oviductal glycoprotein 1, 120kD (mucin 9; Glyco_hydro_18; TM=M; SS=M; 17.48
		431130; NM_006103; Hs.2719; HE4; epididymis-specific, whey-acidic pr; wap; TM=M; SS=Y; 16.59
		400301; X03635; Hs.1657; estrogen receptor 1; F-box, hormone_rec, zf-C4, Oest_recep, adh_zinc, ketoacyl-synt, pp-binding, Acyl_transf, Thioesterase, ketoacyl-synt_C, AAA, E7, RFX_DNA_binding; TM=M; SS=N; 16.11
30		419356; AI656166; Hs.7331; hypothetical protein FLJ22316; Asparaginase_2, none; 15.90
		433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 15.39
		417931; W95642; Hs.82961; trefol factor 3 (intestinal); trefol; 15.39
		400284; ; NM_000125; Homo sapiens estrogen recepto; hormone_rec, zf-C4, Oest_recep; TM=M; SS=M; 15.23
		456662; NM_002448; Hs.1494; msh (Drosophila) homeo box homolog 1 (fo; homeobox, none; 15.04
35		438817; AI023799; Hs.163242; ESTs; none, none; 13.72
		453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none; TM=Y; SS=M; 13.67
		424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin, Peptidase_M10; 13.51
		458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (S; HMG_box; TM=M; SS=N; 13.44
		410001; AB041036; Hs.57771; kallikrein 11; trypsin; TM=M; SS=M; 13.41
40		421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans, K_tetra, asp; 13.27
		449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp; TM=M; SS=M; 12.76
		436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin; TM=Y; SS=M; 12.59
		450693; AW450461; Hs.203965; ESTs; Sema, lg, none; 12.52
		415457; AW081710; Hs.7369; Homo sapiens testes specific A2 homolog ; MORN, sugar_tr; TM=Y; SS=M; 12.46
45		413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; 12.23
		431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none; TM=M; SS=Y; 12.09
		417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK; TM=M; SS=Y; 12.08
		407786; AA687538; Hs.38972; tetraspan 1; transmembrane4; TM=Y; SS=M; 11.91
		444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 11.86
50		446608; N75217; Hs.175622; ESTs; Armadillo_seg, HEAT_PBS; TM=M; SS=M; 11.72
		447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022 hypothetl; none, UQ_con; 11.59
		420181; AI380089; Hs.158951; ESTs; none, lg, pkinase, LRR, LRRCT; 11.49
		451253; H48299; Hs.26126; claudin 10; PMP22_Claudin, Peptidase_M1, K_tetra; TM=Y; SS=M; 11.45
		453968; AA847843; Hs.62711; High mobility group (nonhistone chromoso; HMG_box, none; 11.42
55		448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec, MIP; TM=M; SS=M; 11.37
		421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz, NTR; 11.08
		452367; U71207; Hs.29279; eyes absent (Drosophila) homolog 2; Hydrolase; 11.01
		409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 10.95
		415138; C18356; Hs.295944; tissue factor pathway inhibitor 2; Kunitz_BPTI, none; 10.91
60		416658; U03272; Hs.79432; fibrillin 2 (congenital contractural ara; EGF, TB, granulin, PSI, EB, TIL; TM=M; SS=M; 10.81
		411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A recepto; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 10.72
		438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zf-C4, none; 10.66
		425071; NM_013989; Hs.154424; deliodinase, iodothyronine, type II; T4_deiodinase; TM=M; SS=Y; 10.66
		430832; AI073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior ; none, none; 10.52
		451497; H83294; Hs.284122; Wnt inhibitory factor-1; EGF, WIF; 10.50
65		421478; AI683243; Hs.97258; ESTs, Moderately similar to S29539 ribos; none, none; 10.50
		409231; AA446644; Hs.692; GA733-2 antigen; epithelial glycoprotein; thyroglobulin_1; TM=Y; SS=M; 10.35
		443785; AW449952; Hs.190125; basic-helix-loop-helix-PAS protein; HLH, PAS; TM=M; SS=N; 10.34
		409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, M, SMC_N, SMC_C, DUF164, none; 10.34
70		431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 10.34
		415539; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; pkinase, Activin_rec, PDZ, ZU5, death; 10.31
		411274; NM_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 10.24
		423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin, Peptidase_M10; TM=M; SS=M; 10.24
		441377; BE218239; Hs.202656; ESTs; none, none; 10.17
75		400292; AA250737; Hs.72472; NAME OMITTED ... receptor kinase; pkinase, Activin_rec, PDZ, ZU5, death; 10.17
		452594; AU076405; Hs.29981; solute carrier family 26 (sulfate transp; xan_ur_permease, Sulfate_transp, STAS, HMG_box; 10.12
		429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic ; C2, PLA2_B; TM=M; SS=N; 9.87
		413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT, none; 9.87
		408562; AI436323; Hs.31141; roundabout (axon guidance receptor, Dros; ig, fn3; TM=M; SS=N; 9.86
		428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); melabo; 7tm_3; TM=Y; SS=M; 9.72
80		438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zf-C4, none; 9.68
		411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none, none; 9.53
		450451; AW591528; Hs.202072; ESTs; none, none; 9.53
		456062; AI866286; Hs.71962; ESTs, Weakly similar to B36298 proline-r; none, none; 9.50

- 418113; AI272141; Hs.83484; SRY (sex determining region Y)-box 4; HMG_box,homeobox;TM=M;SS=N; 9.38
 412791; AI131192; Hs.143199; ESTs, Weakly similar to S72481 probable ; pkinase,PBD:none; 9.36
 432435; BE218886; Hs.282070; ESTs; none:none; 9.35
 5 416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyme); trypsin;TM=M;SS=M; 9.32
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.23
 445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM; 9.19
 410407; X66839; Hs.63287; carbonic anhydrase IX; carb_anhydrase;TM=M;SS=M; 9.19
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 9.17
 10 453459; BE047032; Hs.257789; ESTs; none:none; 9.14
 431674; AA098901; Hs.301642; G-protein coupled receptor; none,GCV_H; 9.05
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 9.00
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 8.93
 436954; AA740151; Hs.130425; ESTs; none:none; 8.91
 15 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 8.89
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisolv,HATPase_cc; 8.85
 407792; AI077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 8.80
 451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN cDNA 2810; none:none; 8.79
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 8.72
 20 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxygenase; IDO;TM=M;SS=N; 8.70
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodi; Somatomedin_B,Endonuclease,Phosphodiect;TM=Y;SS=M; 8.69
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phospho; Ribosomal_L20,Na_Pi_cotrans;TM=Y;SS=N; 8.67
 437935; AW939591; Hs.5940; mucin 13, epithelial transmembrane; EGF,SEA;TM=Y;SS=M; 8.56
 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; DPPIV_N_term,Peptidase_S9:none; 8.55
 25 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 8.53
 428187; AI687303; Hs.285529; G protein-coupled receptor 49; 7tm_1:none; 8.49
 448672; AI955511; Hs.374290; ESTs; lig_chan,ANF_receptor,SBP_bac_3;TM=Y;SS=M; 8.44
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 8.40
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 8.40
 452093; AA447453; Hs.27860; Homo sapiens mRNA; cDNA DKFZp586M0723 (f; 7tm_1:none; 8.33
 30 407894; AJ278313; Hs.41143; phosphoinositide-specific phospholipase ; C2,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 8.23
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 8.21
 419508; AW997939; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 8.20
 424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF; 8.20
 408243; Y00787; Hs.624; interleukin 8; IL8;TM=M;SS=N; 8.00
 35 415752; BE314524; Hs.78776; putative transmembrane protein; none;TM=Y;SS=N; 7.99
 422608; AW160644; Hs.118695; potassium voltage-gated channel, subfam; ion_trans,K_tetra;TM=Y;SS=N; 7.99
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none;; 7.95
 409649; AA159216; Hs.55505; hypothetical protein FLJ20442; Y_phosphatase,DSPc;TM=M;SS=N; 7.95
 424078; AB006625; Hs.139033; paternally expressed 3; zf-C2H2,KRAB:none; 7.86
 40 432179; X75208; Hs.2913; EphB3; EPH_lbd,fn3,pkinase,SAM;TM=Y;SS=M; 7.85
 424581; M62062; Hs.150917; catenin (cadherin-associated protein), a; Vinculin,DNA_ligase_ZBD;TM=M;SS=N; 7.84
 420610; AI683183; Hs.99348; distal-less homeo box 5; homeobox;TM=M;SS=N; 7.81
 436856; AI469355; Hs.127310; ESTs; pkinase,rrm;TM=M;SS=N; 7.81
 45 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 7.80
 407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagon; TGF-beta,DAN; 7.78
 424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 BT095 Homo ; none;TM=M;SS=M; 7.65
 418836; AI655499; Hs.161712; ESTs; pkinase,Activin_recpt,PDZ,ZU5,death; 7.64
 435793; AB037734; Hs.4993; KIAA1313 protein; none;TM=M;SS=N; 7.61
 426201; AW182614; Hs.128499; ESTs; SH3:none; 7.59
 50 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; zf-C3HC4;TM=Y;SS=M; 7.55
 410850; AW362867; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 7.55
 453464; AI884911; Hs.32989; receptor (calcitonin) activity modifying; none;TM=Y;SS=N; 7.54
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm,pkinase;; 7.52
 437897; AA770561; Hs.146170; hypothetical protein FLJ22959; zf-DHHC:none; 7.38
 55 443991; NM_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 7.36
 414617; AI339520; Hs.288817; ESTs, Moderately similar to N Chain N, M; hexokinase,hexokinase2;TM=Y;SS=N; 7.35
 422017; NM_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2;; 7.33
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none:none; 7.30
 409041; AB033025; Hs.50081; Hypothetical protein, XP_051860 (KIAA119; none;TM=M;SS=M; 7.28
 60 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;; 7.28
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;SS=N; 7.28
 418506; AA084248; Hs.372651; Unknown protein for MGC:29643 (formerly ; none:none; 7.27
 448913; AA194422; Hs.22564; myosin VI; rrm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M;SS=N; 7.26
 65 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 7.26
 424317; AI865032; Hs.26017; ESTs; none,pkinase; 7.21
 410361; BE391804; Hs.62661; guanylate binding protein 1, interferon-; GBP,GBP_C;TM=Y;SS=M; 7.21
 70 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;SS=N; 7.14
 438707; L08239; Hs.5326; amino acid system N transporter 2; porcu; ACAT,MBOAT;TM=Y;SS=M; 7.05
 423011; NM_000683; Hs.123022; adrenergic, alpha-2C, receptor; 7tm_1;TM=Y;SS=M; 7.03
 435021; AA922192; Hs.73962; ESTs; EPH_lbd,pkinase,fn3,SAM:none; 7.02
 446163; AA026880; Hs.25252; prolactin receptor; none;NA;NA; 7.01
 75 447768; X86400; Hs.19520; FXFD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=M;SS=N; 7.00
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M;SS=N; 6.99
 451035; AU076785; Hs.430; plastin 1 (I isoform); ehand,CH,Adaptin_N; 6.99
 450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta,TGFb_propeptide;; 6.95
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 6.93
 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUIA S-100 pro; none:none; 6.93
 80 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ_con;TM=M;SS=N; 6.92
 419693; AA133749; Hs.301350; FXFD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 6.92
 437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm_1;TM=Y;SS=M; 6.87
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 6.87

- 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 6.86
 410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; Ski_Sno;TM=M;SS=M; 6.86
 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase_M10;; 6.85
 453064; R40334; Hs.89463; potassium large conductance calcium-acti; none,none; 6.83
 452046; AB018345; Hs.27657; KIAA0802 protein; none;TM=M;SS=N; 6.79
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 6.79
 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glut; aldedh,aakinas;TM=M;SS=N; 6.77
 431470; AA832417; Hs.139650; ESTs; none,ig, pkinase,LRR,LRRCT; 6.76
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none,none; 6.75
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory su; SH2,none; 6.74
 417886; AA214584; ; ESTs; SPRY,7tm_3,ANF_receptor,none; 6.72
 412926; A1879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS;; 6.70
 437960; A1669586; Hs.369312; ESTs; none,none; 6.68
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfami; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD;; 6.66
 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; Idl_recept_a,PKD,MHC_I;TM=M;SS=Y; 6.65
 413040; AA193338; Hs.12321; sodium calcium exchanger; Na_Ca_Ex;TM=Y;SS=M; 6.64
 449656; AA002008; Hs.188633; ESTs; PIP5K,none; 6.64
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-induc; pyr_redox;TM=M;SS=N; 6.62
 446063; A1720140; Hs.151079; ESTs; ISK_Channel,none; 6.61
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none,none; 6.60
 421554; AW137676; Hs.97775; ESTs; none,none; 6.59
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 6.55
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase;TM=M;SS=N; 6.54
 448730; AB032983; Hs.21894; KIAA1157 protein; PP2C;TM=M;SS=N; 6.54
 433577; AW007080; Hs.284192; ESTs; none,none; 6.53
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 6.53
 442133; AW874138; Hs.129017; ESTs; type Ia transmembrane protein; LRR,LRRNT,LRRCT;TM=Y;SS=M; 6.52
 430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 6.52
 434263; N34895; Hs.79187; ESTs; ig,none; 6.49
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M;SS=N; 6.48
 419942; U25138; Hs.93841; potassium large conductance calcium-acti; CakB;TM=Y;SS=M; 6.47
 421064; A1245432; Hs.101382; tumor necrosis factor, alpha-induced pro; none;TM=M;SS=N; 6.47
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 6.45
 431685; AW296135; Hs.267659; vav 3 oncogene; CH,DAG_PE-bind,PH,RhoGEF,SH2,SH3,DC1;TM=M;SS=N; 6.44
 428832; AA578229; Hs.324239; ESTs, Moderately similar to ZN91_HUMAN Z; Osteopontin,none; 6.39
 436775; AA731111; Hs.372225; ESTs; none,none; 6.39
 424343; AW956360; Hs.4748; adenylate cyclase activating polypeptide; 7tm_2,HRM,none; 6.37
 421071; A1311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen; none;TM=Y;SS=M; 6.37
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear transi; HLH,PAS,IL8;TM=M;SS=N; 6.37
 438993; AA828995; ; gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens; EGF,metalthio,integrin_B,PSI,none; 6.27
 406400; ; kallikrein 8 (neuropsin/ovasin) (KLK8); trypsin;TM=M;SS=M; 6.27
 429556; AW139399; Hs.314807; ESTs; none;TM=M;SS=N; 6.26
 409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-like; H5AR g; Steroid_dh;TM=Y;SS=M; 6.25
 435732; AF229178; Hs.123136; leucine rich repeat and death domain con; none,none; 6.24
 439668; A1091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 6.24
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (; MIF,sugar_tr,none; 6.23
 436961; AW375974; Hs.156704; ESTs; none,none; 6.23
 434808; AF155108; Hs.256150; NY-REN-41 antigen; none;TM=M;SS=N; 6.22
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-I; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 6.20
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; ethand;; 6.20
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,ig,Neuregulin;TM=M;SS=N; 6.19
 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 6.19
 452551; L27071; Hs.29877; TXK tyrosine kinase; Beach,WD40,SH2,SH3,pkinase;TM=M;SS=N; 6.14
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;SS=N; 6.12
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 6.11
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM,PDZ,pkinase;; 6.11
 449700; L02867; Hs.78358; paraneoplastic antigen; none;TM=M;SS=N; 6.10
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 6.10
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient, yeast, h; HORMA;TM=M;SS=N; 6.09
 433159; AB035898; Hs.150587; kinesin-like protein 2; bZIP,kinesin;; 6.08
 432432; AA541323; Hs.115831; ESTs; ig,Sema,PSI,none; 6.07
 409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG;TM=M;SS=N; 6.04
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M;SS=N; 6.03
 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip;TM=M;SS=Y; 6.03
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.00
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing le; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 6.00
 428677; A1657119; Hs.351582; troponin I, cardiac; none;TM=M;SS=N; 6.00
 450098; W27249; Hs.8109; hypothetical protein FLJ21080; SET,zf-MYND;TM=M;SS=N; 6.00
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, com; C1q,Collagen;; 5.99
 419972; AL041465; Hs.182982; golgin-67; none,none; 5.99
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ;; 5.97
 403362; ; NM_001615; Homo sapiens actin, gamma 2, ; actin;; 5.95
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg;TM=M;SS=N; 5.95
 420253; A1656055; Hs.96200; neighbor of A-kinase anchoring protein 9; none;NA;NA; 5.93
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M;SS=N; 5.93
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 5.92
 450747; A1064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm,zf-RanBP,GAS2; 5.92
 415211; R64730.comp; Hs.155986; DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; DEAD,helicase_C,rm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPc,isp_1,Ribosomal_S21,rvp;TM=M;SS=N; 5.91
 429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin) receptor; 7tm_1;TM=Y;SS=N; 5.90
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazaro; none;TM=Y;SS=N; 5.89
 437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none;TM=Y;SS=M; 5.89
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 5.89

- 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm_2;TM=Y;SS=M; 5.87
- 426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 5.85
- 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 5.85
- 5 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;SS=N; 5.84
- 450502; T08065; Hs.118262; ESTs; ion_trans,ion_trans; 5.84
- 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; none;TM=M;SS=N; 5.83
- 424917; AI636208; Hs.96901; hypothetical protein FLJ23049; none;TM=M;SS=N; 5.83
- 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;SS=N; 5.82
- 10 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M;SS=N; 5.82
- 445133; AW157646; Hs.198689; ESTs; ehfand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FlitD,bZIP,Tropomyosin,Myc-LZ,M,ldh_C,CH,AIP3;TM=M;SS=N; 5.79
- 426215; AW963419; Hs.155223; stanniocalcin 2; Stanniocalcin; 5.78
- 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 5.75
- 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=N; 5.74
- 15 452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox,none; 5.72
- 432201; AI538613; Hs.298241; Transmembrane protease, serine 3; tdl_recept_a,trypsin;TM=Y;SS=M; 5.72
- 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 5.72
- 449458; AI805078; Hs.208261; ESTs; Frizzled,Fz,none; 5.72
- 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 5.71
- 20 418848; AI820961; Hs.193465; ESTs; PDZ,pkinase,none; 5.70
- 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1;TM=Y;SS=M; 5.69
- 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1;TM=M;SS=N; 5.69
- 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin;TM=M;SS=N; 5.69
- 445136; AI348014; Hs.143949; ESTs, Weakly similar to Achaete-Scute ho; ion_trans,ion_trans; 5.69
- 25 409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory su; SH2,SH3,RhoGAP,none; 5.67
- 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y;SS=N; 5.66
- 429638; AI916662; Hs.211577; kinesin 1 (kinesin receptor); bZIP,Tropomyosin,spectrin,LBP,BPI_CETP,B56,M;TM=Y;SS=M; 5.65
- 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2;TM=Y;SS=M; 5.64
- 453950; AA156998; Hs.348037; eukaryotic translation initiation factor; none; 5.64
- 30 425889; M57414; Hs.161305; tachykinin receptor 2; 7tm_1;TM=Y;SS=M; 5.64
- 432527; AW975028; Hs.102754; ESTs; none,none; 5.64
- 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 5.63
- 419080; AW150835; Hs.18878; hypothetical protein FLJ21620; 2OG-Fel1_Oxy;TM=M;SS=N; 5.63
- 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C;TM=M;SS=M; 5.61
- 35 440422; AW452696; Hs.130760; myosin phosphatase, target subunit 2; BTB,Kelch,ank,none; 5.58
- 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome;TM=M;SS=N; 5.58
- 432805; X94630; Hs.3107; CD97 antigen; 7tm_2,EGF,GPS,FecCD;TM=Y;SS=M; 5.55
- 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; Ig,Isodh,Ribosomal_L6,F-box;TM=Y;SS=M; 5.55
- 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; WD40,fn3,Ig;TM=M;SS=N; 5.54
- 40 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none,none; 5.54
- 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 5.53
- 404210; ; NM_005936;Homo sapiens myeloid/lymphoid ; FHA,PDZ,RA,DIL;TM=M;SS=N; 5.53
- 408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 5.53
- 436726; AA324975; Hs.198689; ESTs, Weakly similar to T00079 hypotheti; ehfand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FlitD,bZIP,Tropomyosin,Myc-LZ,M,ldh_C,CH,AIP3;TM=M;SS=N; 5.53
- 45 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none,none; 5.52
- 428667; AI375550; Hs.346868; nucleolar protein p40; homolog of yeast ; none,none; 5.51
- 433907; AW296107; Hs.152686; ESTs; Armadillo_seg,none; 5.50
- 442821; BE391929; Hs.8752; transmembrane protein 4; none; 5.50
- 50 422282; AF019225; Hs.114309; apolipoprotein L; Mota_ExbB;TM=Y;SS=M; 5.49
- 439820; AL360204; Hs.283853; Homo sapiens mRNA full length insert cDN; none,none; 5.49
- 428771; AB028992; Hs.193143; KIAA1069 protein; C2,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 5.48
- 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HE; GDI,7tm_1,none; 5.48
- 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C1; none,none; 5.48
- 55 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 5.47
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR;TM=M;SS=N; 5.47
- 420297; AI628272; Hs.128757; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,TUDOR,none; 5.47
- 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3; 5.46
- 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2,STAT,STAT_bind,STAT_prot,none; 5.45
- 60 441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia vi; pkinase,Recep_L_domain,Furin-like,YLP,none; 5.44
- 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS; 5.43
- 450402; BE218027; Hs.89969; ESTs; SH3,none; 5.42
- 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 5.42
- 65 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 5.42
- 412350; AI659306; Hs.73826; protein tyrosine phosphatase, non-recept; Y_phosphatase,Band_41,PDZ;TM=M;SS=N; 5.42
- 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH,none; 5.41
- 448379; AI097463; Hs.21035; KIAA1130 protein; none,Zip; 5.41
- 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; rrm;TM=M;SS=N; 5.41
- 70 411817; BE302900; Hs.72241; mitogen-activated protein kinase kinase ; pkinase;TM=M;SS=M; 5.40
- 445413; AA151342; Hs.12677; CGI-147 protein; UPF0099;TM=M;SS=M; 5.39
- 451863; AL120634; Hs.331803; ATPase, Ca transporting, plasma membrane; cpn60_TCP1,E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase; 5.38
- 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra,DUF51,none; 5.38
- 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrola; PAF-AH_Ib,Lipase_GDSL;TM=M;SS=N; 5.36
- 75 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin; 5.34
- 441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C,G-alpha,arf;TM=M;SS=M; 5.33
- 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/pep; PTR2;TM=Y;SS=N; 5.33
- 435391; AA704588; Hs.58934; ESTs; PIP5K,none; 5.33
- 411779; AA292811; Hs.72050; non-metastatic cells 5, protein expresse; NDK; 5.33
- 80 422170; AI791949; Hs.112432; anti-Mullerian hormone; TGF-beta; 5.32
- 447350; AI735572; Hs.172634; v-erb-a avian erythroblastic leukemia vi; pkinase,Recep_L_domain,Furin-like,YLP,none; 5.32
- 449964; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase;TM=M;SS=N; 5.31
- 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 5.30
- 430407; H23551; Hs.30974; ESTs; pkinase,PBD,none; 5.29

- 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3;TM=M;SS=N; 5.27
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; ig,kringle,pkinase,Fz;TM=Y;SS=M; 5.27
 424596; AB020639; Hs.151017; estrogen-related receptor gamma; hormone_rec,zf-C4;TM=M;SS=N; 5.27
 428013; AF151020; Hs.181444; hypothetical protein; none;TM=Y;SS=M; 5.26
 447384; AI377221; Hs.40528; ESTs; SH3,Sorb,none; 5.26
 441824; AB007871; Hs.7977; KIAA0411 gene product; SH3,RhoGAP;TM=M;SS=N; 5.26
 438493; AI130740; Hs.6241; phosphoinositide-3-kinase, regulatory su; SH2,SH3,RhoGAP;TM=M;SS=N; 5.26
 428579; NM_005756; Hs.184942; G protein-coupled receptor 64; 7tm_2,GPS;TM=Y;SS=M; 5.25
 414359; M62194; Hs.75929; cadherin 11, type 2, OB-cadherin (osteob; cadherin,Cadherin_C_term;TM=Y;SS=M; 5.25
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 5.24
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;SS=N; 5.24
 423685; BE350494; Hs.49753; uveal autoantigen with coiled coil domai; ank,bZIP,M,DUF164,AIP3;; 5.23
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-pho; MORN,sugar_tr;TM=Y;SS=M; 5.23
 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M;SS=N; 5.23
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF;; 5.23
 412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 5.23
 426770; AI948618; Hs.150178; ESTs; Sulfate_transp,STAS;TM=Y;SS=N; 5.23
 422583; AA410506; Hs.27973; KIAA0874 protein; ank,G-alpha;TM=M;SS=N; 5.22
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 5.22
 448093; AW977382; Hs.15898; 2,4-dienoyl CoA reductase 2, peroxisomal; adh_short;; 5.21
 443646; AI085198; Hs.164226; Thrombospondin 1; EGF,tsp_1,vwc,TSPN,tsp_3,none; 5.18
 457916; BE085271; Hs.8834; ring finger protein 3; pkinase,none; 5.18
 433933; AI754389; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none;NA;NA; 5.18
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none;; 5.17
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC_tran,arf;TM=M;SS=M; 5.17
 450511; R07423; Hs.85092; thyroid hormone receptor interactor 11; Myosin_tail,EGF; 5.16
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 no; none;TM=M;SS=N; 5.15
 454438; AA224053; Hs.172405; cell division cycle 27; SPRY,7tm_3,ANF_receptor; 5.14
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 5.14
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial; mito_carr;TM=M;SS=N; 5.14
 415474; NM_014252; Hs.78457; solute carrier family 25 (mitochondrial; mito_carr;TM=M;SS=N; 5.14
 411704; AI499220; Hs.71573; hypothetical protein FLJ10074; pkinase;TM=M;SS=N; 5.13
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 5.13
 454128; AL031259; Hs.367900; programmed cell death 2; zf-MYND;TM=M;SS=N; 5.13
 431322; AW970622; Hs.376626; gb:EST382704 MAGE resequences, MAGK Homo; none,none; 5.13
 444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none;TM=Y;SS=M; 5.12
 422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; tsp_3,EGF;; 5.12
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 5.11
 436494; AA720997; Hs.128295; ESTs; none,CAP_GLY,HCO3_cotransp,Glyco_hydro_63,PH; 5.11
 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA synthetas; WHEP-TRS,tRNA-synt_1b,none; 5.10
 453387; AI990741; Hs.252809; ESTs; Na_Ca_Ex,none; 5.07
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M;SS=N; 5.07
 456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3;TM=M;SS=N; 5.07
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanlylate_kin,PDZ,SH3; 5.07
 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase,DCX;TM=M;SS=N; 5.06
 413745; AW247252; Hs.75514; nucleoside phosphorylase; Mtap_PNP;; 5.06
 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, y; none,Ribosomal_S13,Galactosyl_T,Zip,adh_short,zf-C3HC4; 5.06
 421369; NM_005089; Hs.171909; U2 small nuclear ribonucleoprotein auxil; rrm,zf-CCCH,lectin_c,integrin_B;TM=M;SS=N; 5.06
 412170; D16532; Hs.73729; very low density lipoprotein receptor; ldl_recept_a,ldl_recept_b,EGF;TM=M;SS=M; 5.06
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;SS=N; 5.05
 421109; L32832; Hs.101842; AT-binding transcription factor 1; HMG14_17,homeobox,zf-C2H2;TM=M;SS=M; 5.05
 453880; AI803166; Hs.135121; ESTs, Weakly similar to 138022 hypotheti; HSP70,none; 5.05
 431512; BE270734; Hs.2795; lactate dehydrogenase A; ldh,ldh_C,SH3,pkinase,UBA;TM=M;SS=N; 5.05
 435411; AW444619; Hs.138211; ESTs; none,pkinase; 5.04
 419088; AI538323; Hs.367688; Integrin, beta 8; integrin_B,none; 5.04
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX; Troponin,Exo_endo_phos,IQ;TM=M;SS=N; 5.04
 428376; AF119665; Hs.184011; pyrophosphatase (inorganic); Pyrophosphatase;TM=M;SS=N; 5.03
 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9;TM=M;SS=M; 5.03
 436415; BE265254; Hs.343258; proliferation-associated 2G4, 38kD; Peptidase_M24,Furin-like,pkinase,Recep_L_domain,efhand; 5.01
 449674; AW444937; Hs.233482; ESTs; C2,PI-PLC-Y,PI-PLC-X,none; 5.01
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras,arf,TK;; 5.01
 412133; U83460; Hs.104557; solute carrier family 31 (copper transpo; none;TM=Y;SS=N; 5.01
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;; 5.00
 449474; AA019344; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; ThiF,UBACT,pkinase,UCH-2,UCH-1,rrm,zf-C2H2,zf-RanBP,G-patch; 5.00
 416365; U15131; Hs.79265; suppression of tumorigenicity 5; DENN,dDENN,uDENN;TM=M;SS=N; 5.00
 421351; AU076667; Hs.103755; receptor-interacting serine-threonine ki; CARD,pkinase;TM=M;SS=N; 4.99
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 4.98
 442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; rrm,IRK;; 4.95
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT; none,none; 4.95
 426310; NM_000909; Hs.169266; neuropeptide Y receptor Y1; 7tm_1;TM=Y;SS=M; 4.95
 457718; F18572; Hs.22978; ESTs, Weakly similar to ALU4_HUMAN ALU S; pkinase,pkinase; 4.94
 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase;TM=M;SS=N; 4.94
 427541; AI798983; Hs.375835; solute carrier family 35 (CMP-sialic aci; none,none; 4.94
 452792; AB037765; Hs.30652; KIAA1344 protein; thiores;TM=M;SS=M; 4.93
 430713; AA351647; Hs.2642; eukaryotic translation elongation factor; GTP_EFTU,GTP_EFTU_D3,GTP_EFTU_D2;; 4.93
 444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP,none; 4.93
 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin (neuronal; HNH,cadherin,Cadherin_C_term;TM=M;SS=N; 4.92
 421302; T34462; Hs.103291; neuritin; none;TM=M;SS=Y; 4.91
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisi; pkinase;TM=M;SS=N; 4.91
 408657; AA782601; Hs.378649; ESTs; B56,none; 4.91
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 4.91
 421462; AF016495; Hs.104624; aquaporin 9; MIP;TM=Y;SS=M; 4.90
 424503; NM_002205; Hs.149609; integrin, alpha 5 (fibronectin receptor;; integrin_A,FG-GAP;TM=Y;SS=N; 4.89

- 438564; AA381553; Hs.198253; major histocompatibility complex, class ; ig,MHC_II_alpha,none; 4.89
 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 4.88
 434521; NM_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg,IBB;TM=M;SS=N; 4.88
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig;TM=Y;SS=M; 4.88
 424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosp; perilipin;; 4.88
 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; DEAD,helicase_C,PRK,ALP3;TM=M;SS=N; 4.87
 417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone H; voltage_CLC,CBS,none; 4.86
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C; Phosphodiester,Somatomedin_B,Endonuclease,none; 4.86
 417666; AI345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4;TM=M;SS=N; 4.86
 453864; AW021407; Hs.21068; hypothetical protein; none,none; 4.86
 453082; H18835; Hs.31608; hypothetical protein FLJ20041; ion_trans;TM=Y;SS=M; 4.85
 413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like ; SH2,SAM,Exo_endo_phos;; 4.85
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;; 4.85
 435652; N32388; Hs.334370; uncharacterized hypothalamus protein HBE; none;TM=M;SS=N; 4.84
 419355; AA428520; Hs.90061; progesterone binding protein; heme_1;TM=Y;SS=M; 4.83
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 4.83
 408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC_tran,ABC_membrane,PRK,Bac_export_3;TM=Y;SS=N; 4.83
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 4.82
 435232; NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank;TM=M;SS=N; 4.81
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,pkinase;TM=M;SS=N; 4.81
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.81
 453354; W55946; Hs.234863; Homo sapiens cDNA FLJ12082 fis, clone HE; transmembrane4,none; 4.81
 450883; NM_001348; Hs.25619; death-associated protein kinase 3; pkinase;TM=M;SS=N; 4.79
 429736; AF125304; Hs.212680; tumor necrosis factor receptor superfam; TNFR_c6;TM=M;SS=M; 4.79
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept;TM=M;SS=M; 4.79
 409960; BE261944; Hs.355264; hexokinase 1; none,none; 4.78
 422795; AB033109; Hs.375610; KIAA1283 protein; 7tm_1,kazal,A2M,A2M_N;TM=Y;SS=M; 4.78
 423619; T48691; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm_1,7tm_2;TM=Y;SS=M; 4.78
 429305; AF095727; Hs.287832; myelin protein zero-like 1; ig,transmembrane4;TM=Y;SS=M; 4.78
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPC;TM=M;SS=N; 4.77
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 4.76
 444672; Z95636; Hs.11669; laminin, alpha 5; laminin_EGF,laminin_G,EGF,TNFR_c6,laminin_B,laminin_Nterm,metalthio,Tropomyosin,DUF164,p450;TM=M;SS=N; 4.76
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; pfbK;TM=M;SS=N; 4.75
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 4.75
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_Oxidase;; 4.75
 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;; 4.75
 425548; AA890023; Hs.1906; prolactin receptor; ln3;TM=Y;SS=M; 4.73
 434158; T86534; Hs.14372; ESTs; adenylatekinase,none; 4.73
 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypotheti; none,SH3,myosin_head,IQ; 4.73
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 4.73
 434503; T96231; Hs.17762; ESTs; SH3,Sorb,none; 4.73
 446342; BE298665; Hs.14846; solute carrier family 7 (cationic amino ; none;TM=M;SS=N; 4.72
 427418; AA402587; Hs.356667; LAT1-3TM protein; none,none; 4.71
 449433; AI672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-bind; Frizzled,Fz,Frizzled,Fz; 4.71
 418910; Z25821; Hs.89466; Homo sapiens, Similar to dodecenoyl-Coen; ECH;; 4.70
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,tRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M; 4.70
 442199; BE277633; Hs.372542; etoposide-induced mRNA; none;TM=Y;SS=M; 4.69
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 4.69
 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 ; none;; 4.69
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domai; death,DED;; 4.68
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;SS=N; 4.68
 443323; BE560621; Hs.9222; estrogen receptor binding site associate; none;TM=M;SS=M; 4.68
 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor;; integrin_A,FG-GAP;TM=Y;SS=N; 4.68
 418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodi; Phosphodiester;TM=Y;SS=M; 4.67
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,integrin_B;; 4.67
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 4.66
 407844; AW073716; Hs.8037; ESTs; transmembrane4,none; 4.66
 450656; AA010539; Hs.18912; unnamed protein product; zf-C2H2;; 4.66
 420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-530115; none,none; 4.65
 404287; ; FGENESH predicted novel CUB-domain conta; none,none; 4.64
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd_glycop;TM=Y;SS=M; 4.63
 426680; AA320160; Hs.171811; adenylate kinase 2; adenylatekinase;TM=M;SS=N; 4.63
 430397; AI924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;SS=N; 4.63
 447656; NM_003726; Hs.19126; src kinase-associated phosphoprotein of ; SH3,PH;TM=M;SS=N; 4.63
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M;SS=N; 4.62
 429126; AW172356; Hs.99083; ESTs; 7tm_1,none; 4.61
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 4.60
 409220; BE243323; Hs.51233; tumor necrosis factor receptor superfam; TNFR_c6,death,Lipoprotein_5,TIL;TM=Y;SS=M; 4.60
 421921; H83363; Hs.355993; translocase of inner mitochondrial membr; zf-Tim10_DDP,efhand,CH,spectrin,serpin;TM=M;SS=N; 4.60
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 4.59
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; none,Cys_knot; 4.59
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans;TM=Y;SS=M; 4.59
 409645; AI142265; Hs.55498; geranylgeranyl diphosphate synthase 1; polyprenyl_synt;TM=M;SS=N; 4.59
 427373; AB007972; Hs.130760; myosin phosphatase, target subunit 2; ank;TM=M;SS=N; 4.58
 437212; AI765021; Hs.210775; ESTs; UDPGT,none; 4.58
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZUS,EGF,kringle,trypsin,Nebulin,LIM;; 4.57
 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 4.56
 416041; AA345547; Hs.53263; hypothetical protein FLJ13287; WD40;; 4.55
 434511; R28982; Hs.18106; ESTs; pkinase,Glyco_hydro_39; 4.55
 410174; AA306007; Hs.59461; DKFZP434C245 protein; none,DSPC; 4.55
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M;SS=N; 4.55
 451367; AA923729; Hs.26322; cell cycle related kinase; pkinase;TM=M;SS=N; 4.54

- 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR,LRRNT,LRRCT;TM=Y;SS=M; 4.54
 411296; BE207307; Hs.10114; growth suppressor 1; ZOG-Fell_Oxy;TM=M;SS=M; 4.53
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph); Ham1p_like;TM=M;SS=N; 4.53
 431992; NM_002742; Hs.2891; protein kinase C, mu; pkinase,DAG_PE-bind,PH;TM=M;SS=M; 4.53
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 4.53
 428005; AW302245; Hs.181390; casein kinase 1, gamma 2; pkinase;TM=M;SS=N; 4.52
 407775; NM_004914; Hs.38772; RAB36, member RAS oncogene family; ras,arf;TM=M;SS=N; 4.52
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 4.51
 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HE; none,none; 4.51
 405484; ; C3002124;gij12737280[ref]XP_006682.2[k]; none; 4.50
 443605; H06865; Hs.134131; ESTs; efhand,ion_trans,none; 4.50
 431738; AW237726; Hs.288549; hypothetical protein FLJ14710; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 4.50
 422112; BE540240; Hs.111783; Lsm1 protein; Sm,BAG; 4.49
 418869; AW516555; ; gb:xq01d05.x1 Soares_NHCeC_cervical_tumo; none,RasGAP,WW,IQ; 4.48
 447898; AW969638; Hs.112318; 6.2 kd protein; none,none; 4.48
 450607; AL050373; Hs.25213; hypothetical protein; SH3;TM=M;SS=N; 4.48
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; ig;TM=Y;SS=M; 4.48
 424823; NM_006226; Hs.153322; phospholipase C, epsilon; C2,PH,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 4.48
 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chlo; none;TM=Y;SS=N; 4.47
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase,Recep_L_domain,YLP,none; 4.47
 435615; Y15065; Hs.4975; potassium voltage-gated channel, KQT-like; ion_trans,KCNQ1_channel;TM=Y;SS=N; 4.47
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_inh; 4.47
 428727; AF078847; Hs.78452; general transcription factor IIH, polype; PHO4,LIM;TM=M;SS=N; 4.46
 412760; AW379030; Hs.41324; ESTs; Cbl_N,Cbl_N2,Cbl_N3,UBA,zf-C3HC4,none; 4.46
 409093; BE243834; Hs.50441; CGI-04 protein; Ribosomal_L37ae, pkinase,POLO_box,tRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M; 4.46
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate aps; APS_kinase,ATP-sulfurylase,PRK,Thymidylate_kin; 4.46
 447434; R16890; Hs.137135; ESTs; pkinase,fn3,jg, pkinase,fn3; 4.45
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar_lr; 4.45
 414108; AI267592; Hs.75761; SFPS protein kinase 1; ank,PH,Oxysterol_BP, pkinase;TM=M;SS=N; 4.44
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;SS=N; 4.44
 409686; AK000002; Hs.55879; Homo sapiens mRNA; cDNA DKFZp434L0827 (f; ABC_tran,ABC_membrane;TM=M;SS=M; 4.44
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3,none; 4.44
 436823; AW749865; Hs.117077; ESTs, Weakly similar to I38022 hypotheti; aa_permeases,zf-C2H2,KRAB,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_Pi4_kinase,FAT,FATC,BolA,RUN,TFIIS;TM=M;SS=N; 4.44
 450505; NM_004572; Hs.25051; plakophilin 2; Armadillo_seg;TM=M;SS=N; 4.43
 437915; AI637993; Hs.202312; Homo sapiens clone N11 Ntera2D1 teratoca; none,none; 4.43
 417412; X16896; Hs.82112; interleukin 1 receptor, type I; ig,TIR;TM=M;SS=M; 4.43
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 4.43
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor; ; inositol_P;ig;TM=M;SS=N; 4.43
 452124; AA454220; Hs.61170; ESTs; pkinase,none; 4.43
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) ; NDK,PH,Oxysterol_BP; 4.42
 416202; AW964492; Hs.169624; ESTs; none;TM=M;SS=N; 4.42
 441518; AW161697; Hs.294150; ESTs; Y_phosphatase,DSPc,none; 4.42
 441680; AW444598; Hs.7940; RAP1, GTP-GDP dissociation stimulator 1; Armadillo_seg;TM=M;SS=N; 4.42
 431429; AF072813; Hs.252831; reticulon 3; Reticulon,Fz,ig,kringle, pkinase;TM=Y;SS=N; 4.42
 453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 fis, clone L; FG-GAP,integrin_A,NIF; 4.41
 421242; AW161386; Hs.13561; hypothetical protein MGC4692; none;NA;NA; 4.41
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M;SS=N; 4.41
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death,ZU5; 4.41
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M;SS=N; 4.41
 413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;SS=N; 4.41
 458097; AW341135; Hs.58104; ESTs; none,SH3,PID; 4.40
 458246; BE407379; Hs.108082; ESTs, Weakly similar to T31636 hypotheti; C1q,Collagen;TM=M;SS=Y; 4.40
 427681; AB018263; Hs.284232; tumor necrosis factor receptor superfam; death,TNFR_c6,PH,Xlink,RhoGEF,Metallothio_5;TM=M;SS=M; 4.40
 443693; AI344782; Hs.9683; DnaJ (Hsp40) homolog, subfamily C, membe; rm,DnaJ,TPR;TM=M;SS=N; 4.40
 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating pr; bromodomain;TM=M;SS=N; 4.39
 453891; AB037751; Hs.301242; Homo sapiens mRNA full length insert cDN; none,none; 4.39
 442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 4.39
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig;TM=Y;SS=M; 4.37
 445817; NM_003642; Hs.13340; histone acetyltransferase 1; none;TM=M;SS=N; 4.37
 444895; AI674383; Hs.22891; solute carrier family 7 (cationic amino ; ASC,death,TNFR_c6; 4.37
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg;TM=M;SS=M; 4.37
 432108; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3,PDZ,Guanylate_kin,none; 4.37
 418283; S79895; Hs.83942; cathepsin K (pseudosostosis); Peptidase_C1; 4.37
 445826; BE313754; Hs.13350; Homo sapiens mRNA; cDNA DKFZp586D0918 (f; ig,lsp_1,ZU5,Nucleoside_tran; 4.37
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=Y;SS=N; 4.36
 400257; ; Hs.76366; ENSP00000000452:BAD protein (BCL-2 bindi; none;TM=M;SS=N; 4.36
 431476; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT; 4.36
 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none;TM=M;SS=N; 4.36
 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD,none; 4.36
 427716; L38951; Hs.180446; karyopherin (importin) beta 1; Armadillo_seg,HEAT;TM=M;SS=N; 4.35
 425843; BE313280; Hs.159627; death associated protein 3; myb_DNA-binding,PAH,BAH,bromodomain,PHD,SET;TM=M;SS=N; 4.35
 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms; pkinase,ig, pkinase,ig,p450,SET,PWWP; 4.35
 445926; AF054284; Hs.334826; splicing factor 3b, subunit 1, 155kD; none;TM=M;SS=N; 4.35
 410726; AI623859; Hs.15936; ESTs; pkinase,pro_isomerase,none; 4.35
 433996; AW135357; Hs.192374; ESTs; HSP90,HATPase_c,UDG; 4.34
 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog) ; none;TM=M;SS=N; 4.34
 437103; AW139408; Hs.152940; ESTs; Choline_kinase,none; 4.34
 410068; AI633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3;TM=M;SS=N; 4.34
 427349; AA360154; Hs.177415; Finkel-Biskis-Reilly murine sarcoma viru; ubiquitin;TM=M;SS=N; 4.33
 439807; AA376417; Hs.374608; hypothetical protein MGC5244; ; abhydrolase_2;TM=M;SS=M; 4.33
 453308; AW959731; Hs.323099; ESTs; none, pkinase,Activin_recp; 4.33
 424893; AW295112; Hs.153648; Homo sapiens cDNA FLJ13303 fis, clone OV; SAM; 4.33

444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-S; DSPc;TM=M;SS=N; 4.33
 429655; U48959; Hs.211582; myosin, light polypeptide kinase; pkinase,fn3,ig,none; 4.32
 409121; AA902256; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR,none; 4.32
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 4.32
 423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbon; HCO3_cotransp;TM=Y;SS=M; 4.29
 425654; AB033022; Hs.158654; KIAA1196 protein; zf-C2H2;TM=M;SS=N; 4.29
 457500; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm,pkinase;TM=M;SS=N; 4.29
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 4.29
 447191; NM_014521; Hs.17667; SH3-domain binding protein 4; SH3;TM=M;SS=N; 4.29
 408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc;TM=M;SS=N; 4.29
 441130; AI160734; Hs.267604; Homo sapiens PNAS-129 mRNA, complete cds; BTB,Kelch,K_tetra,DSPc;TM=M;SS=N; 4.28
 430057; AW450303; Hs.2534; bone morphogenetic protein receptor, typ; Activin_rec,pkinase;TM=Y;SS=M; 4.28
 430250; NM_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;SS=N; 4.28
 406774; AW518383; Hs.177592; ribosomal protein, large, P1; 60s_ribosomal; 4.28
 413809; L25851; Hs.851; integrin, alpha E (antigen CD103, human; vwa,integrin_A,FG-GAP;TM=M;SS=Y; 4.27
 443960; AI093577; Hs.255416; hypothetical protein FLJ21986; TTL;TM=M;SS=N; 4.27
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE;TM=M;SS=N; 4.27
 412204; AI125507; Hs.24937; ESTs; ig,rrm,none; 4.26
 439506; AI361238; Hs.41136; ESTs; MAM,pkinase,Nucleoplasmin,none; 4.26
 451295; AI557212; Hs.17132; ESTs; Moderately similar to I54374 gene; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.26
 452488; N74921; Hs.184389; ESTs; none;TM=M;SS=N; 4.26
 450973; AF012072; Hs.25732; eukaryotic translation initiation factor; W2,MA3,MIF4G;TM=M;SS=N; 4.26
 452437; AA026237; Hs.181272; ESTs; efhand,ion_trans,none; 4.26
 438204; AI589645; Hs.128690; ESTs; none;7tm_1; 4.25
 424756; AW504657; Hs.152931; lamin B receptor; ERG4_ERG24,FKBP;TM=Y;SS=N; 4.25
 430570; AI417881; Hs.292464; ESTs; 7tm_2,Fz,Frizzled,none; 4.25
 445709; H02592; Hs.74280; ESTs; PDZ,none; 4.25
 428134; AA421773; Hs.161008; ESTs; Armadillo_seg,none; 4.24
 434149; Z43829; Hs.244624; hypothetical protein MGC5469; none;TM=M;SS=M; 4.24
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M;SS=N; 4.24
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 4.24
 447818; W79940; Hs.355279; Homo sapiens clone 24670 mRNA sequence; none,pkinase; 4.24
 450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig;TM=Y;SS=M; 4.23
 435542; AA687376; Hs.351226; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 4.23
 426224; BE085860; Hs.374468; karyopherin (importin) beta 2; Armadillo_seg,HEAT;TM=M;SS=N; 4.23
 413284; AU077055; Hs.289107; baculoviral IAP repeat-containing 2; zf-C3HC4,CARD,BIR,death,ig;TM=M;SS=N; 4.22
 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P14_kinase,PI3Ka;TM=M;SS=N; 4.22
 431239; AL039971; Hs.251216; hypothetical protein DKFZp434A196; SH2,ank,WH2; 4.22
 419685; W76083; Hs.134185; ESTs; none;TM=M;SS=N; 4.22
 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha; FG-GAP,Rhabd_glycop,integrin_A;TM=Y;SS=M; 4.22
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none; 4.21
 422219; AW978073; Hs.1010; regulator of mitotic spindle assembly 1; pkinase,none; 4.21
 450746; D82673; Hs.278589; general transcription factor II, i; none,SH3,PX; 4.21
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone L; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 4.21
 416907; W60909; ; gb:zd29g10.s1 Soares_fetal_heart_NbHH19W; ion_trans,none; 4.21
 411768; NM_013371; Hs.71979; interleukin 19; IL10; 4.21
 425262; D87119; Hs.155418; GS3955 protein; pkinase; 4.21
 430035; NM_003463; Hs.227777; protein tyrosine phosphatase type IVA, m; Y_phosphatase,DSPc;TM=M;SS=N; 4.21
 411789; AF245505; Hs.72157; Adican; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 4.15
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none,none; 4.14
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 4.13
 431745; AW972448; Hs.163425; Novel FGENESH predicted cadherin repeat; none,none; 4.10
 416965; N26223; Hs.160436; MDAC1; none;NA;NA; 3.94
 426890; AA393167; Hs.41294; ESTs; none,none; 3.88
 442438; AA995998; Hs.370007; gb:os26b03.s1 NCI_CGAP_Kld5 Homo sapiens; none,DNA_pol_B,DNA_pol_B_exo; 3.86
 412314; AA825247; Hs.356084; downstream of: G protein-coupled recepto; 7tm_1;TM=Y;SS=M; 3.84
 448243; AW369771; Hs.367688; integrin, beta 8; integrin_B,none; 3.64
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2,CytC_asm,GPS;TM=Y;SS=M; 3.61
 415999; AA172179; Hs.294029; ESTs; none,none; 3.60
 429466; M85835; Hs.12827; ESTs; none,none; 3.45
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none;TM=M;SS=Y; 3.34
 400517; ; lingsin; none;TM=M;SS=N; 3.17
 439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.88
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.84
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 2.81
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C; 2.70
 438167; R28363; Hs.24286; chemokine binding protein 2 (CCBP2), mRNA; none;TM=Y;SS=M; 2.68
 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestin; cadherin;TM=Y;SS=M; 2.17

TABLE 23B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409745	MH1944_5	BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI0129864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
438993	2580163_1	AI926361 AA834879 AA828995

418869 12789_14 AA229762 AA230035
416907 1112245_1 W60909 W61051 M78905 BG959483

TABLE 23C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
406400	9256298	Plus	1553-1712, 1878-2140, 4252-4385, 5922-6077
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404287	2326514	Plus	53134-53281
405484	5922025	Plus	199214-199579, 199672-199920, 200262-20049
400517	9796686	Minus	49996-50346

TABLE 24A: 571 GENES UP-REGULATED IN HEAD AND NECK TUMORS COMPARED WITH NORMAL BODY TISSUES

Table 24A lists about 571 genes up-regulated in head and neck tumors compared with normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
R1: 70th percentile of AI for head and neck cancer samples vs. the 80th percentile of the AI for normal body tissues

Pkey	ExAccn	UnigenelD	Unigene Title	R1
421155	H87879	Hs.102267	lysyl oxidase	166.00
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	156.00
434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	80.00
438274	AI918906	Hs.55080	ESTs	28.00
401486				121.00
446999	AA151520	Hs.334822	hypothetical protein MGC4485	126.00
423887	AL080207	Hs.134585	DKFZP434G232 protein	13.00
419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	98.00
428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00
420602	AF060877	Hs.99236	regulator of G-protein signalling 20	35.00
445019	AI205540	Hs.281295	ESTs	93.00
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	270.62
449722	BE280074	Hs.23960	cyclin B1	9.81
423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	373.00
424086	AI351010	Hs.102267	lysyl oxidase	200.00
447078	AW885727	Hs.301570	ESTs	184.00
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	177.00
409506	NM_006153	Hs.54589	NCK adaptor protein 1	170.00
426471	M22440	Hs.170009	transforming growth factor, alpha	158.00
413268	AL039079	Hs.75256	regulator of G-protein signalling 1	155.00
419948	AB041035	Hs.93847	NADPH oxidase 4	140.00
451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	139.00
442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	111.00
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	109.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	106.00
416283	NM_005429	Hs.79141	vascular endothelial growth factor C	95.00
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	92.00
449101	AA205847	Hs.23016	G protein-coupled receptor	92.00
442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	86.00
438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	85.68
414132	AI801235	Hs.48480	ESTs	85.00
447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	83.00
402047	AK001921	Hs.169575	hypothetical protein MGC2550	80.00
414972	BE263782	Hs.77695	KIAA0008 gene product	74.00
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	74.00
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	71.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	70.19
449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	66.25
418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	66.00
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	64.00
414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	63.00
432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	60.00
431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	58.00
411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	57.00
418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	57.00
438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	54.00
452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	54.00
423020	AA383092	Hs.1608	replication protein A3 (14kD)	49.00

	422426	W79117	Hs.58559	ESTs	49.00
	406747	AI925153	Hs.217493	annexin A2	46.00
	445828	F05802	Hs.81907	ESTs	46.00
5	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	44.00
	452909	NM_015368	Hs.30985	pannexin 1	43.95
	432226	AW182766	Hs.273558	phosphate cytidyltransferase 1, cholin	43.00
	458027	L49054	Hs.85195	myeloid leukemia factor 1	43.00
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	43.00
10	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	42.00
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	40.00
	433859	AW896758	Hs.273789	ESTs	38.00
	426753	T89832	Hs.170278	ESTs	37.00
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	36.00
	402034				35.00
15	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	34.00
	458424	AI084049	Hs.206761	ESTs	34.00
	435159	AA668879	Hs.116649	ESTs	33.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	32.00
20	444361	W76027	Hs.23920	hypothetical protein FLJ11105	31.00
	439128	AI949371	Hs.153089	ESTs	29.20
	420795	AA323037	Hs.128645	sorting nexin 16	26.00
	422505	AL120862	Hs.124165	ESTs	25.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	24.00
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	22.10
25	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	19.00
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	19.00
	414869	AA157291	Hs.21479	ubiquitin 1	17.37
	453049	BE537217	Hs.30343	ESTs	16.00
30	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	14.00
	435243	AW292886	Hs.261373	hypothetical protein dJ434O14.3	13.00
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	10.80
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	10.00
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	9.60
35	414231	AI468004	Hs.278956	hypothetical protein FLJ12929	9.00
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	8.09
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	8.07
	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.07
	417791	AW965339	Hs.111471	ESTs	8.04
40	436486	AA742221	Hs.120633	ESTs	7.23
	432731	R31178	Hs.287820	fibronectin 1	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	5.18
	435039	AW043921	Hs.130526	ESTs	5.00
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	4.25
45	457001	J03258	Hs.2062	vitamin D (1,25- dihydroxyvitamin D3) re	4.24
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	3.74
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	3.19
	458531	AA367718	Hs.159083	ESTs	3.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	2.53
50	411388	X72925	Hs.69752	desmocollin 1	1.00
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	1.00
	429370	C19097	Hs.89709	glutamate-cysteine ligase, modifier subu	1.00
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	1.00
	449467	AW205006	Hs.197042	ESTs	1.00
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00
	453637	NM_002589	Hs.34073	BH-protocadherin (brain-heart)	1.00
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	517.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	616.00
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	226.00
60	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	278.00
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	56.11
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	264.00
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	124.00
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.00
65	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	1.00
	415511	AI732617	Hs.182362	ESTs	1.00
	406467				141.00
	422330	D30783	Hs.115263	epiregulin	98.00
	452461	N78223	Hs.108106	transcription factor	159.00
70	415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypotheti	1.00
	413324	V00571	Hs.75294	corticotropin releasing hormone	1.00
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (7.60
	443211	AI128388	Hs.143655	ESTs	99.00
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00
75	441877	AW273802	Hs.11340	hypothetical protein FLJ23047	3.00
	439926	AW014875	Hs.137007	ESTs	2.79
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	94.00
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	1.22
	448062	AW295923	Hs.255472	KIAA1843 protein	1.00
80	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.27
	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	1.00
	421187	NM_014721	Hs.102471	KIAA0680 gene product	5.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	89.00
	437214	BE092336		gb:IL2-BT0734-240400-072-A12 BT0734 Homo	1.00

	449773	R76294	Hs.302383	ESTs	1.00
	443054	A1745185	Hs.8939	yes-associated protein 65 kDa	90.00
	432097	X51730	Hs.2905	progesterone receptor	1.00
5	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	0.38
	430184	AB013802	Hs.234790	contactin 5	1.00
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.23
	415025	AW207091	Hs.72307	ESTs	1.00
	416575	W02414	Hs.38383	ESTs	1.00
10	443171	BE281128	Hs.9030	TONDU	0.92
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	20.30
	400844				0.60
	409402	AF208234	Hs.695	cystatin B (stefin B)	1.96
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.38
15	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.60
	400751				1.34
	436361	AA825814	Hs.149065	ESTs	0.92
	455612	BE042896	Hs.274848	ESTs	0.81
	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	1.55
	404148				0.77
20	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	1.00
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.47
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.92
	442994	AI026718	Hs.16954	ESTs	0.40
25	415327	H22769		gb:ym54c02.r1 Soares infant brain 1N1B H	0.47
	418624	A1734080	Hs.104211	ESTs	1.90
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-lin	0.54
	401747			Homo sapiens keratin 17 (KRT17),	7.22
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	5.10
30	418259	AA215404	Hs.137289	ESTs	1.28
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	8.13
	403381				21.00
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	0.00
	418216	AA662240	Hs.283099	AF15q14 protein	11.29
35	444649	AW207523	Hs.197628	ESTs	0.10
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	4.64
	402230				1.64
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.97
40	447334	AA515032	Hs.91109	ESTs	0.62
	432829	W60377	Hs.57772	ESTs	0.86
	418686	Z36830	Hs.87268	annexin A8	8.44
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.68
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	2.22
45	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	78.00
	425721	AC002115	Hs.159309	uroplakin 1A	0.86
	420370	Y13645	Hs.97234	uroplakin 2	0.87
	417720	AA205625	Hs.208067	ESTs	5.83
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.07
	431753	X76029	Hs.2841	neuromedin U	7.00
50	402075				286.00
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	363.00
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.81
	405064				1.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	2.00
55	441233	AA972965	Hs.135568	ESTs	1.00
	456034	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCL_CGAP_Su	1.23
	414221	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCL_CGAP_Su	0.65
	412296	AW936233		gb:QV0-DT0020-090200-107-a06 DT0020 Homo	1.00
	405494				1.00
60	407189	AA598927		gb:ae37e03.s1 Gessler Wilms tumor Homo s	1.00
	403085				1.00
	408633	AW963372	Hs.46677	PRO2000 protein	2.46
	435257	AA677026	Hs.191217	ESTs	1.00
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00
65	445182	AW189787	Hs.147474	ESTs	0.50
	417275	X63578	Hs.295449	parvalbumin	1.00
	418406	X73501	Hs.84905	cytokeratin 20	1.00
	421110	AJ250717	Hs.1355	cathepsin E	1.00
	406081				2.13
70	449448	D60730	Hs.57471	ESTs	123.00
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.37
	408243	Y00787	Hs.624	interleukin 8	3.35
	436246	AW450963	Hs.119991	ESTs	51.00
	440304	BE159984	Hs.125395	ESTs	1.00
75	402778				1.00
	406117				1.00
	406360				71.00
	435347	AW014873	Hs.116963	ESTs	1.00
	445550	AI242754	Hs.137306	ESTs	1.00
80	451359	H85334	Hs.336623	ESTs	1.00
	419559	Y07828	Hs.91096	ring finger protein	1.00
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	58.00
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00
	402901				0.85

	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	0.87
	417715	AW969587	Hs.86366	ESTs	5.12
	442577	AA292998	Hs.163900	ESTs	2.19
5	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.54
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	1.11
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	1.27
	414683	S78296	Hs.76888	hypothetical protein MGC12702	0.67
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	0.03
10	403903				0.87
	405033				0.13
	422282	AF019225	Hs.114309	apolipoprotein L	2.13
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.05
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.59
15	430168	AW968343	Hs.24255	DKFZP434I1735 protein	1.69
	459702	AI204995			1.00
	446082	AI274139	Hs.156452	ESTs	0.60
	400843				0.76
	417409	BE272506	Hs.82109	syndecan 1	1.78
20	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	1.20
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	0.50
	404875				0.80
	436293	AI601188	Hs.120910	ESTs	1.40
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.03
25	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	0.94
	404977			Insulin-like growth factor 2 (somatomedi	0.99
	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.10
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	0.85
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.20
	420876	AA918425	Hs.177744	ESTs	0.85
30	422119	AI277829	Hs.111862	KIAA0590 gene product	0.71
	400846			sortilin-related receptor, L(DLR class)	0.75
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	4.01
	430152	AB001325	Hs.234642	aquaporin 3	1.74
	402777				0.70
35	417151	AA194055	Hs.293858	ESTs	0.99
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.48
	405034	AL035754	Hs.2474	toll-like receptor 1	1.00
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	18.68
40	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.94
	453134	AA032211	Hs.118493	ESTs	0.70
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.19
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	0.25
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	2.74
45	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.07
	438315	R56795	Hs.82419	ESTs	0.65
	418937	T71508	Hs.13861	ESTs, Weakly similar to T42383 probable	1.18
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	0.85
	444444	AI149332	Hs.14855	ESTs	0.59
50	407581	R48402	Hs.173508	P3ECSL	0.82
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	0.92
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	0.62
	446024	AB040946	Hs.284227	KIAA1513 protein	0.92
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.42
55	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.68
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptiona	1.57
	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	0.08
	446009	AI989885	Hs.231926	ESTs	1.00
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	0.98
60	415949	H10562	Hs.21691	ESTs	0.61
	420281	AI623693	Hs.191533	ESTs	7.01
	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	0.72
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.21
	414792	BE314949	Hs.87128	hypothetical protein FLJ23309	0.99
65	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	0.54
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.06
	426900	AW163564	Hs.142375	ESTs	0.48
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	0.83
	402305				0.89
70	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	0.04
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.49
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	0.65
	423916	AW993496	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	0.63
	405932				1.76
75	401760				2.61
	452240	AI591147	Hs.61232	ESTs	453.00
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	1.04
	421373	AA808229	Hs.167771	ESTs	17.00
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.16
80	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	1.68
	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.19
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.73
	453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal ki	1.00
	454789	BE156314		gb:QV0-HT0367-150200-114-d02 HT0367 Homo	1.00

	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	0.06
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.45
	418067	AI127958	Hs.83393	cystatin E/M	1.41
5	441801	AW242799	Hs.86366	ESTs	140.00
	423536	L22075	Hs.1666	guanine nucleotide binding protein (G pr	2.45
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	58.00
	400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	1.17
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	0.86
10	427587	BE348244	Hs.202628	ESTs, Weakly similar to I78885 serine/th	0.91
	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	1.00
	453204	R10799	Hs.191990	ESTs	1.13
	437240	AA747537		gb:nx85c05.s1 NCL_CGAP_GCB1 Homo sapiens	1.00
	405531				0.92
15	440249	AI246590	Hs.337275	ESTs	1.32
	426783	Z19084	Hs.172210	MUF1 protein	1.17
	434192	AW387314	Hs.34371	ESTs	1.00
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	87.14
	402001				37.00
20	433967	AF113018	Hs.284302	PRO1621 protein	1.00
	451592	AI805416	Hs.213897	ESTs	10.00
	422170	AI791949	Hs.112432	anti-Mullerian hormone	0.67
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	1.00
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	0.99
25	441940	AW298115	Hs.128152	ESTs	0.88
	425048	H05468	Hs.164502	ESTs	0.33
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.01
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.06
	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	0.45
30	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	0.62
	410348	AW182663	Hs.95469	ESTs	1.00
	419078	M93119	Hs.89584	insulinoma-associated 1	0.04
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.04
	441795	N58115	Hs.21137	AD024 protein	10.00
35	418583	AA604379	Hs.86211	hypothetical protein	1.22
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	106.67
	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	2.30
	441495	AW294603	Hs.127039	ESTs	0.44
	417933	X02308	Hs.82962	thymidylate synthetase	2.48
40	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	1.00
	411880	AW872477		gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens	1.00
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	1.44
	430034	X60155	Hs.227767	zinc finger protein 41	1.00
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.87
45	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	0.54
	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	2.27
	417599	AA204688	Hs.136201	ESTs	1.01
	438366	AA805760	Hs.303567	ESTs	1.00
	438746	AI885815	Hs.184727	ESTs	1.47
50	409691	T89983	Hs.246042	Homo sapiens, clone MGC:5437, mRNA, comp	1.00
	408827	AW275730	Hs.254825	ESTs	1.00
	414735	BE468016	Hs.281904	ESTs	1.00
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	5.21
	412719	AW016610	Hs.129911	ESTs	494.00
55	417034	NM_006183	Hs.80962	neurotensin	1.00
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	23.36
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	6.98
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	7.50
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	9.77
60	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	445.00
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	13.93
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	12.77
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	45.00
	418663	AK001100	Hs.41690	desmocollin 3	10.89
65	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.29
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	0.88
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	38.31
	421948	L42583	Hs.334309	keratin 6A	36.81
	431846	BE019924	Hs.271580	uroplakin 1B	1.37
70	424098	AF077374	Hs.139322	small proline-rich protein 3	8.85
	453964	AI961486	Hs.12744	ESTs	0.40
	446856	AI814373	Hs.164175	ESTs	1.16
	443648	AI085377	Hs.143610	ESTs	2.15
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	4.39
75	431384	BE158000		gb:MR2-HT0377-150200-202-e03 HT0377 Homo	1.18
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.22
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	164.00
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	9.85
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	5.59
80	441020	W79283	Hs.35962	ESTs	5.76
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.97
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.09
	444371	BE540274	Hs.239	forkhead box M1	2.44
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.39

5	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.53
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	1.67
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	2.30
	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.04
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.11
10	401781				11.07
	401780				9.54
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.62
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	1.12
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	947.00
15	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.79
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.16
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.08
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	5.20
	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	2.53
20	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	72.00
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	19.96
	409103	AF251237	Hs.112208	XAGE-1 protein	0.47
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	0.66
	428471	X57348	Hs.184510	stratifin	3.39
25	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	1.61
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.31
	451541	BE279383	Hs.26557	plakophilin 3	1.82
	418203	X54942	Hs.83758	CDC28 protein kinase 2	5.60
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.78
30	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.01
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.18
	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.58
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.63
	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.25
35	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	11.88
	430677	Z26317	Hs.94560	desmoglein 2	1.38
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.09
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.09
	422963	M79141	Hs.13234	ESTs	2.28
40	418462	BE001596	Hs.85266	integrin, beta 4	1.40
	450832	AW970602	Hs.105421	ESTs	13.31
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.25
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.89
	458933	AI638429	Hs.24763	RAN binding protein 1	1.54
45	439394	AA149250	Hs.56105	ESTs	3.89
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.77
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.52
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.11
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.10
50	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.84
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	0.61
	439606	W79123	Hs.58561	G protein-coupled receptor 87	303.00
	453884	AA355925	Hs.36232	KIAA0186 gene product	10.55
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.38
55	451743	AW074266	Hs.23071	ESTs	2.90
	413129	AF292100	Hs.104613	RP42 homolog	2.38
	406974	M57293		gb:Human parathyroid hormone-related pep	1.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	5.92
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	2.18
60	416819	U77735	Hs.80205	pim-2 oncogene	1.01
	451320	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	0.67
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.19
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.55
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	3.06
65	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	1.64
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	7.04
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	203.00
	435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33
	430337	M36707	Hs.239600	calmodulin-like 3	1.32
70	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	81.00
	448993	AI471630	Hs.8127	KIAA0144 gene product	1.03
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	28.00
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.24
	425245	AI751768	Hs.155314	KIAA0095 gene product	1.40
75	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.55
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00
	418678	NM_001327	Hs.167379	cancer/testis antigen	0.82
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00
	427335	AA448542	Hs.251677	G antigen 7B	0.91
80	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	6.53
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	1.35
	421917	AB028943	Hs.109445	KIAA1020 protein	0.94
	404440				38.57
	409582	R27430	Hs.271565	ESTs	3.19
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	2.45
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.61
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	1.95

	408380	AF123050	Hs.44532	diubiquitin	7.23
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.35
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	0.81
5	446102	AW168067	Hs.252956	ESTs	1.03
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	137.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.91
	423761	NM_006194	Hs.132576	paired box gene 9	36.00
10	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.35
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	207.00
	440659	AF134160	Hs.7327	claudin 1	3.06
	434360	AW015415	Hs.127780	ESTs	3.89
	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.28
	438898	AI819863	Hs.106243	ESTs	1.73
15	441553	AA281219	Hs.121296	ESTs	1.47
	418379	AA218940	Hs.137516	fidgetin-like 1	40.42
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	14.25
	429413	NM_014058	Hs.201877	DESC1 protein	5.17
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.95
20	415380	F07953	Hs.16085	putative G-protein coupled receptor	0.18
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.09
	429538	BE182592	Hs.11261	small proline-rich protein 2A	6.14
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00
25	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	44.00
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	149.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	127.00
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	20.00
	404996				147.00
30	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	54.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	139.00
	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR	22.00
	438702	AI879064	Hs.54618	ESTs	1.00
35	444378	R41339	Hs.12569	ESTs	1.00
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	41.00
	407839	AA045144	Hs.161566	ESTs	7.50
	439223	AW238299	Hs.250618	UL16 binding protein 2	3.39
	409041	AB033025	Hs.50081	KIAA1199 protein	245.00
40	429228	AI553633	Hs.337139	ESTs	10.89
	409757	NM_001898	Hs.123114	cystatin SN	3.19
	411089	AA456454	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	0.78
	436511	AA721252	Hs.291502	ESTs	0.23
	449207	AL044222	Hs.23255	nucleoporin 155kD	1.68
45	453331	AI240665	Hs.8895	ESTs	5.21
	409935	AW511413	Hs.278025	ESTs	0.75
	428969	AF120274	Hs.194689	artemin	1.17
	445443	AV653838	Hs.322971	ESTs	1.00
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	11.42
50	401785				2.76
	412723	AA648459	Hs.335951	hypothetical protein AF301222	107.00
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	2.17
	405770				2.42
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.24
55	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	4.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.95
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.44
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00
	454098	V27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.33
60	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	1.11
	427441	AA412605	Hs.178053	SPANX family, member C	5.00
	403478				0.78
	400842				0.16
	441525	AW241867	Hs.127728	ESTs	0.79
65	452865	AI924046	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	1.50
	405646				1.05
	427260	AA663848		gb:ae70b06.s1 Stratagene schizo brain S1	0.79
	431413	AA504777	Hs.105293	ESTs	1.00
	401994				3.25
70	402420				0.05
	404298				0.64
	404927				88.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	0.96
	436961	AW375974	Hs.156704	ESTs	3.58
75	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	0.92
	426067	AW664691	Hs.97053	ESTs	0.97
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	0.66
	426897	AW976570	Hs.97387	ESTs	1.29
	443892	AI889572	Hs.134791	ESTs	1.00
80	413223	AI732182	Hs.191866	ESTs	0.79
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	1.51
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	2.59
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.39
	420758	AW297536	Hs.33053	ESTs	0.89

5	423816	AL031985	Hs.133034	hypothetical protein	1.00
	447534	AW953935	Hs.30837	ESTs	1.88
	451919	W05086	Hs.114256	ESTs, Weakly similar to 178885 serine/th	0.11
	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell	0.92
	403715				0.89
10	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	37.00
	436839	AA767346	Hs.291614	ESTs	1.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	59.00
	413573	AI733859	Hs.149089	ESTs	78.00
15	430686	NM_001942	Hs.2633	desmoglein 1	127.08
	438993	AA828995		gbrod77b08.s1 NCI_CGAP_Ov2 Homo sapiens	1.00
	448243	AW369771	Hs.52620	integrin, beta 8	133.00
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	232.00
	426427	M86699	Hs.169840	TTK protein kinase	66.00
20	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	148.00
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	40.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	13.00
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	106.00
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	159.00
25	415989	AI267700	Hs.317584	ESTs	196.00
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	32.44
	453160	AI263307	Hs.239884	H2B histone family, member L	7.00
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.13
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	45.00

TABLE 24B

30 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accessions: Genbank accession numbers

35	Pkey	CAT number	Accessions
40	411880	1263110_1	AW872477 BE088101 T05990
	412296	1288043_1	AW936233 AW936272
	413804	1390710_1	T64682 BE168190 BE168256
	414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363
45	415327	1534137_1	H22769 R35182 Z43545 F05783 N92089 H71928
	427260	276598_1	AA663848 AA400100 AA401424
	431322	331543_1	AW970622 AA503009 AA502998 AA502805 T92188
	431384	33264_1	BE158000 BE157999 H75671 H70965 C18895 BE386512 BE385815 BE390298 AI341995 BE074534 AA055592 AA132265 AI733757
			AA134504 BE145037 AA055887 BE070191 R66492 AW858018 AW858058 AW817057 AW862031 AW861688 AW862029 AW858805 AW858792
50			AW862028 AW858017 AW819164 AW853698 AI522161 AW854789 AW817408 BE152005 AI732411 AA133084
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
	437214	434730_1	BE092336 BE092259 BE092497 BE092051 AA746882 AI336378
	437240	435139_1	AA747537 BE089068 BE089070
	438993	467651_1	AA828995 AA834879 AI926361
55	439780	47673_1	AL109688 R23665 R26578
	444163	593658_1	AI126098 AI184746 AI148521
	451844	888230_1	T61430 AI820546 AI821336
	453823	982526_1	AL137967 BE064160 BE064186
	454789	1234742_1	BE156314 BE156316 AW820750
60	456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 24C

65 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

70	Pkey	Ref	Strand	Nt_position
75	400751	7331445	Minus	35395-35533
	400842	1927148	Plus	90462-90673
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
	400844	9188605	Plus	24746-24872,25035-25204
	400846	9188605	Plus	39310-39474
80	401486	7341763	Plus	32585-32756,36261-36540,40791-40933,44018-44179
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
	402001	9501818	Plus	68052-68223

402034	7684482	Minus	86227-86451
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
402305	7328724	Plus	40832-41362
402420	9796339	Plus	129750-129919
402777	9588235	Plus	126786-126948
402778	9588235	Plus	128560-128702
402901	8894222	Minus	175426-175667
403085	8954241	Plus	165035-165334,165420-165713
403381	9438267	Minus	26009-26178
403478	9958258	Plus	116458-116564
403715	7239669	Plus	85128-85292
403903	7710671	Minus	101165-102597
404148	9863703	Plus	78218-78418,79571-79709
404298	9944263	Minus	73591-73723
404440	7528051	Plus	80430-81581
404875	9801324	Plus	96588-96732,97722-97831
404927	7342002	Plus	68690-69563
404977	3738341	Minus	43081-43229
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405033	7107731	Minus	142358-142546
405064	7658416	Plus	81207-81416
405494	8050952	Minus	70284-70518
405531	9665194	Plus	35602-35803
405646	4914350	Plus	741-969
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713
406081	9123861	Minus	38115-38691
406117	9142932	Plus	54304-54584
406360	9256107	Minus	7513-7673
406467	9795551	Plus	182212-182958

TABLE 25A: 691 genes upregulated in head and neck cancer relative to normal body tissues

Table 25A lists about 691 genes upregulated in head and neck cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1 85th percentile of head and neck cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prot.Domains; R1

422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psorias; efhand,S_100;TM=M;SS=N; 46.25
 408522; AI541214; Hs.46320; Small proline-rich protein SPRK [human; none; Cornifin; 40.37
 417366; BE185289; Hs.1076; small proline-rich protein 1B (cornifin); Cornifin;TM=M;SS=N; 38.94
 401781; ; Target Exon; filament;TM=M;SS=N; 29.74
 422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap;TM=M;SS=Y; 29.54
 401780; ; NM_005557; Homo sapiens keratin 16 (foca; filament;filament; 28.58
 424098; AF077374; Hs.139322; small proline-rich protein 3; Cornifin;TM=M;SS=N; 28.55
 421948; L42583; Hs.334309; keratin 6A; filament;RhoGAP,DUF286,bZIP,Tropomyosin,tubulin,DUF164,TBCA,Collagen;TM=M;SS=N; 25.74
 428471; X57348; Hs.184510; stratifin; 14-3-3;TM=M;SS=N; 23.65
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; 21.02
 421574; AJ000152; Hs.105924; defensin, beta 2; Defensin_beta;TM=M;SS=M; 20.83
 409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyperkeratosis); filament,bZIP,UvrD-helicase,TBCA;TM=M;SS=N; 20.72
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_recpt;TM=M;SS=Y; 19.63
 446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium_transp,FecCD;TM=Y;SS=M; 19.53
 420783; AI659838; Hs.99923; lectin, galactoside-binding, soluble, 7; Gal-bind_lectin;TM=M;SS=N; 19.12
 407788; BE514982; Hs.38991; S100 calcium-binding protein A2; efhand,S_100,S_100,efhand; 17.93
 416091; AF295370; Hs.283082; defensin, beta 3; Defensin_beta;TM=M;SS=M; 17.63
 431211; M86849; Hs.323733; gap junction protein, beta 2, 26kD (conn; connexin;TM=Y;SS=M; 16.94
 429259; AA420450; Hs.380088; Plakophilin; none;none; 14.92
 417515; L24203; Hs.82237; ataxia-telangiectasia group D-associated; zf-B_box,zf-UBR1;TM=M;SS=N; 14.75
 423634; AW959908; Hs.1690; heparin-binding growth factor binding pr; none;TM=M;SS=M; 14.45
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (interstitial; hemopexin,Peptidase_M10,Astacin,PG_binding_1; 13.02
 409632; W74001; Hs.55279; serine (or cysteine) proteinase inhibitor; serpin; 12.82
 406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 12.81
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin,Cadherin_C_term;TM=Y;SS=M; 12.45
 446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL4; 11.71
 401760; ; Target Exon; none;bromodomain; 11.68
 407839; AA045144; Hs.161566; ESTs; cadherin,cadherin; 11.65
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh; 11.56
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associated prote; UPAR_LY6,lactamase_B; 11.31

- 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none; TM=Y; SS=M; 11.03
 424012; AW368377; Hs.137569; tumor protein 63 kDa with strong homolog; SAM, P53; TM=M; SS=N; 10.75
 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin; TM=M; SS=N; 10.58
 419693; AA133749; Hs.301350; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8; TM=Y; SS=M; 10.30
 411274; NM_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 10.25
 441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none; TM=M; SS=M; 9.84
 446989; AK001898; Hs.16740; hypothetical protein FLJ11036; none; TM=Y; SS=N; 9.74
 402075; ; ENSP00000251056; Plasma membrane calcium; none; 9.50
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 9.50
 431009; BE149762; Hs.48956; gap junction protein, beta 6 (connexin 3; connexin; TM=Y; SS=M; 9.48
 439310; AF086120; Hs.102793; ESTs; casein_kappa, pkinase, ig, none; 9.43
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M; SS=N; 9.33
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh; TM=M; SS=M; 9.14
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); ehand, spectrin, GAS2, SH3, Plectin, RA, Xylose_isom, FliD, bZIP, Tropomyosin, Myc-LZ, M, Idh, C, CH, AIP3; TM=M; SS=N; 9.12
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg; TM=M; SS=N; 9.11
 425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin; TM=M; SS=M; 8.66
 452240; AI591147; Hs.61232; ESTs; none, none; 8.57
 429228; AI553633; Hs.356828; ESTs; none, none; 8.46
 400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin, Peptidase_M10, Astacin; 8.44
 425071; NM_013989; Hs.154424; delodinas, Iodothyronine, type II; T4_delodinas; TM=M; SS=Y; 8.15
 407242; M18728; ; gb:Human nonspecific crossreacting antig; ig; TM=M; SS=M; 8.05
 407944; R34008; Hs.239727; desmocollin 2; cadherin, Cadherin_C_term, Hanta_G2; TM=Y; SS=M; 7.90
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 7.82
 428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase_M10; 7.82
 417308; H60720; Hs.81892; KIAA0101 gene product; none; TM=M; SS=N; 7.77
 413753; U17760; Hs.75517; laminin, beta 3 (nicein (125kD), kalinin; laminin_EGF, laminin_Nterm; 7.76
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolys; Kunitz_BPTI, fn3, vwa, Collagen, beta-lactamase; TM=M; SS=M; 7.71
 430686; NM_001942; Hs.2633; desmoglein 1; cadherin, Cadherin_C_term; TM=Y; SS=M; 7.69
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha, arf; TM=M; SS=N; 7.54
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_Pi4_kinase, FAT, FATC, BoA, RUN; TM=M; SS=N; 7.53
 418663; AK001100; Hs.41690; desmocollin 3; cadherin, Cadherin_C_term, none; 7.30
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide, TGF-beta, none; 7.28
 429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin; TM=Y; SS=M; 7.26
 412719; AW016610; Hs.816; ESTs; none, none; 7.17
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin; 7.10
 423961; D13666; Hs.136348; periostin (OSF-2os); Fasciclin; TM=M; SS=M; 7.09
 427666; AI791495; Hs.180142; calmodulin-like skin protein (CLSP); ehand; TM=M; SS=N; 7.08
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 7.06
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin, Peptidase_M10; TM=M; SS=M; 7.03
 401747; ; ; Homo sapiens keratin 17 (KRT17); none, bromodomain; 7.01
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT, none; 6.98
 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg; TM=M; SS=N; 6.96
 432239; X81334; Hs.2936; matrix metalloproteinase 13 (collagenase; hemopexin, Peptidase_M10; 6.87
 417715; AW969587; Hs.86366; ESTs; none, none; 6.72
 422440; NM_004812; Hs.116724; aldo-keto reductase family 1, member B10; aldo_ket_red, ROK; TM=M; SS=N; 6.50
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-in; hemopexin, Peptidase_M10; TM=M; SS=M; 6.39
 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase, PLAT; TM=M; SS=N; 6.38
 420039; NM_004605; Hs.376147; sulfotransferase family, cytosolic, 2B, ; Sulfotransfer; 6.38
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB, DNA_topoisolV, HATPase_c; 6.35
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3, ank; TM=M; SS=N; 6.30
 409420; Z15008; Hs.54451; laminin, gamma 2 (nicein (100kD), kalini; laminin_B, laminin_EGF; 6.28
 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 atrophin-; ras; TM=M; SS=N; 6.27
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 6.23
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin, Peptidase_M10; 6.22
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none; TM=M; SS=N; 6.21
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3; TM=Y; SS=M; 6.12
 423017; AW178761; Hs.227948; serine (or cysteine) proteinase inhibitor; serpin; 6.08
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none, none; 6.08
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; SS=M; 6.04
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretoglobulin, fa; none; 5.81
 439223; AW238299; Hs.250618; UL16 binding protein 2; ldi_recept_a, PKD, MHC_1; TM=M; SS=Y; 5.77
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR, Lysyl_oxidase; TM=M; SS=M; 5.72
 454098; W27953; Hs.217493; Plakophilin; none, none; 5.71
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevi; WD40; TM=M; SS=N; 5.70
 435505; AF200492; Hs.211238; interleukin-1 homolog 1; IL1; TM=M; SS=N; 5.69
 406685; M18728; ; gb:Human nonspecific crossreacting antig; ig; TM=M; SS=M; 5.67
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3, none; 5.63
 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none; TM=Y; SS=M; 5.61
 449722; BE280074; Hs.23960; cyclin B1; cyclin, cyclin_C; TM=M; SS=N; 5.61
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1; TM=Y; SS=M; 5.60
 452862; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like and metallo; Pep_M12B_propep, tsp_1, Reprolysin, none; 5.58
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras, ABC_tran, arf; TM=M; SS=M; 5.57
 411296; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell_Oxy; TM=M; SS=M; 5.55
 433848; AF095719; Hs.93764; carboxypeptidase A4; Zn_carbOpeptLPropep_M14; 5.54
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase; 5.48
 428368; BE440042; Hs.83326; matrix metalloproteinase 3 (stromelysin ; hemopexin, Peptidase_M10, Astacin; 5.47
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig, Rhabd_glycop; TM=Y; SS=M; 5.46
 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase, abhydrolase_2; TM=Y; SS=M; 5.42
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; 5.35
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 5.28
 418462; BE001596; Hs.85266; integrin, beta 4; fn3, integrin_B, Calx-beta, EGF; TM=M; SS=M; 5.26

- 429554; NM_012275; Hs.207224; interleukin 1, delta; IL1; TM=M; SS=N; 5.14
 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN; HIN; TM=M; SS=N; 5.13
 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none; TM=M; SS=N; 5.11
 427099; AB032953; Hs.173560; odd Oz/ten-m homolog 2 (Drosophila, mous; NHL; TM=M; SS=N; 5.11
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 5.08
 436396; AI683487; Hs.152213; wingless-type MMTV integration site fami; wnt; none; 5.07
 406690; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; ig; TM=M; SS=M; 5.05
 453905; NM_002314; Hs.36566; LIM domain kinase 1; pkinase, LIM, PDZ, zf-PARP; TM=M; SS=N; 5.04
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor; serpin; 5.00
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH, death, TNFR_c6, Acyl-CoA_hydro; 4.96
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK; TM=M; SS=N; 4.93
 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like (rabkines; kinesin, Tropomyosin; TM=M; SS=N; 4.92
 445537; AJ245671; Hs.12844; EGF-like domain, multiple 6; EGF, MAM; 4.91
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily; 60s_ribosomal, Ribosomal_L10, TNFR_c6, DEAD; 4.90
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig; HSP70, Ppx-GppA; TM=M; SS=N; 4.89
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none, none; 4.84
 430024; AI808780; Hs.227730; integrin, alpha 6; integrin_A, FG-GAP; TM=Y; SS=M; 4.81
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH; none, none; 4.80
 444371; BE540274; Hs.239; forkhead box M1; Fork_head; TM=M; SS=N; 4.75
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 4.74
 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPc; 4.69
 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha; FG-GAP, Rhabd_glycop, integrin_A; TM=Y; SS=M; 4.69
 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none, pkinase, fn3, ig; 4.68
 418067; AI127958; Hs.83393; cystatin E/M; cystatin; 4.66
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle, trypsin, plant_thionins; 4.64
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM, PDZ, pkinase; 4.62
 410418; D31382; Hs.63325; transmembrane protease, serine 4; Idl_recept_a, trypsin; TM=Y; SS=M; 4.60
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen, COL1I, TSPN, laminin_G, CorA; 4.60
 438113; AI467908; Hs.8882; ESTs; 7tm_1, none; 4.60
 418140; BE613836; Hs.83551; microfibrillar-associated protein 2; none; TM=M; SS=M; 4.57
 408380; AF123050; Hs.44532; diubiquitin; ubiquitin; TM=M; SS=N; 4.55
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 4.50
 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin, Peptidase_M10; 4.50
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domain; death, DED; 4.49
 408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1; TM=Y; SS=M; 4.48
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD, helicase_C, rrm, Ndr, Cys_knot, TIL, vwa, vwc, vwd, IQ, RIIa, abhydrolase, TGF-beta, DUF139, TPR, DSPc, tsp_1, Ribosomal_S21, rvp; TM=M; SS=N; 4.47
 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.47
 411789; AF245505; Hs.72157; Adican; ig, LRR, LRRNT, LRRCT; TM=M; SS=M; 4.47
 414561; AI064813; Hs.195155; Homo sapiens amino acid transport system; Aa_trans; TM=Y; SS=N; 4.47
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR; TM=M; SS=N; 4.45
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6, ET, PLA2_inh; 4.43
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase, DSPc; TM=M; SS=N; 4.42
 409041; AB033025; Hs.50081; Hypothetical protein, XP_051850 (KIAA119; none; TM=M; SS=M; 4.41
 406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gen; none, none; 4.40
 450701; H39960; Hs.288467; hypothetical protein XP_098151 (leucine-; none, LRRCT, LRR; 4.40
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2, SH3, pkinase; TM=M; SS=N; 4.38
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cytactin); EGF, fn3, fibrinogen_C, toxin_2, Keratin_B2; TM=M; SS=Y; 4.38
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT_bind, STAT_prot; TM=M; SS=N; 4.32
 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; none; TM=M; SS=N; 4.32
 411573; AB029000; Hs.70823; KIAA1077 protein; Sulfatase; TM=M; SS=N; 4.31
 408243; Y00787; Hs.624; interleukin 8; HLH, PAS, IL8; TM=M; SS=N; 4.31
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 4.30
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC; none; 4.29
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, ig, FAD_Synth, Idh, Idh_C, pkinase; 4.29
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 4.29
 404996; ; ; Target Exon; Peptidase_C1; TM=M; SS=M; 4.29
 416539; Y07909; Hs.79368; epithelial membrane protein 1; PMP22_Claudin, oxidored_g5_N; TM=Y; SS=M; 4.28
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, M, SMC_N, SMC_C, DUF164, none; 4.25
 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg, HEAT; TM=M; SS=N; 4.25
 424503; NM_002205; Hs.149609; integrin, alpha 5 (fibronectin receptor; integrin_A, FG-GAP; TM=Y; SS=N; 4.24
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y; SS=N; 4.24
 439720; AI935202; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF, sugar_tr; 4.23
 437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none; TM=M; SS=M; 4.23
 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta, TGFb_propeptide, Tub; 4.20
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA, ABC_tran, CoaE; TM=M; SS=N; 4.20
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK; TM=M; SS=Y; 4.19
 407137; T97307; ; gb:ye53h05.s1 Soares fetal liver spleen ; GDA1_CD39, none; 4.18
 419235; AW470411; Hs.288433; neurotrimin; none, none; 4.18
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema, PSI, TIG, integrin_B; TM=Y; SS=M; 4.18
 456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4, Cbl_N, Cbl_N2, Cbl_N3; TM=M; SS=N; 4.17
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moi; NUDIX; TM=M; SS=M; 4.17
 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor; integrin_A, FG-GAP; TM=Y; SS=N; 4.14
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; SS=N; 4.13
 445417; AK001058; Hs.12680; a disintegrin-like and metalloprotease w; tsp_1, Reprolysin, Pep_M12B_propep, none; 4.12
 433895; AI287912; Hs.3628; mitogen-activated protein Kinase kinase ; pkinase, zf-C4, CNH, ERM; TM=M; SS=N; 4.12
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M; SS=N; 4.09
 419121; AA374372; Hs.89626; parathyroid hormone-like hormone; none, none; 4.08
 416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF, vwc, TSPN; 4.07
 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1; TM=Y; SS=M; 4.07
 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase; TM=M; SS=N; 4.06
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M; SS=N; 4.03
 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PSI, integrin_B; TM=Y; SS=N; 4.02

414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 4.02
 413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic; sugar_tr; TM=Y; SS=M; 4.01
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 4.01
 406906; Z25424; ; gb:H.sapiens protein-serine/threonine ki; none; none; 3.98
 450375; AA009647; Hs.352537; a disintegrin and metalloproteinase doma; Reprolysin, Pep_M12B_propep, disintegrin, Reprolysin, Pep_M12B_propep, disintegrin; 3.98
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_Oxidase;; 3.96
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM; TM=Y; SS=M; 3.95
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated kinase; pkinase, pkinase_C; TM=M; SS=M; 3.95
 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR, LRRNT, LRRCT; TM=Y; SS=M; 3.95
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfam; SRP14, TNFR_c6;; 3.93
 407792; AI077715; Hs.39384; putative secreted ligand homologous to f; none; TM=M; SS=Y; 3.91
 424441; X14850; Hs.147097; H2A histone family, member X; histone, CBFD_NFYB_HMF;; 3.91
 415989; AI267700; Hs.351201; ESTs; none; none; 3.90
 423189; M59371; Hs.171596; EphA2; fn3, pkinase, SAM, EPH_lbd; TM=Y; SS=M; 3.90
 443859; NM_013409; Hs.9914; follistatin; kazal;; 3.89
 429612; AF062649; Hs.252587; pituitary tumor-transforming 1; none;; 3.89
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death, ZU5;; 3.88
 450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig; TM=Y; SS=M; 3.88
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1, pkinase; TM=M; SS=N; 3.86
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2, SH3; TM=M; SS=N; 3.84
 377763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP, pkinase, DAG, PE-bind, RBD; 3.83
 436291; BE568452; Hs.344037; protein regulator of cytokinesis 1; none; TM=M; SS=N; 3.82
 417512; X76534; Hs.82226; glycoprotein (transmembrane) nmb; PKD; TM=Y; SS=M; 3.81
 427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20653 fis, clone KA; none, pkinase; 3.80
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none; TM=M; SS=Y; 3.80
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside_tra2, none; 3.80
 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfam; IL2;; 3.79
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase, hexokinase2, none; 3.78
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M; SS=N; 3.78
 417720; AA205625; Hs.208067; ESTs; none; none; 3.77
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP, none; 3.77
 449029; N28989; Hs.22891; solute carrier family 7 (cationic amino; aa_permeases; TM=Y; SS=M; 3.76
 413436; AF238083; Hs.68061; sphingosine kinase 1; DAGK; TM=M; SS=N; 3.75
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated; ig, ITAM, Zn_clus; TM=Y; SS=M; 3.74
 413281; AA861271; Hs.222024; transcription factor BMAL2; HLH, PAS;; 3.74
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ_con; TM=M; SS=N; 3.74
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa, integrin_A, FG-GAP; TM=Y; SS=M; 3.74
 424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosp; perlipin;; 3.73
 426471; M22440; Hs.170009; transforming growth factor, alpha; EGF; TM=M; SS=M; 3.72
 422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; EGF, vwd, AMOP;; 3.72
 450125; AA005418; Hs.158186; ESTs; CIDE-N, 7tm_1, none; 3.71
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 3.70
 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; Idl_recept_a, PKD, MHC_I; TM=M; SS=Y; 3.70
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF, sugar_lr; 3.70
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; SS=N; 3.69
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-i; fn3, Y_phosphatase, carb_anhydrase; TM=Y; SS=M; 3.68
 443759; BE390832; Hs.134729; FYD domain-containing ion transport reg; ATP1G1_PLM_MAT8; TM=Y; SS=M; 3.68
 452344; AI264357; Hs.55405; hypothetical protein MGC16212; Sulfate_transp, STAS;; 3.68
 439625; AF086453; Hs.58611; ESTs; Fork_head, glycolytic_enz, Na_sulph_symp; 3.66
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 3.66
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement comp; C1q, Collagen;; 3.65
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (; SH3, PH, RhoGEF; TM=M; SS=N; 3.64
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos; TM=M; SS=M; 3.64
 438707; L08239; Hs.5326; amino acid system N transporter 2; porcu; ACAT, MBOAT; TM=Y; SS=M; 3.64
 422596; AF063611; Hs.118633; 2'-5'-oligoadenylate synthetase-like; ubiquitin;; 3.63
 449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN cDNA 5730; none; TM=M; SS=N; 3.62
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin, Guanylate_kin, PDZ, SH3; 3.62
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M; SS=Y; 3.62
 452696; AI826645; Hs.211534; ESTs; ArfGap, PH, ank, Guanylate_kin, PDZ, SH3; 3.60
 407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc; Galactosyl_T; TM=M; SS=Y; 3.59
 423575; C18863; Hs.163443; intron of periostin (OSF-2os); Fasciclin, none; 3.59
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor tran; ig, none; 3.58
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig, pkinase; TM=Y; SS=M; 3.58
 419912; AF249745; Hs.6066; Rho guanine nucleotide exchange factor (; SH3, PH, RhoGEF; TM=M; SS=N; 3.58
 431457; NM_012211; Hs.256297; integrin, alpha 11; FG-GAP, vwa; TM=Y; SS=M; 3.57
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans; TM=Y; SS=M; 3.55
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none; TM=Y; SS=M; 3.55
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E coli Re; none; 3.53
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2, PI-PLC-Y; TM=M; SS=N; 3.53
 429556; AW139399; Hs.314807; ESTs; none; TM=M; SS=N; 3.52
 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1; TM=Y; SS=M; 3.52
 432636; AA340864; Hs.278562; claudin 7; PMP22, Claudin; TM=Y; SS=M; 3.51
 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none; TM=Y; SS=M; 3.51
 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran, ABC_membrane, SRP54, Thymidylate_kin; TM=Y; SS=M; 3.49
 425566; AW162943; Hs.250618; UL16 binding protein 2; Idl_recept_a, PKD, MHC_I; TM=M; SS=Y; 3.48
 402447; ; C1000201.gij204416[gb]AA02627.1 (L0519; none; TM=Y; SS=M; 3.48
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept; TM=M; SS=M; 3.48
 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 3.48
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3, TPR; TM=M; SS=N; 3.48
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease (APEX; Troponin, Exo_endo_phos, IQ; TM=M; SS=N; 3.47
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese;; 3.44
 446051; BE048061; Hs.37054; ephrin-A3; Ephrin, A_deamin, dsrm, z-alpha; 3.43
 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin, Reprolysin, Pep_M12B_propep, EGF; TM=Y; SS=M; 3.42

417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,integrin_B;; 3.42
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-asso; kinesin;TM=M;SS=N; 3.42
 430044; AA464510; Hs.152812; ESTs; none,none; 3.42
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;; 3.39
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1;TM=Y;SS=M; 3.39
 428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino a; eIF6,SDF;TM=M;SS=N; 3.39
 443648; AI085377; Hs.143610; ESTs; Fork_head,none; 3.39
 418869; AW516565; ; gb:xq01d05.x1 Soares_NHCeC_cervical_tumo; none,RasGAP,WW,IQ; 3.38
 432179; X75208; Hs.2913; EphB3; EPH_lbd,fn3,ptkinase,SAM;TM=Y;SS=M; 3.38
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; ig;TM=Y;SS=M; 3.38
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 3.37
 408716; AI567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein, ; UvrD-helicase,RNB,Runt;TM=M;SS=N; 3.37
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;SS=N; 3.37
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 3.37
 421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 3.36
 400298; AA032279; Hs.61635; six transmembrane epithelial antigen of ; none;TM=Y;SS=N; 3.35
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;; 3.33
 400261; ; Hs.1802; Eos Control; ig,MHC_II_beta;TM=Y;SS=M; 3.33
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3;TM=M;SS=N; 3.32
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none,lectin_c; 3.32
 416065; BE267931; Hs.78996; proliferating cell nuclear antigen; PCNA,PCNA_C;TM=M;SS=N; 3.31
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg,UQ_con,none; 3.31
 426840; BE244217; Hs.172890; diacylglycerol kinase, alpha (80kD); ehand,DAG_PE-bind,DAGKa,DAGKc,DC1;TM=M;SS=N; 3.31
 434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPc;TM=M;SS=N; 3.31
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M;SS=N; 3.31
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 3.31
 423973; AF038461; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase,PLAT;TM=M;SS=N; 3.30
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; ig,pkinase;TM=Y;SS=M; 3.30
 449027; AJ271216; Hs.22880; dipeptidylpeptidase II; Peptidase_M49,EGF,ig,Neuregulin;TM=M;SS=N; 3.28
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 3.28
 426457; AW894667; Hs.380138; chimerin (chimaerin) 1; DAG_PE-bind,RhoGAP,SH2;TM=M;SS=N; 3.28
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 3.27
 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M;SS=N; 3.27
 430397; AI924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;SS=N; 3.27
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3_PI4_kinase,FAT,FATC;TM=M;SS=N; 3.26
 446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 3.26
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH,none; 3.25
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 3.25
 405932; ; C15000305:gil3806122[gb]AAC69198.1[(AFO; ras;TM=M;SS=N; 3.25
 400205; ; Hs.81848; NM_006265; Homo sapiens RAD21 (S. pombe); DUF173; 3.25
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3;TM=M;SS=Y; 3.24
 412942; AL120344; Hs.75074; mitogen-activated protein kinase-activat; pkinase;TM=M;SS=N; 3.23
 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; ig;TM=M;SS=M; 3.22
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 3.22
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 3.22
 427318; AF186081; Hs.175783; zinc transporter; Zip;TM=Y;SS=M; 3.22
 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 3.22
 448698; AA852773; Hs.334838; KIAA1866 protein; none;NA;NA; 3.22
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M;SS=N; 3.22
 415149; X12451; Hs.78056; cathepsin L; Peptidase_C1; 3.21
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD;TM=M;SS=N; 3.21
 424618; L29472; Hs.1802; major histocompatibility complex, class ; ig,MHC_II_beta;TM=Y;SS=M; 3.20
 438564; AA381553; Hs.198253; major histocompatibility complex, class ; ig,MHC_II_alpha,none; 3.20
 456181; L36463; Hs.1030; ras inhibitor; RA,SH2,VPS9;TM=M;SS=N; 3.20
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase ; pkinase,CNH;TM=M;SS=N; 3.19
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin,bZIP;TM=M;SS=N; 3.18
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threon; ank,pkinase,UPF0073;; 3.16
 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8;; 3.16
 450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin,ld_recept_a,none; 3.16
 426395; BE151985; Hs.355669; hypothetical protein FLJ23316; pkinase,none; 3.15
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor; none,none; 3.15
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;; 3.15
 410668; BE379794; Hs.159651; hypothetical protein; death,TNFR_c6;TM=Y;SS=M; 3.15
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 3.15
 432251; AW972983; Hs.232165; polycythemia rubra vera 1; cell surface ; none;TM=M;SS=M; 3.15
 407844; AW073716; Hs.8037; ESTs; transmembrane4,none; 3.14
 408634; AW407254; Hs.356216; calmodulin 2 (phosphorylase kinase, delt; none,none; 3.14
 423061; AI290473; Hs.44807; ESTs; integrin_B,Sema,PSI,TIG,none; 3.14
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ;; 3.13
 431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 3.13
 425394; AA356730; Hs.323949; kangai 1 (suppression of tumorigenicty ; transmembrane4,none; 3.13
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIII (25-hy; p450;; 3.13
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; ig,isodh,Ribosomal_L6,F-box;TM=Y;SS=M; 3.13
 429305; AF095727; Hs.287832; myelin protein zero-like 1; ig,transmembrane4;TM=Y;SS=M; 3.12
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M;SS=N; 3.12
 417386; AL037228; Hs.301957; D123 gene product; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 3.11
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion_trans,SPRY,RYDR,ITPR,RyR,MIR;TM=Y;SS=N; 3.11
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-li; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 3.10
 406467; ; Target Exon; ehand,Acyltransferase,none; 3.10
 422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell transformi; BRCT,RhoGEF;TM=M;SS=N; 3.10
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 3.09
 437016; AU076916; Hs.5398; guanine monophosphate synthetase; PHD,SET,zf-
 CXXC,EGF,ank,notch,WW,FCH,GATase,GMP_synt_C,Occludin,YEATS,metalthio,EB,heme_1,RCC1,ZZ,FeThRed_A,ENTH,Band_41,HECT;TM=M;SS=N; 3.09

- 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 3.09
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none,none; 3.09
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 3.09
 5 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;SS=N; 3.08
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 3.08
 402233; ; NM_030760; Homo sapiens endothelial diff; 7tm_1;TM=Y;SS=M; 3.07
 430066; A1929659; Hs.237825; signal recognition particle 72kD; TPR,AIRC,SAICAR_synt; 3.07
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 3.06
 434263; N34895; Hs.79187; ESTs; ig,none; 3.06
 10 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 3.05
 409378; U42387; Hs.54428; pancreatic polypeptide receptor 1; 7tm_1;TM=Y;SS=M; 3.05
 410165; BE560228; Hs.71869; apoptosis-associated speck-like protein ; PAAD_DAPIN,CARD;TM=M;SS=N; 3.05
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; fn3; 3.05
 15 449003; X76342; Hs.389; alcohol dehydrogenase 7 (class IV), mu o; adh_zinc;TM=M;SS=N; 3.05
 420189; AW296380; Hs.95821; osteoclast stimulating factor 1; SH3,ank; 3.05
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 doma; SH2; 3.05
 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase, pkinase_C;TM=M;SS=N; 3.04
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M;SS=N; 3.03
 20 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-
 binding, THF_DHG_CYH, THF_DHG_CYH_C, CAP_GLY, AAA, LON, Peptidase_C9, bZIP, M, xan_ur_permease, HCO3_cotransp;TM=M;SS=N; 3.03
 449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp;TM=M;SS=M; 3.03
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 3.02
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra,DUF51,none; 3.02
 25 436576; A1458213; Hs.77542; ESTs; 7tm_1,DnaJ; 3.02
 446269; AW263155; Hs.14559; hypothetical protein FLJ10540; none;TM=M;SS=N; 3.02
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 3.01
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 3.00
 421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, polyp; pkinase, pkinase_C;TM=M;SS=N; 3.00
 30 409705; M37762; Hs.56023; brain-derived neurotrophic factor; NGF; 2.99
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory su; CDK5_activator,none; 2.99
 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 2.98
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin_B,EGF,PSI;TM=Y;SS=M; 2.97
 410026; A1912061; Hs.55016; hypothetical protein FLJ21935; none,none; 2.97
 35 448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitte; SNF;TM=Y;SS=N; 2.97
 432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2;TM=M;SS=N; 2.97
 453035; AW581943; Hs.334; Rho guanine nucleotide exchange factor (; none,none; 2.97
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 2.97
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase,Furin-like,Recep_L_domain,none; 2.96
 40 441389; AF134838; Hs.7835; endocytic receptor (macrophage mannose r; fn2,lectin_c;TM=Y;SS=M; 2.95
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (; MIF,sugar_tr,none; 2.94
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm_1,none; 2.94
 402558; ; c1000201:gil204416[gb]AAA02627.1 (L0519; none;TM=Y;SS=M; 2.94
 425852; AK001504; Hs.159551; death receptor 6, TNF superfamily member; death, TNFR_c6;TM=Y;SS=M; 2.94
 45 424080; AW444761; Hs.72901; ESTs; ank; 2.94
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 2.93
 444809; BE207568; Hs.208219; oculoplanin; transmembrane4;TM=Y;SS=N; 2.93
 449843; R55337; Hs.24030; solute carrier family 31 (copper transpo; none;TM=Y;SS=M; 2.93
 416110; Z42262; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 2.93
 50 453768; BE382670; Hs.198511; Homo sapiens mRNA; cDNA DKFZp7611177 (fr; arf, G-alpha,none; 2.92
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian ; Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 2.92
 421429; NM_014922; Hs.104305; death effector filament-forming Ced-4-li; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC,NA;NA; 2.92
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 2.91
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;SS=N; 2.91
 55 422127; AW504286; Hs.112049; SET binding factor 1; dDENN,DENN,GRAM,PH; 2.91
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 2.90
 430451; AA836472; Hs.297939; cathepsin B; Peptidase_C1,pro_isomerase; 2.90
 424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibitor; serpin;TM=M;SS=N; 2.89
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,IRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M; 2.89
 60 429619; AL120751; Hs.211568; eukaryotic translation initiation factor; none,none; 2.89
 413879; AA132961; Hs.212533; Homo sapiens cDNA: FLJ22572 fis, clone H; none,none; 2.89
 417018; M16038; Hs.80887; v-src-1 Yamaguchi sarcoma viral related ; SH2,SH3,pkinase;TM=M;SS=N; 2.89
 422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, s; IRK;TM=Y;SS=N; 2.89
 405556; ; homeodomain-interacting protein kinase 3; trypsin;TM=M;SS=N; 2.89
 65 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 2.89
 425262; D87119; Hs.155418; GS3955 protein; pkinase; 2.88
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) ; NDK,PH,Oxysterol_BP; 2.88
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 2.88
 414703; BE243877; Hs.380063; ATPase, Na+ transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 2.87
 70 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2,none; 2.86
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF;TM=Y;SS=M; 2.86
 458039; AA835884; Hs.130685; leukotriene b4 receptor (chemokine recep; CIDE-N,none; 2.86
 434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp586F2224 (f; DSPc,none; 2.86
 425802; Y14838; chemokine-like receptor 1; 7tm_1,none; 2.86
 75 403112; ; Target Exon; ehand,C2,PH,PI-PLC-Y,PI-PLC-X; 2.86
 435563; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=N; 2.85
 442117; AW664964; Hs.128899; ESTs; hypothetical protein for IMAGE:447; none,none; 2.84
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein FLJ20522; none,none; 2.84
 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD,none; 2.83
 408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delt; none,none; 2.83
 446947; AF146747; Hs.232165; polycythemia rubra vera 1; cell surface ; none;TM=M;SS=M; 2.83
 80 448386; AB037750; Hs.21061; KIAA1329 protein; PKD,BNR;TM=Y;SS=M; 2.82
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin_head,IQ,zf-MYND;TM=M;SS=M; 2.82
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC;TM=Y;SS=M; 2.82

459707; AA631362; Hs.120866; gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens; 7tm_1,none; 2.82
 422699; BE410590; Hs.119257; ems1 sequence (mammary tumor and squamous); SH3,HS1_rep;TM=M;SS=N; 2.82
 438108; A1471795; Hs.287776; vanilloid receptor-related osmotically a; ank,ion_trans;TM=Y;SS=N; 2.82
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;SS=N; 2.82
 448595; AB014544; Hs.21572; KIAA0644 gene product; LRR,LRRCT;TM=Y;SS=M; 2.81
 423598; BE247600; Hs.377968; ESTs; 7tm_1;TM=Y;SS=M; 2.81
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSpc;; 2.81
 414198; AW505308; Hs.75812; phosphoenolpyruvate carboxykinase 2 (mit; PEPCK;; 2.81
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 2.81
 432314; AA533447; Hs.285173; ESTs; Xlink,none; 2.81
 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, comp; none;TM=Y;SS=M; 2.80
 446985; AL038704; Hs.156827; ESTs, Weakly similar to ALU1_HUMAN ALU S; SAM,SH3,HS1_rep; 2.80
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone L;
 aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 2.80
 432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M;SS=N; 2.80
 426006; R49031; Hs.22627; ESTs; pkinase,TBC; 2.79
 414217; A1309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 2.79
 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;; 2.79
 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheti; ABC_tran,ABC_membrane,ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 2.78
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 2.78
 421448; AF033850; Hs.104519; phospholipase D2; PH,PLDc,PX;TM=M;SS=N; 2.78
 410226; A1831958; Hs.61053; hypothetical protein; SH3,TPR;TM=M;SS=N; 2.78
 433535; AF111106; Hs.3382; protein phosphatase 4, regulatory subunit; HEAT;TM=M;SS=N; 2.78
 424503; AF147078; Hs.375031; p53-responsive gene 5; K_tetra,ion_trans,none; 2.77
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/H; TPR,PDZ,WW,Guanylate_kin;TM=M;SS=N; 2.77
 454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M;SS=N; 2.77
 440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK;TM=M;SS=N; 2.77
 449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep_L_domain,none; 2.76
 422667; H25642; Hs.132821; ESTs; FMO-like,FMO-like; 2.76
 415012; NM_004383; Hs.77793; c-src tyrosine kinase; SH2,SH3,pkinase;TM=M;SS=N; 2.76
 402316; ; NM_013447;Homo sapiens egf-like module c; 7tm_2,GPS;TM=M;SS=M; 2.75
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 2.75
 447250; A1878909; Hs.17883; protein phosphatase 1G (formerly 2C); ma; PP2C;TM=M;SS=N; 2.75
 438629; A1187380; Hs.257170; ESTs, Weakly similar to T12515 hypotheti; TNFR_c6,none; 2.75
 451144; AW956103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme; HATPase_c,none; 2.74
 408543; N78098; Hs.44289; ESTs; none;TM=M;SS=N; 2.74
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 2.74
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; ptkB;TM=M;SS=N; 2.73
 420602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS;TM=M;SS=N; 2.73
 407217; AA477136; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 2.73
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSpc,Y_phosphatase;TM=M;SS=N; 2.73
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 2.73
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 2.73
 438022; AW517524; Hs.135201; NOD2 protein; LRR,CARD,GTP_CDC,Viral_helicase1;TM=M;SS=N; 2.72
 420929; A1694143; Hs.326248; programmed cell death 4; MA3;TM=M;SS=N; 2.72
 421155; H87879; Hs.102267; lysyl oxidase; Lysyl_oxidase,Aldose_epim,Epimerase; 2.72
 448564; AL044962; Hs.21453; inositol 1,4,5-trisphosphate 3-kinase C; IPK; 2.71
 449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain,none; 2.71
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ig;TM=Y;SS=M; 2.71
 412259; A1560292; Hs.279909; protein phosphatase 2 (formerly 2A), reg; WD40;TM=M;SS=N; 2.71
 419569; A1971651; Hs.91143; jagged 1 (Alagille syndrome); DSL,EGF,laminin_EGF_vwc,metalthio;TM=M;SS=M; 2.71
 452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-induced pro; Xlink,CUB;; 2.71
 458190; BE561793; Hs.21446; KIAA1716 protein; ASC,Galactosyl_T,none; 2.70
 432126; AA865239; Hs.37196; ESTs; 7tm_1;TM=Y;SS=M; 2.70
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M;SS=N; 2.70
 424717; H03754; Hs.152213; wingless-type MMTV integration site fam; wnt,none; 2.70
 414108; A1267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol_BP,pkinase;TM=M;SS=N; 2.70
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep;TM=M;SS=N; 2.70
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none,none; 2.69
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;SS=N; 2.69
 404891; ; Target Exon; none,none; 2.69
 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 2.69
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2,SH3,pkinase;TM=M;SS=N; 2.68
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; ig,kringle,pkinase,Fz;TM=Y;SS=M; 2.68
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor;; ig,pkinase;TM=Y;SS=N; 2.68
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, fo; ig,pkinase;TM=Y;SS=M; 2.68
 436856; A1469355; Hs.127310; ESTs; pkinase,rrm;TM=M;SS=N; 2.68
 437429; H79981; Hs.5613; Homo sapiens mRNA; cDNA DKFZp564E2222 (f; SH2,SH3,BTB; 2.67
 450690; AA296696; Hs.333418; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 2.67
 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 2.67
 445330; R52656; Hs.21691; ESTs; 7tm_1,none; 2.67
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 2.67
 419754; H52299; Hs.308467; Homo sapiens mRNA; cDNA DKFZp566I0523 (f; none;TM=M;SS=N; 2.67
 434237; AF119908; Hs.235516; hypothetical protein PRO2955; none;; 2.67
 445826; BE313754; Hs.13350; Homo sapiens mRNA; cDNA DKFZp566D0918 (f; ig,isp_1,ZU5,Nucleoside_tran; 2.66
 446698; AF279265; Hs.298476; solute carrier family 26, member 6; Sulfate_transp,STAS,xan_ur_permease;TM=Y;SS=N; 2.66
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 2.66
 413745; AW247252; Hs.75514; nucleoside phosphorylase; Mtap_PNP;; 2.66
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 2.66
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 2.66
 449030; A1365582; Hs.57100; Homo sapiens mRNA for FLJ00016 protein, ; transmembrane4;TM=Y;SS=M; 2.66
 434979; A1953054; Hs.89643; transketolase (Wernicke-Korsakoff syndr; ASC,transketolase,transket_pyr,transketolase_C,pkinase; 2.66
 408137; ; NM_000179;Homo sapiens mutS (E. coli) h; MutS_C,PWWP,MutS_N;TM=M;SS=N; 2.66

- 412935; BE267045; Hs.75064; tubulin-specific chaperone c; none;; 2.66
 408633; AW963372; Hs.222088; PRO2000 protein; bromodomain,AAA,Sigma54_activat;; 2.66
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subu; PC_rep; TM=M;SS=N; 2.65
 452682; AA456193; Hs.374574; progesterone membrane binding protein; homeobox; none; 2.65
 401752; ; RAN binding protein 3; SH2,STAT,STAT_bind,STAT_prot,ion_trans,PAC,PAS,Orexin; 2.65
 450747; AI064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm,zf-RanBP,GAS2; 2.65
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM; TM=Y;SS=M; 2.64
 452701; NM_005110; Hs.30332; glutamine-fructose-6-phosphate transamin; GATase_2,SIS; TM=M;SS=N; 2.64
 433933; AI754389; Hs.355397; Homo sapiens clone TCCCAC0164 mRNA sequ; none;NA;NA; 2.64
 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 2.64
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none;; 2.64
 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese; none; 2.64
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH; TM=M;SS=N; 2.64
 437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor, ; Tropomyosin,pkinase,LRR,LRRCT,Hydantoinase_B,Hydantoinase_A; TM=M;SS=N; 2.63
 458946; AA009716; Hs.42311; ESTs; none,DSPc,Y_phosphatase; 2.63
 447217; BE465754; Hs.17778; neuroligin 2; CUB,MAM,F5_F8_type_C; TM=M;SS=M; 2.63
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 2.63
 425075; AA506324; Hs.1852; acid phosphatase, prostate; acid_phosphat; TM=Y;SS=M; 2.63
 405588; ; NM_000299; Homo sapiens plakophilin 1 (e; Armadillo_seg; TM=M;SS=N; 2.63
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH; none; 2.63
 448243; AW369771; Hs.367688; integrin, beta 8; integrin_B; none; 2.63
 452012; AA307703; Hs.279766; kinesin family member 4A; kinesin,DNA_topoisolV,K-box; TM=M;SS=N; 2.63
 412182; AA205588; Hs.73737; Splicing factor, arginine/serine-rich, 4; rrm,hormone_rec,zf-C4,sugar_tr; 2.63
 423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC_tran; TM=Y;SS=N; 2.63
 417497; AV402482; Hs.82212; CD53 antigen; transmembrane4; TM=Y;SS=M; 2.62
 413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like ; SH2,SAM,Exo_endo_phos;; 2.62
 414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c; TM=Y;SS=M; 2.62
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin_c,sushi; TM=M;SS=M; 2.62
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone; TM=M;SS=N; 2.62
 401812; ; sorting nexin 14; AAA,NB-ARC,APS_kinase,cdc48_N,cdc48_2; none; 2.61
 417886; AA214584; ; ESTs; SPRY,7tm_3,ANF_receptor; none; 2.61
 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substra; SH3; TM=M;SS=N; 2.61
 428512; AI018187; Hs.375624; Human DNA sequence from clone RP11-243J1; none;; 2.61
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Pribosyltran,OMPdecase; TM=M;SS=N; 2.61
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT; none; 2.61
 421077; AK000061; Hs.101590; hypothetical protein; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN; TM=M;SS=N; 2.60
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase; TM=M;SS=N; 2.60
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain,rrm; TM=M;SS=N; 2.60
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF;; 2.60
 411133; AW819204; ; gb:CM1-ST0283-071299-061-h03 ST0283 Homo; ANF_receptor; none; 2.60
 405602; ; Target Exon; pkinase;; 2.60
 400440; X83957; Hs.83870; nebulin; SH3,Nebulin;; 2.60
 424848; AI263231; Hs.327090; EST; SH3,PDZ,Guanylate_kin; none; 2.59
 432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase; TM=M;SS=N; 2.59
 452690; AI536070; Hs.15085; ESTs; pou,homeobox,lig_chan,ANF_receptor; 2.59
 422753; AI928995; Hs.1575; small nuclear ribonucleoprotein D3 polyp; Srm;; 2.59
 428028; U52112; Hs.182018; interleukin-1 receptor-associated kinase; death,pkinase; TM=M;SS=N; 2.58
 433573; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G-type rece; 7tm_2,EGF,cadherin,laminin_EGF,laminin_G,Tyran_glycop,GPS,HRM; TM=Y;SS=M; 2.58
 422785; AI824114; Hs.289088; heat shock 90kD protein 1, alpha; zf-C2H2; none; 2.58
 418685; U76376; Hs.87247; harakiri, BCL2-interacting protein (cont; none; TM=M;SS=M; 2.58
 452329; N36626; Hs.29106; mitogen-activated protein kinase phosphatase; DSPc; TM=M;SS=N; 2.58
 428405; Y00762; Hs.2266; cholinergic receptor, nicotinic, alpha p; Neur_chan_LBD,Neur_chan_memb; TM=Y;SS=M; 2.58
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ; 2.57
 407245; X90568; Hs.172004; titin; tn3,ig,SGXXSG,pkinase; TM=M;SS=N; 2.57
 422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic; sugar_lr; TM=Y;SS=M; 2.57
 401751; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_prot,ion_trans,PAC,PAS; none; 2.57
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED; TM=M;SS=N; 2.57
 422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExbB; TM=Y;SS=M; 2.57
 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; lipoxygenase,PLAT,lipoxygenase,PLAT; 2.57
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2; TM=Y;SS=N; 2.57
 401218; ; eukaryotic translation elongation factor; ion_trans; TM=Y;SS=N; 2.57
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L OR; PLDc; TM=M;SS=N; 2.57
 444743; AA045648; Hs.301957; nudix (nucleoside diphosphate linked moi; NUDIX,secY,E1_dehydrog,transkeL_pyr; TM=Y;SS=M; 2.56
 429782; NM_005754; Hs.220689; Ras-GTPase-activating protein SH3-domain; rrm,NTF2; TM=M;SS=N; 2.56
 442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 2.56
 456602; AA411607; Hs.118964; ESTs, Weakly similar to KIAA1150 protein; none,pkinase; 2.56
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3,PX; TM=M;SS=N; 2.56
 441699; AW511126; Hs.127572; ESTs; none,Aa_trans; 2.56
 447912; AW576549; Hs.165728; ESTs, Weakly similar to I38022 hypotheti; none,GSHPx,ABC_tran; 2.56
 442945; AI024849; Hs.131853; ESTs; pkinase; none; 2.56
 453199; AI336266; Hs.32353; mitogen-activated protein kinase kinase ; pkinase; TM=M;SS=N; 2.56
 451477; AI798425; Hs.42710; ESTs; SH3; none; 2.56
 415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-Coenzyme A sy; HMG_CoA_synt; 2.55
 413529; U11874; Hs.846; interleukin 8 receptor, beta; 7tm_1; TM=Y;SS=N; 2.55
 425345; AU077297; Hs.155894; protein tyrosine phosphatase, non-recept; Y_phosphatase,DSPc; TM=M;SS=M; 2.55
 401321; ; receptor tyrosine kinase-like orphan rec; none; TM=M;SS=N; 2.55
 446999; AA151520; Hs.351416; hypothetical protein MGC4485; none; none; 2.55
 401057; ; eukaryotic translation elongation factor; ion_trans,IQ; TM=Y;SS=N; 2.55
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4; TM=Y;SS=M; 2.55
 408204; AA454501; Hs.43666; protein tyrosine phosphatase type IVA, m; Y_phosphatase; TM=M;SS=N; 2.54
 424539; I02911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK; pkinase,Activin_rec; TM=M;SS=M; 2.54
 459060; H89244; Hs.303627; heterogeneous nuclear ribonucleoprotein ; rrm,pkinase; TM=M;SS=N; 2.54
 450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2; TM=M;SS=N; 2.54

- 425966; NM_001761; Hs.1973; cyclin F; cyclin,F-box,cyclin_C;TM=M;SS=N; 2.54
 446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 2.54
 412834; R77123; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm_1,none; 2.54
 457255; AL133011; Hs.253920; Homo sapiens mRNA; cDNA DKFp434P201 (fr; none,none; 2.54
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit,; proteasome;TM=M;SS=N; 2.53
 417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2,PID,zf-C2H2,SCAN,AMP-binding,KRAB;TM=M;SS=N; 2.53
 414570; Y00285; Hs.76473; insulin-like growth factor 2 receptor; fn2,CIMR;TM=M;SS=M; 2.53
 444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP,none; 2.53
 422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR,SH2,SH3,pkinase;TM=Y;SS=M; 2.53
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none,none; 2.53
 400702; ; Target Exon; lig_chan,SBP_bac_3,ANF_receptor;TM=Y;SS=M; 2.53
 432336; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm,pkinase;TM=M;SS=N; 2.53
 442643; U82756; Hs.374973; PRP4/STK/WD splicing factor; WD40;; 2.52
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN2; ABC_tran,IRK,SWIB; 2.52
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22,Claudin,none; 2.52
 428975; NM_004672; Hs.194694; mitogen-activated protein kinase kinase ; pkinase; 2.52
 407608; A1928218; Hs.380063; ATPase, Na? transporting, beta 3 polypep; none,none; 2.51
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 2.51
 410293; AK000047; Hs.61960; hypothetical protein; K_tetra;TM=M;SS=N; 2.51
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, ; C2,PLA2_B;TM=M;SS=N; 2.51
 425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;SS=N; 2.51
 457013; AA037145; Hs.172865; cleavage stimulation factor, 3' pre-RNA; WD40;TM=M;SS=N; 2.51
 439221; AA737106; Hs.32250; ESTs, Moderately similar to I78885 serin; adh_short,Bcl-2,BH4,none; 2.51
 405429; ; Target Exon; Y_phosphatase,none; 2.51
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible Ik; pkinase,RIO1;TM=M;SS=N; 2.51
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 2.50
 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 2.50
 414419; F06829; Hs.76090; tumor necrosis factor, alpha-induced pro; K_tetra;TM=M;SS=N; 2.50
 405369; ; NM_005569; Homo sapiens LIM domain kinase; pkinase,LIM,PDZ; 2.50
 418216; AA662240; Hs.283099; AF15q14 protein; Hemagglutinin,squash;TM=Y;SS=N; 2.50
 404321; ; C7001741;gij4299629]sp]Q63932]MPK2_MOUSE; none,none; 2.50
 430900; U91939; Hs.248123; G protein-coupled receptor 25; 7tm_1;TM=Y;SS=M; 2.49
 440861; BE244115; Hs.7482; KIAA0682 gene product; rrm,Guanylate_kin;TM=M;SS=N; 2.49
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; ig;TM=Y;SS=N; 2.49
 418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosom; pkinase,Activin_recp,pkinase,Activin_recp; 2.49
 417034; NM_006183; Hs.80962; neurotensin; none; 2.49
 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none,none; 2.49
 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase;TM=M;SS=N; 2.49
 418255; AW135405; Hs.37251; ESTs; pkinase,none; 2.49
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase;TM=M;SS=N; 2.44
 417791; AW965339; Hs.44269; ESTs; none,fer2,FAD_binding_5,Ald_Xan_dh_C,fer2_2,Ald_Xan_dh_C2,CO_deh_flav_C; 2.44
 453941; U39817; Hs.36820; Bloom syndrome; DEAD,helicase_C,HRDC;TM=M;SS=N; 2.41
 417849; AW291587; Hs.82733; nidogen 2; EGF,Idl_recept_b,thyroglobulin_1;TM=M;SS=M; 2.39
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;; 2.32
 428513; BE220806; Hs.184697; plexin C1; PSI,none; 2.31
 426761; A1015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 2.31
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q,Collagen;; 2.28
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M;SS=N; 2.28
 452461; N78223; Hs.108106; transcription factor; zf-C3HC4,ubiquitin,PHD,YDG_SRA;TM=M;SS=N; 2.26
 429547; AW009166; Hs.99376; FGENESH predicted novel secreted protein; none,none; 2.15
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; SNF2_N,helicase_C;TM=M;SS=N; 2.15
 401486; ; C4000647;gij4758508]ref]NP_004253.1] ai; none;TM=Y;SS=M; 2.15
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient, yeast, h; HORMA;TM=M;SS=N; 2.14
 424399; A1905687; Hs.348419; A1905687:IL-BT095-190199-019 BT095 Homo ; none;TM=M;SS=M; 2.14
 423761; NM_006194; Hs.132576; paired box gene 9; PAX;TM=M;SS=N; 2.13
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC004858 3 U1 sm; none,none; 2.13
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2,CytC_asm,GPS;TM=Y;SS=M; 2.03
 445019; A1205540; Hs.281295; ESTs; none,none; 2.00
 443211; A1128388; Hs.143655; ESTs; none,none; 1.98
 449448; D60730; Hs.57471; ESTs; none,none; 1.92
 435243; AW292886; Hs.348932; hypothetical protein dJ434O14.3; IRF,none; 1.85
 406360; ; Target Exon; WD40;TM=M;SS=N; 1.84
 411388; X72925; Hs.69752; desmocollin 1; cadherin;TM=Y;SS=N; 1.84
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm_2;TM=Y;SS=M; 1.79
 419183; U60669; Hs.89663; cytochrome P450, subfamily XXIV (vitamin; p450;; 1.78
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 1.77
 432842; AW674093; Hs.334822; hypothetical protein MGC4485; Ribosomal_L4;TM=M;SS=N; 1.76
 419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA sequence; none,none; 1.73
 426427; M86699; Hs.169840; TTK protein kinase; pkinase;; 1.62
 437915; A1637993; Hs.202312; Homo sapiens clone N11 Ntera2D1 teratoca; none,none; 1.58
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz,NTR;; 1.50
 434377; AW137148; Hs.306593; intron of periostin (OSF-2os); Fasciclin,none; 1.47
 451592; A1805416; Hs.213897; ESTs; none,none; 1.47
 404927; ; Target Exon; Galactosyl_T;TM=M;SS=Y; 1.28
 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;; 1.27
 427335; AA448542; Hs.278444; G antigen 7B; none;; 1.25
 431808; M30703; Hs.270833; amphiregulin (schwannoma-derived growth ; EGF;TM=Y;SS=M; 1.24
 447993; AW139525; Hs.170362; ESTs; none,none; 1.21
 428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_HUMAN G ANT; none;TM=M;SS=N; 1.18
 453637; NM_002589; Hs.34073; BH-protocadherin (brain-heart); cadherin;TM=Y;SS=M; 1.14
 438274; A1918906; Hs.55080; ESTs; PAX,none; 1.14
 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin,Idl_recept_a,none; 1.10
 413268; AL039079; Hs.75256; regulator of G-protein signalling 1; RGS;TM=M;SS=N; 1.07

429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen, COLFI, TSPN, laminin_G, CorA;; 1.00
452795; AW392555; Hs.18878; hypothetical protein FLJ21620; 2OG-Fell_Oxy; TM=M; SS=N; 1.00

TABLE 25B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
406685	0_0	M18728
418869	12789_14	AA229762 AA230035
425802	8884_3	AA122298 AA360788
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
411133	1070995_1	AW819203 AW819204 AW819197 AW819202 AW819211 BE158469 AW819221 BE158473 AW819235 AW819207 AW819220 AW819208 AW819238
AW819198	AW819234	

TABLE 25C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
405932	7767812	Minus	123525-123713
406467	9795551	Plus	182212-182958
402233	7690102	Plus	90281-91477
402558	9863760	Plus	19047-19145,21133-21293,33968-34069
405556	1552511	Plus	163497-163623,164715-164968,165369-16550
403112	8980973	Minus	113051-113195
402316	7527774	Minus	10751-10919,18817-19052,22131-22328
404891	7329392	Plus	84974-85125
406137	9166422	Minus	30487-31058
401752	9828651	Plus	144600-144794
405588	5002511	Plus	46180-46366
401812	7407975	Minus	55084-55391
405602	4753260	Plus	44647-44778
401751	9828651	Plus	139165-139322
401218	9929301	Minus	40793-41031
401321	9863631	Minus	104278-104748
401057	8117645	Plus	158309-159238
400702	8118856	Minus	11457-11585,26311-26536,27902-28067,3204
405429	7321905	Minus	51577-51723
405369	2078469	Minus	34183-34357,35686-35751
404321	9665209	Minus	76594-77805
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
406360	9256107	Minus	7513-7673
404927	7342002	Plus	68690-69563

TABLE 26A: 834 GENES UP-REGULATED IN EWING'S SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 26A lists about 834 genes up-regulated in Ewing's sarcoma compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 1.5. The "average" kidney cancer level was set to the 75th percentile amongst Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 7.5th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UniGeneID: UniGene number
UniGene Title: UniGene gene title
R1: Ratio of Ewing sarcoma to normal tissue

Pkey	ExAccn	UniGeneID	UniGene Title	R1
101447	M21305		gb:Human alpha satellite and satellite 3	38.4
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	34.2
110278	AF061573	Hs.19492	protocadherin 8	32.2
121362	AF050147	Hs.97932	chondromodulin I precursor	30.3
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	26.3

	121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	24.4
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidyseri	23.4
	104659	AW969769	Hs.105201	ESTs	20.2
5	106533	AL134708	Hs.145998	ESTs	16.9
	124006	AI147155	Hs.270016	ESTs	15.0
	110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	14.8
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	14.6
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	14.5
10	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	13.7
	121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	12.3
	129526	S69681	Hs.177582	surfactant, pulmonary-associated protein	12.1
	119791	AA554907	Hs.58291	ESTs	11.7
	116301	AW969706	Hs.293332	ESTs	11.2
15	123308	C14187	Hs.103538	ESTs	10.9
	127742	AW293496	Hs.180138	ESTs	10.8
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	10.7
	127489	AA650250	Hs.272076	ESTs	10.6
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.6
20	101063	D54745	Hs.80247	cholecystokinin	10.6
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	10.5
	100299	D49493	Hs.2171	growth differentiation factor 10	10.1
	127987	AI022103	Hs.124511	ESTs	10.1
	131313	R96290	Hs.336629	ribosomal protein L44	9.2
25	126799	AW753865	Hs.74376	olfactomedin related ER localized protei	8.5
	125847	AW161885	Hs.249034	ESTs	7.0
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	6.9
	114837	BE244930	Hs.166895	ESTs	6.6
	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	6.6
30	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.5
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous r	6.5
	125186	AA610620	Hs.181244	major histocompatibility complex, class	6.4
	118644	AA443241	Hs.336629	ribosomal protein L44	6.3
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	6.3
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	6.1
	113003	AW292315	Hs.7215	ESTs	5.8
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.7
	101050	AU077324	Hs.1832	neuropeptide Y	5.7
	116790	AW161357	Hs.101174	microtubule-associated protein tau	5.5
40	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	5.1
	132315	AF091086	Hs.44563	hypothetical protein	5.0
	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	4.9
	126077	M78772	Hs.210836	ESTs	4.7
	126426	AA125984		gb:zn27h06.r1 Stralagene neuroepithelium	4.6
45	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	4.5
	123619	AA602964		gb:no97c02.s1 NCL_CGAP_Pr2 Homo sapiens	4.4
	128361	AW172570	Hs.130246	ESTs	4.3
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	4.3
	100020				4.2
50	125556	AB033064	Hs.334806	KIAA1238 protein	4.2
	105316	AI671245	Hs.24835	hypothetical protein FLJ14594	4.0
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.0
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (3.9
	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	3.9
55	129012	R81936	Hs.336629	ribosomal protein L44	3.9
	125447	AI582222	Hs.128686	ESTs	3.8
	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	3.6
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	3.6
	128391	AW188326	Hs.170652	ESTs	3.5
60	123829	AF251237	Hs.112208	XAGE-1 protein	3.4
	123949	AA621665	Hs.208957	EST	3.4
	126872	AW450979		gb:U1-H-BI3-ala-a-12-0-UI.s1 NCL_CGAP_Su	3.4
	101266	L36645	Hs.73964	EphA4	3.3
	121309	AA293834	Hs.97312	ESTs	3.3
65	130637	AA356764	Hs.17109	integral membrane protein 2A	3.2
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	3.2
	135175	M91463	Hs.95958	solute carrier family 2 (facilitated glu	3.2
	107599	AW664072	Hs.60136	ESTs	3.2
	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.2
70	131688	AI935413	Hs.30692	p21 (CDKN1A)-activated kinase 2	3.1
	120147	AI917116	Hs.155376	hemoglobin, beta	3.1
	110343	AW136703	Hs.17268	ESTs	3.1
	127664	AA806164	Hs.116502	ESTs	3.0
	103076	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	3.0
75	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	3.0
	125558	R59305		gb:yh16c10.r1 Soares infant brain 1NIB H	3.0
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.9
	133421	AF134160	Hs.7327	claudin 1	2.8
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.8
80	113577	AI300699	Hs.278937	PRO0470 protein	2.8
	118397	BE139479	Hs.161492	ESTs	2.8
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	2.8
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	2.8
	127262	AA828125		gb:od71a09.s1 NCL_CGAP_Ov2 Homo sapiens	2.8

	106472	AI207162	Hs.3815	stathmin-like-protein RB3	2.7
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	2.7
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	2.7
5	126600	AA699949	Hs.191385	ESTs	2.7
	120325	AA195651	Hs.104106	ESTs	2.7
	127256	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN	2.7
	117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	2.7
	126735	M69113	Hs.226795	glutathione S-transferase pi	2.7
10	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	2.7
	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (2.6
	129706	AA443241	Hs.336629	ribosomal protein L44	2.6
	107731	AA016086	Hs.272106	ESTs, Weakly similar to I38022 hypotheti	2.6
	128283	AI076570	Hs.134053	ESTs	2.6
15	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	2.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
	105577	AW852257	Hs.171391	C-terminal binding protein 2	2.6
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	2.6
	130262	D63216	Hs.153684	frizzled-related protein	2.6
20	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.6
	102479	NM_001991	Hs.194669	enhancer of zeste (Drosophila) homolog 1	2.6
	128531	H03721	Hs.2953	ribosomal protein S15a	2.6
	126165	AI741816	Hs.125897	ESTs	2.6
	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	2.5
25	118967	AI668670	Hs.216756	ESTs	2.5
	120830	AI568170	Hs.96886	ESTs	2.5
	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.5
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	2.5
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	2.5
30	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	2.5
	133761	AF041430	Hs.75922	brain protein I3	2.5
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.5
	126693	C05723		gb:C05723 Human pancreatic islet Homo sa	2.5
35	126021	AA775894	Hs.187516	ESTs	2.5
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	2.5
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	2.5
	125743	H17151		gb:ym37a05.r1 Soares infant brain 1NIB H	2.5
	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	2.5
40	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	2.4
	123110	AA486256	Hs.193510	EST	2.4
	113283	T66813	Hs.12947	EST	2.4
	107711	W96141	Hs.220687	ESTs	2.4
	128992	H04150	Hs.107708	ESTs	2.4
	106111	AW875398	Hs.6451	PRO0659 protein	2.4
45	129948	AI537162	Hs.263988	ESTs	2.4
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	2.4
	116728	F13687	Hs.227976	EST	2.4
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	2.4
50	124971	T23800	Hs.151001	hypothetical protein FLJ14728	2.4
	131019	W28614	Hs.306155	chorionic somatomammotropin hormone 1 (p	2.4
	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory s	2.4
	111795	AI435437	Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCL	2.4
	119127	AA708035	Hs.12248	ESTs	2.4
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	2.4
55	111898	R38944	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.4
	131916	AA025976	Hs.34569	ESTs	2.4
	130850	AB040922	Hs.20237	DKFZP566C134 protein	2.4
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	2.4
	126722	N66148	Hs.11125	HSPC033 protein	2.4
60	123720	AA609734	Hs.112755	EST	2.4
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovir	2.4
	131136	AB033099	Hs.23413	KIAA1273 protein	2.4
	129001	AA443323	Hs.107812	BPOZ protein	2.4
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	2.4
65	107593	AI093688	Hs.60051	ESTs	2.4
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	2.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	2.4
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	2.4
	128367	AW611791	Hs.150742	ESTs	2.4
70	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	2.4
	112342	AW410273	Hs.92614	longevity assurance (LAG1, S. cerevisiae	2.3
	114721	D61939	Hs.103822	ESTs	2.3
	127768	AW085002	Hs.156187	ESTs	2.3
	127706	AI174238	Hs.186982	ESTs	2.3
75	126029	AA704253	Hs.169359	ESTs	2.3
	124250	AA350256	Hs.323875	EST, Weakly similar to 2109260A B cell	2.3
	117265	AA451966	Hs.43005	RAB9-like protein	2.3
	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	2.3
	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	2.3
80	127252	AI049545	Hs.94	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
	129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	2.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.3
	109252	BE440157	Hs.85944	ESTs	2.3
	127889	AI147408	Hs.144941	ESTs	2.3

	121292	AA401807		gb:zv65f11.s1 Soares_total_fetus_Nb2HFB_	2.3
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte sec	2.3
	132985	AL045579	Hs.62113	KIAA0717 protein	2.3
5	125174	W51835	Hs.231082	EST	2.3
	125401	AI204637	Hs.337585	ESTs, Highly similar to KIAA0350 [H.sapi	2.3
	135278	AA399542	Hs.229671	EST, Moderately similar to PEPTIDYL-PROL	2.3
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN	2.3
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	2.3
10	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	2.3
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	2.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC	2.3
	101086	AA382524	Hs.250959	histatin 1	2.3
	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	2.3
15	126879	D90391	Hs.1265	branched chain keto acid dehydrogenase E	2.3
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	2.3
	124691	R05835	Hs.110153	ESTs	2.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	2.3
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	2.2
20	129052	BE275031	Hs.158210	hypothetical protein MGC2555	2.2
	129248	W04606	Hs.171637	hypothetical protein MGC2628	2.2
	100780	BE561958	Hs.302063	immunoglobulin heavy constant mu	2.2
	135416	BE281018	Hs.99969	fusion, derived from t(12;16) malignant	2.2
	129928	AI338993	Hs.134535	ESTs	2.2
25	103319	X83492	Hs.82359	tumor necrosis factor receptor superfam	2.2
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	2.2
	120734	AA299948		gb:EST12544 Uterus tumor 1 Homo sapiens	2.2
	111777	AK001100	Hs.41690	desmocollin 3	2.2
	128963	J03890	Hs.1074	surfactant, pulmonary-associated protein	2.2
30	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	2.2
	134964	AI803516	Hs.272891	hippocalcin-like protein 4	2.2
	127248	AA364195		gb:EST75015 Pineal gland II Homo sapiens	2.2
	125761	R68351		gb:yh99b03.r1 Soares placenta Nb2HP Homo	2.2
35	101358	M10058	Hs.12056	asialoglycoprotein receptor 1	2.2
	101613	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.2
	107121	AB015427	Hs.250493	zinc finger protein 219	2.2
	118751	N74210	Hs.50454	ESTs	2.2
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	2.2
40	126581	W73306	Hs.306668	Homo sapiens cDNA FLJ14089 fis, clone MA	2.2
	127634	AA633469	Hs.193283	ESTs, Weakly similar to unnamed protein	2.2
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	2.2
	132867	AF226667	Hs.58553	CTP synthase II	2.2
	126323	N77584	Hs.68644	Homo sapiens microsomal signal peptidase	2.2
45	111790	AW769683	Hs.6734	ESTs, Weakly similar to S26650 DNA-bind	2.2
	125549	R20215		gb:ygl8b09.r1 Soares infant brain 1N1B H	2.2
	128059	AA972446	Hs.145096	ESTs	2.2
	132342	AW162758	Hs.45232	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.2
	125722	H29796	Hs.269622	ESTs	2.2
50	106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	2.2
	127644	N88858	Hs.155101	ATP synthase, H+ transporting, mitochond	2.2
	128179	AW293689	Hs.127116	ESTs	2.2
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	2.2
	126962	R12014	Hs.20976	ESTs	2.2
55	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	2.2
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	2.2
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypothet	2.2
	108743	AI580150	Hs.71074	ESTs	2.2
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	2.2
	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	2.2
60	109929	AA773187	Hs.294027	ESTs	2.2
	129059	AW069534	Hs.279583	CGI-81 protein	2.2
	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	2.2
	116962	H79677		gb:yu76g10.s1 Soares fetal liver spleen	2.2
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	2.2
65	106711	BE390125	Hs.143187	hypothetical protein	2.2
	135191	X16866	Hs.301086	cytochrome P450, subfamily IID (debrisoq	2.2
	125822	H03162	Hs.268768	ESTs	2.2
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	2.2
	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	2.2
70	126250	AL050391	Hs.321247	Homo sapiens mRNA; cDNA DKFZp586A181 (fr	2.2
	103392	X94563		gb:H.sapiens dbi/acbp gene exon 1 & 2.	2.2
	129794	AF161399	Hs.23259	hypothetical protein FLJ13433	2.2
	100253	D38024	Hs.157425	double homeobox, 2	2.2
	130743	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.2
75	125466	R08234	Hs.180461	ESTs	2.2
	122682	AA984531	Hs.159293	ESTs	2.2
	133347	BE257758	Hs.71475	acid cluster protein 33	2.2
	104455	AL110261	Hs.157211	DKFZP586B0621 protein	2.2
80	116332	AA491208	Hs.62620	chromosome 6 open reading frame 1	2.2
	131163	AA099524	Hs.23754	ESTs	2.2
	109592	AI198059	Hs.26370	ESTs	2.2
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.1
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	2.1
	128434	AI190914	Hs.143880	ESTs	2.1

	103163	AU077018	Hs.3235	keratin 4	2.1
	112379	AK001713	Hs.17860	hypothetical protein FLJ10851	2.1
	127507	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	2.1
5	133097	W03512	Hs.6479	hypothetical protein MGC13272	2.1
	126153	H85692	Hs.40730	ESTs	2.1
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	2.1
	100554	M95923		gb:Human 12-lipoxygenase mRNA, partial c	2.1
	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	2.1
10	132664	AI740461	Hs.54542	ESTs	2.1
	114620	AA642974		gb:nr60h01.s1 NCL_CGAP_Lym3 Homo sapiens	2.1
	115348	AA281562	Hs.292100	ESTs	2.1
	133231	AK000517	Hs.6844	hypothetical protein FLJ20510	2.1
	133160	N54968	Hs.66309	hypothetical protein MGC11061	2.1
15	124656	AW297702	Hs.102915	ESTs	2.1
	133576	M19650	Hs.150741	2',3'-cyclic nucleotide 3' phosphodiester	2.1
	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypothet	2.1
	126505	AA282881	Hs.190057	ESTs	2.1
	118865	AA736405	Hs.54530	ESTs	2.1
20	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	2.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	2.1
	133493	AW998046	Hs.194369	arginine-glutamic acid dipeptide (RE) re	2.1
	112853	T02843		gb:FB11H5 Fetal brain, Stratagene Homo s	2.1
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU	2.1
25	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	2.1
	134869	AL157518	Hs.90421	PRO2463 protein	2.1
	128869	AA768242	Hs.80618	hypothetical protein	2.1
	129179	AW969025	Hs.109154	ESTs	2.1
	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	2.1
30	101651	AL037111	Hs.75641	galactose-1-phosphate uridylyltransferase	2.1
	129726	H15474	Hs.132898	fatty acid desaturase 1	2.1
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	126271	AI250773	Hs.270012	ESTs	2.1
	116925	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-ce	2.1
35	128468	T23625	Hs.150580	putative translation initiation factor	2.1
	116031	AA452239	Hs.103329	KIAA0970 protein	2.1
	130724	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	2.1
	121897	AA427419	Hs.229162	EST, Weakly similar to ZN91_HUMAN ZINC	2.1
	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	2.1
40	122333	AA625872	Hs.98977	ESTs, Moderately similar to T34561 hypot	2.1
	127841	AW136558	Hs.125246	ESTs	2.1
	100023				2.1
	113002	BE243513	Hs.7212	hypothetical protein PP1044	2.1
	111567	F12628	Hs.334786	hypothetical protein MGC16040	2.1
45	113697	T97183	Hs.17992	Homo sapiens mRNA; cDNA DKFZp434J1726 (f	2.1
	128033	AI248705	Hs.149321	ESTs	2.1
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	2.1
	112370	AF052095	Hs.167344	Homo sapiens clone 23911 mRNA sequence	2.1
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	2.1
50	113226	AI821008	Hs.10697	ESTs	2.1
	117997	N52090	Hs.47420	EST	2.1
	116996	H83935	Hs.40535	ESTs	2.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	2.1
	122591	AI188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	2.1
55	107279	S57296	Hs.323910	v-erb-b2 avian erythroblastic leukemia	2.1
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	2.1
	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	2.1
	127447	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	2.1
	128352	AW137413	Hs.169942	ESTs	2.1
60	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.0
	128275	AI218235	Hs.131240	ESTs	2.0
	125976	AA436760		gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_	2.0
	120820	AA347417	Hs.96869	EST	2.0
	134937	AI251449	Hs.171939	ESTs	2.0
65	129602	AI282193	Hs.198298	v-src avian sarcoma (Schmidt-Ruppin A-2)	2.0
	129535	AA397972	Hs.169965	chimerin (chimaerin) 1	2.0
	106095	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.0
	128538	R44214	Hs.101189	ESTs	2.0
	105593	AA279341	Hs.174151	aldehyde oxidase 1	2.0
70	105788	AB009698	Hs.23965	solute carrier family 22 (organic anion	2.0
	128148	AA918175	Hs.126637	ESTs	2.0
	125982	R98091		gb:yr30e11.r1 Soares fetal liver spleen	2.0
	125746	AL137506	Hs.274256	hypothetical protein FLJ23563	2.0
	127835	AA748762	Hs.163113	ESTs, Weakly similar to I38022 hypotheti	2.0
75	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	2.0
	124282	AA018408	Hs.110287	ESTs	2.0
	126926	AA179472	Hs.832	ESTs, Highly similar to A41029 integrin	2.0
	100221	D28383		gb:Human mRNA for ATP synthase B chain,	2.0
	126053	H64450		gb:yu62d01.r1 Weizmann Olfactory Epithel	2.0
80	100944	L07518	Hs.159593	mucin 6, gastric	2.0
	125581	AI272848	Hs.75309	eukaryotic translation elongation factor	2.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.0
	114612	AI124557	Hs.95456	ESTs	2.0
	130453	U80735	Hs.173854	PAX transcription activation domain inte	2.0

	135060	AK001887	Hs.259842	protein kinase, AMP-activated, gamma 2 n	2.0
	114419	AI248013	Hs.106532	ESTs, Weakly similar to I38588 reverse t	2.0
	126283	N40359	Hs.271896	ESTs	2.0
5	112003	AW978731	Hs.301824	hypothetical protein PRO1331	2.0
	127391	AW380893	Hs.11039	hypothetical protein MGC2722	2.0
	127717	F12209	Hs.173380	CK2 interacting protein 1; HQ0024c prote	2.0
	126893	AJ252060	Hs.26320	TRABID protein	2.0
	106798	BE252749	Hs.20558	hypothetical protein FLJ20345	2.0
10	103760	AA642973	Hs.183842	ubiquitin B	2.0
	118922	AW206193	Hs.91065	hypothetical protein DKFZp761B2423	2.0
	133195	AI434760	Hs.279949	KIAA1007 protein	2.0
	133424	AA350994	Hs.20281	KIAA1700	2.0
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	2.0
15	132347	BE271016	Hs.169850	ESTs, Weakly similar to T21554 hypotheti	2.0
	125599	H13295	Hs.106135	ESTs	2.0
	114459	AW445217	Hs.103362	ESTs	2.0
	128478	AA708205	Hs.100343	ESTs	2.0
	127271	H96820		gb:yy99b03.r1 Soares melanocyte 2NbHM Ho	2.0
20	111122	N63753	Hs.16492	DKFZP564G2022 protein	2.0
	130695	T97205	Hs.17998	ESTs, Weakly similar to 2109260A B cell	2.0
	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	2.0
	119244	AW407564	Hs.275865	ribosomal protein S18	2.0
	127603	AI016798	Hs.9925	hypothetical protein FLJ20772	2.0
25	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	2.0
	128115	AI435590	Hs.130168	ESTs	2.0
	117639	AA377165	Hs.44833	ESTs	2.0
	127033	AF169301	Hs.9098	sulfate transporter 1	2.0
	112411	R43090	Hs.271510	ESTs, Moderately similar to ALU1_HUMAN A	2.0
30	114601	AA075566		gb:zm88f06.s1 Stratagene ovarian cancer	2.0
	127573	AA594196	Hs.269464	ESTs, Weakly similar to S65657 alpha-1C-	2.0
	125500	AW952654	Hs.244624	ESTs	2.0
	119416	T97186		gb:ye50h09.s1 Soares fetal liver spleen	2.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	2.0
35	128902	AA036637	Hs.107052	ESTs	2.0
	127684	AA658631	Hs.32556	KIAA0379 protein	2.0
	126288	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	2.0
	122059	AA431737	Hs.98749	EST, Moderately similar to T42671 hypoth	2.0
	125486	AI023895	Hs.190587	ESTs	2.0
40	128895	AW467000	Hs.106985	ESTs	2.0
	105301	AW352357	Hs.7457	MAGE1 protein	2.0
	125536	F08266	Hs.77948	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	121387	AA405854		gb:zu66g08.s1 Soares_testis_NHT Homo sap	2.0
	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	2.0
45	126860	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.0
	102907	BE409861	Hs.202833	heme oxygenase (decycling) 1	2.0
	127804	AA740634	Hs.292084	ESTs	2.0
	130566	R85474	Hs.16073	ESTs	1.9
	113782	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	1.9
50	124119	AA040123	Hs.248953	solute carrier family 27 (fatty acid tra	1.9
	132490	NM_001290	Hs.4980	LIM domain binding 2	1.9
	125494	AU077029	Hs.177543	antigen identified by monoclonal antibod	1.9
	100237	D30715	Hs.306333	Human PAP (pancreatitis-associated prot	1.9
	127687	AW772383	Hs.300635	ESTs	1.9
55	103136	AF087917	Hs.247936	olfactory receptor, family 1, subfamily	1.9
	125704	R55094	Hs.26239	Human DNA sequence from clone RP11-438B2	1.9
	126208	N22588	Hs.288548	Homo sapiens cDNA FLJ12368 fis, clone MA	1.9
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	1.9
	128660	AA011597	Hs.177398	ESTs	1.9
60	118049	N53145		gb:yy55f09.s1 Soares fetal liver spleen	1.9
	134624	AF035119	Hs.8700	deleted in liver cancer 1	1.9
	127432	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.9
	126414	AI363157	Hs.24756	hepatocyte growth factor-regulated tyros	1.9
	120861	AA350394	Hs.96952	ESTs	1.9
65	124669	AI571594	Hs.102943	hypothetical protein MGC12916	1.9
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	1.9
	103891	NM_007212	Hs.124186	ring finger protein 2	1.9
	128727	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.9
	126831	AI929107	Hs.79933	cyclin I	1.9
70	125360	AW898892	Hs.189741	ESTs	1.9
	124276	H83465		gb:ys91a11.s1 Soares retina N2b5HR Homo	1.9
	126524	Z45455	Hs.182447	heterogeneous nuclear ribonucleoprotein	1.9
	126647	AK000283	Hs.270502	hypothetical protein FLJ20276	1.9
	125957	H41694		gb:yo06b06.r1 Soares adult brain N2b5HB5	1.9
75	121782	AW452957	Hs.334698	Homo sapiens, clone MGC:15203, mRNA, com	1.9
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1.9
	130945	U20582	Hs.2149	actin like protein	1.9
	126348	T16243	Hs.6473	Homo sapiens cDNA FLJ13992 fis, clone Y7	1.9
	103558	BE616547	Hs.2785	keratin 17	1.9
80	126982	AA211419		gb:zn55g05.s1 Stratagene muscle 937209 H	1.9
	125613	AA765957	Hs.21077	KIAA0532 protein	1.9
	129601	AB032964	Hs.115726	KIAA1138 protein	1.9
	126007	H51097	Hs.143261	ESTs	1.9
	123627	AA909619	Hs.112668	ESTs	1.9

	111587	AI125867	Hs.20734	ESTs	1.9
	135231	BE613615	Hs.74280	hypothetical protein FLJ22237	1.9
	128897	AW979134	Hs.10700	hypothetical protein	1.9
5	109891	H04757	Hs.323176	ESTs	1.9
	127704	AA679609		gb:ag72c02.s1 Gessler Wilms tumor Homo s	1.9
	129340	H75334	Hs.11050	F-box only protein 9	1.9
	126502	T10077	Hs.13453	hypothetical protein FLJ14753	1.9
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	1.9
10	127136	R36277	Hs.7773	Homo sapiens ubiquitin conjugating enzyme	1.9
	110636	H72868	Hs.19110	ESTs	1.9
	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	1.9
	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.9
	130829	BE262530	Hs.2006	glutathione S-transferase M3 (brain)	1.9
	125768	AI557486	Hs.119122	ribosomal protein L13a	1.9
15	123613	AA609158	Hs.291166	EST	1.9
	127506	T61039	Hs.252574	ribosomal protein L10a	1.9
	123546	AA608817	Hs.112597	EST	1.9
	126516	R95872	Hs.117572	chemokine binding protein 2	1.9
20	103973	AA305729	Hs.18272	amino acid transporter system A1	1.9
	127426	AA854756	Hs.124076	ESTs	1.9
	112339	R56570	Hs.50547	ESTs	1.9
	129101	NM_013403	Hs.108665	zinedin	1.9
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	1.9
25	118103	AA401733	Hs.184134	ESTs	1.9
	125752	AW136622	Hs.206673	ESTs	1.9
	102926	W28363	Hs.239752	nuclear receptor subfamily 2, group F, m	1.9
	133975	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.9
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.9
30	127329	AW160551	Hs.124021	soggy-1 gene	1.8
	126659	T16245		gb:NIB1005R Normalized Infant brain, Ben	1.8
	127297	AW629485	Hs.140720	GSK-3 binding protein FRAT2	1.8
	127640	AI557486	Hs.119122	ribosomal protein L13a	1.8
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	1.8
35	127964	F06298		gb:HSC13F081 normalized infant brain cDN	1.8
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	1.8
	128193	AJ224442	Hs.155020	putative methyltransferase	1.8
	115173	BE612940	Hs.88252	ESTs	1.8
	125532	AI734146	Hs.271800	ESTs, Weakly similar to alternatively sp	1.8
40	126541	AJ271671	Hs.7854	zinc/iron regulated transporter-like	1.8
	127309	AI669765	Hs.133184	ESTs	1.8
	129062	AA452970	Hs.155218	E1B-55kDa-associated protein 5	1.8
	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	1.8
	127775	AA128808	Hs.179902	transporter-like protein	1.8
45	126994	AA455265	Hs.86686	ESTs, Moderately similar to I54374 gene	1.8
	130734	AW137091	Hs.18624	KIAA1052 protein	1.8
	114461	AA531187	Hs.126705	ESTs	1.8
	100842	U05597		gb:Human anion exchanger 3 cardiac isofo	1.8
	127389	T65126	Hs.12743	carnitine O-octanoyltransferase	1.8
50	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	1.8
	107736	AA016239	Hs.60715	ESTs	1.8
	125669	R51308	Hs.333256	ESTs, Weakly similar to ALU8_HUMAN ALU	1.8
	100370	D79989	Hs.184884	KIAA0167 gene product	1.8
	113479	AI023133	Hs.10739	ESTs	1.8
55	105165	BE280787	Hs.16079	hypothetical protein FLJ10233	1.8
	120602	AA808018	Hs.109302	ESTs	1.8
	112399	R60920	Hs.296770	KIAA1719 protein	1.8
	123474	AA599209		gb:ag34b11.s1 Jia bone marrow stroma Hom	1.8
	134212	AA654353	Hs.17719	EBP50-PDZ interactor of 64 kD	1.8
60	104204	AK001691	Hs.57655	hypothetical protein FLJ10829	1.8
	127464	AW971875	Hs.292071	ESTs	1.8
	116715	AL117440	Hs.170263	tumor protein p53-binding protein, 1	1.8
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	1.8
	132380	AW373665	Hs.46853	ESTs	1.8
65	120087	AF186780	Hs.79219	RalGDS-like gene; KIAA0959 protein	1.8
	116356	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	1.8
	125499	H10543		gb:ym04c06.r1 Soares infant brain 1NIB H	1.8
	128846	AA730767	Hs.285753	SCG10-like-protein	1.8
	123869	AA620924	Hs.112923	EST	1.8
70	108889	AA135722	Hs.61481	ESTs	1.8
	126528	Z24895		gb:HSB67F122 STRATAGENE Human skeletal m	1.8
	127629	AA293279	Hs.29173	hypothetical protein FLJ20515	1.8
	130004	AA703684	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN A	1.8
	130847	AI672483	Hs.20220	lipase protein	1.8
75	111620	R14853	Hs.307478	EST, Weakly similar to I39058 hypotheti	1.8
	131971	BE567100	Hs.154938	hypothetical protein MDS025	1.8
	121360	AA405635	Hs.96854	ESTs, Weakly similar to DYLX_HUMAN CYTOP	1.8
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	1.8
80	124687	AA833902	Hs.270745	ESTs	1.8
	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	1.8
	126730	AA442429		gb:zv70g02.r1 Soares_totai_fetus_Nb2HF8_	1.8
	127916	AI239950	Hs.294111	ESTs, Moderately similar to B34087 hypo	1.8
	128408	AI183407	Hs.143704	EST	1.8
	128440	AW090340	Hs.14337	Homo sapiens cDNA FLJ14407 fis, clone HE	1.8

	123783	AA610112		gb:af19g05.s1 Soares_tetal_fetus_Nb2HF8_	1.8
	109152	AW380723	Hs.73451	ESTs, Weakly similar to S55024 nebulin,	1.8
	107242	AB020672	Hs.175411	KIAA0865 protein	1.8
5	132804	AI805943	Hs.326067	hypothetical protein MGC5178	1.8
	125387	AJ243669	Hs.8127	KIAA0144 gene product	1.8
	121578	AA398791	Hs.178185	ESTs	1.8
	132944	T96641	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	1.8
	126295	AI281459	Hs.270114	ESTs	1.8
10	133335	BE251012	Hs.263812	nuclear distribution gene C (A.nidulans)	1.8
	129879	AK001696	Hs.13109	Ran binding protein 11	1.7
	125175	W52355	Hs.303030	EST	1.7
	126919	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	1.7
	127773	AA725863	Hs.120508	ESTs	1.7
15	126495	AB029021	Hs.137732	KIAA1098 protein	1.7
	126948	AW968535	Hs.14328	hypothetical protein FLJ20071	1.7
	126671	C03105	Hs.285847	CGI-19 protein	1.7
	115428	AA284112	Hs.94680	ESTs, Weakly similar to I78885 serine/t	1.7
	128232	AI830319	Hs.334641	hypothetical protein DKFZp43411916	1.7
20	126082	H81188	Hs.269571	ESTs	1.7
	120467	AW292562	Hs.187628	ESTs	1.7
	124041	AW590171	Hs.101413	ESTs	1.7
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	1.7
	123951	AB012922	Hs.173043	metastasis-associated 1-like 1	1.7
25	126449	AF223944	Hs.325443	breast cell glutaminase	1.7
	124554	N65961		gb:za27d03.s1 Soares fetal liver spleen	1.7
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2	1.7
	126780	R12421	Hs.5811	chromosome 21 open reading frame 59	1.7
	125661	AA491830	Hs.25689	ESTs	1.7
30	125888	H18298		gb:yn48b09.r1 Soares adult brain N2b5HB5	1.7
	127245	AA323958		gb:EST26810 Cerebellum II Homo sapiens c	1.7
	111223	AA852773	Hs.334838	KIAA1866 protein	1.7
	115611	R44789	Hs.33191	Homo sapiens, Similar to transmembrane r	1.7
	124846	R59977	Hs.158196	transcriptional adaptor 3 (ADA3, yeast	1.7
	100397	D84424	Hs.57697	hyaluronan synthase 1	1.7
35	127180	T27097	Hs.22790	ESTs	1.7
	102598	BE250742	Hs.106673	eukaryotic translation initiation factor	1.7
	134076	AF086215		gb:Homo sapiens full length insert cDNA	1.7
	115659	W99382	Hs.283709	lipopolysaccharide specific response-7 p	1.7
40	125555	R19382	Hs.117869	ESTs	1.7
	128382	AI138886	Hs.143243	ESTs	1.7
	127710	AA682867	Hs.191901	ESTs	1.7
	125445	AI452722	Hs.7709	WW domain binding protein 1	1.7
	129951	AL110282	Hs.268024	Homo sapiens, clone IMAGE:3873720, mRNA	1.7
45	119898	R93325	Hs.58690	ESTs	1.7
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	1.7
	133531	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.7
	119726	AF086289	Hs.234766	skin-specific protein	1.7
	125198	W69474	Hs.323140	ESTs	1.7
50	121414	AW291477	Hs.188763	testis expressed sequence 13A	1.7
	112542	AI458867	Hs.24276	ESTs	1.7
	101368	M13058	Hs.73952	proline-rich protein HaeIII subfamily 2	1.7
	125820	AA730136	Hs.75561	teratocarcinoma-derived growth factor 1	1.7
	129091	AA056483	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	1.7
55	132609	U20165	Hs.53250	bone morphogenetic protein receptor, typ	1.7
	119447	W31714	Hs.122656	ESTs, Highly similar to formin 2-like pr	1.7
	113675	T81034	Hs.14841	ESTs	1.7
	113701	T97301	Hs.18026	ESTs	1.7
	116180	AA463902	Hs.13522	ESTs, Weakly similar to I38022 hypothet	1.7
60	127133	AA280740	Hs.292072	ESTs, Moderately similar to A46010 X-lin	1.7
	113316	T70318	Hs.268581	ESTs	1.7
	123316	AI290561	Hs.155361	ESTs	1.7
	122638	AL137476	Hs.123609	Homo sapiens mRNA; cDNA DKFZp43410623 (f	1.7
	105053	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.7
65	103305	X82279		gb:H.sapiens Fas, Apo-1 gene (promoter a	1.7
	110384	H45282	Hs.268798	ESTs	1.7
	115626	AW630870	Hs.86674	ESTs, Weakly similar to hypothetical pro	1.7
	126905	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	1.7
	130820	AL353934	Hs.288798	hypothetical protein FLJ21012	1.7
70	112394	AK000373	Hs.8358	hypothetical protein FLJ20366	1.7
	129589	AW504292	Hs.11517	ESTs	1.7
	126446	NM_015670	Hs.118926	sentrin/SUMO-specific protease 3	1.7
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3	1.7
	120287	AF219946	Hs.102237	tubby super-family protein	1.7
75	129991	R28386	Hs.179925	ESTs, Weakly similar to ALU8_HUMAN ALU	1.7
	123912	AA621283	Hs.332855	EST	1.7
	102071	AL120051	Hs.144700	ephrin-B1	1.7
	121046	AB033083	Hs.97377	KIAA1257 protein	1.7
	128403	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	1.7
80	104268	AL043864	Hs.70604	ATPase, Class II, type 9A	1.7
	111598	R11505	Hs.268912	ESTs	1.7
	128109	AW269421	Hs.128093	ESTs	1.7
	125435	R08480	Hs.272138	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.7
	133104	AI091195	Hs.65029	growth arrest-specific 1	1.7

	126826	AA099764		gb:zn61f12.r1 Stratagene muscle 937209 H	1.7
	106483	NM_006548	Hs.30299	IGF-II mRNA-binding protein 2	1.7
	129765	M86933	Hs.1238	amelogenin (Y chromosome)	1.7
5	115904	AI167560	Hs.61297	ESTs	1.7
	125514	AB040912	Hs.191098	hypothetical protein FLJ11598	1.7
	125797	H03117	Hs.111497	similar to mouse neuronal protein 15.6	1.7
	133179	U81599	Hs.66731	homeo box B13	1.7
	115167	AA749209	Hs.43728	hypothetical protein	1.7
10	118036	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.7
	124540	N63232		gb:yz39a12.s1 Morton Fetal Cochlea Homo	1.7
	126183	BE018708	Hs.81972	SHC (Src homology 2 domain-containing) t	1.7
	127897	AA773681		gb:af77b12.r1 Soares_NhHMPu_S1 Homo sapi	1.7
	126680	F07097	Hs.133865	transmembrane 6 superfamily member 1	1.7
15	126972	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	1.7
	130605	BE514362	Hs.306024	FK506-binding protein 3 (25kD)	1.7
	127541	AA573449	Hs.171515	ESTs	1.7
	127392	AI816736	Hs.14896	DHHC1 protein	1.7
	106879	AI190785	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA,	1.7
20	128303	AI096444	Hs.7187	hypothetical protein FLJ10707	1.7
	126469	BE384361	Hs.182885	ESTs, Weakly similar to JC5024 UDP-galac	1.7
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	1.7
	132332	AW978906	Hs.45005	hypothetical protein FLJ12960	1.6
	127142	AW452942	Hs.130393	ESTs	1.6
25	128416	F13165	Hs.12549	ESTs, Weakly similar to 2109260A B cell	1.6
	103790	AL122044	Hs.331633	hypothetical protein DKFZp566N034	1.6
	134578	AL110193	Hs.224137	hypothetical protein	1.6
	110023	AW294701	Hs.31040	ESTs	1.6
	125511	AJ271379	Hs.76194	ribosomal protein S5	1.6
30	111483	R06569	Hs.269534	ESTs	1.6
	127363	AF064104	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	1.6
	126231	AA991766	Hs.300793	ESTs	1.6
	106181	AI803651	Hs.191608	ESTs	1.6
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	1.6
35	119929	W86464	Hs.304825	ESTs	1.6
	132542	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f	1.6
	127155	AA284993		gb:zt23e10.r1 Soares ovary tumor NbHOT H	1.6
	125956	AK000214	Hs.129014	hypothetical protein FLJ20207	1.6
	126854	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.6
40	131330	D13969	Hs.184669	zinc finger protein 144 (Mel-18)	1.6
	129445	W52452	Hs.29797	ribosomal protein L10	1.6
	113427	T85105	Hs.15471	ESTs	1.6
	106124	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	1.6
45	128135	AA954381	Hs.269721	ESTs, Moderately similar to ALU1_HUMAN	1.6
	111460	R02728	Hs.117331	ESTs	1.6
	125636	H12382	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	1.6
	134118	BE336680	Hs.182877	KIAA0116 protein	1.6
	111570	AF059203	Hs.20580	sterol O-acyltransferase 2	1.6
	113511	T89578	Hs.189740	ESTs	1.6
50	113296	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	1.6
	109875	H03260	Hs.30385	ESTs	1.6
	105930	AF016371	Hs.9880	peptidyl prolyl isomerase H (cyclophilin	1.6
	105564	BE616694	Hs.288042	hypothetical protein FLJ14299	1.6
	128063	AI377750	Hs.167177	ESTs	1.6
55	109779	AB029396	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur	1.6
	125334	T86569	Hs.182118	ESTs	1.6
	127206	AW816490	Hs.337508	ESTs	1.6
	108845	AW362901	Hs.68864	ESTs, Weakly similar to phosphatidylseri	1.6
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.6
60	114062	AI560984	Hs.27283	ESTs	1.6
	122550	AA451859	Hs.99253	ESTs	1.6
	113413	R08872	Hs.186512	ESTs	1.6
	127019	AI929355	Hs.286128	hypothetical protein FLJ23329	1.6
	106251	R12607	Hs.35101	proline-rich Gla (G-carboxyglutamic acid	1.6
65	112670	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	1.6
	114913	AI435199	Hs.58940	ESTs, Weakly similar to I38022 hypotheti	1.6
	126604	AI023299	Hs.269806	ESTs	1.6
	125324	R07785		gb:yf15c06.r1 Soares fetal liver spleen	1.6
	121438	AW445024	Hs.139389	ESTs	1.6
70	127289	AI041014	Hs.220752	ESTs, Weakly similar to unnamed protein	1.6
	126935	AI198535	Hs.89463	potassium large conductance calcium-acti	1.6
	132430	AW973652	Hs.283105	ESTs	1.6
	133541	H75334	Hs.11050	F-box only protein 9	1.6
	102612	U65402	Hs.248124	G protein-coupled receptor 31	1.6
75	120228	AI192528	Hs.164537	ESTs	1.6
	122652	AA454641		gb:zx99d05.s1 Soares_NhHMPu_S1 Homo sapi	1.6
	103456	AA496425	Hs.9629	papillary renal cell carcinoma (transloc	1.6
	105355	AL031447	Hs.26938	Homo sapiens, clone IMAGE:4053044, mRNA,	1.6
	108043	AA042873	Hs.160412	ESTs	1.6
80	128695	NM_003478	Hs.101299	cullin 5	1.6
	127984	AA846377	Hs.193706	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.6
	124405	AA228137	Hs.25005	hypothetical protein MGC3329	1.6
	103934	BE278111	Hs.134200	DKFZP564C186 protein	1.6
	124195	H83034		gb:yq48e07.r1 Soares fetal liver spleen	1.6

	110938	N48982	Hs.38034	Homo sapiens cDNA FLJ12924 fis, clone NT	1.6
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.6
	121226	AA364109	Hs.177990	ESTs	1.6
5	120415	AA235810		gb:zs41a03.s1 Soares_NhHMPu_S1 Homo sapi	1.6
	123864	AA620882		gb:at95g01.s1 Soares_testis_NHT Homo sap	1.6
	125045	AI114630	Hs.208334	Homo sapiens cDNA: FLJ21874 fis, clone H	1.6
	133425	AA444390	Hs.155482	hydroxyacyl glutathione hydrolase	1.6
	126578	AF151861	Hs.107528	androgen induced protein	1.6
10	102406	U43177		(NONE)	1.6
	114126	BE566962	Hs.7063	Homo sapiens cDNA: FLJ20913 fis, clone A	1.6
	125233	W85713	Hs.110092	ESTs	1.6
	109635	F04296	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.6
	125675	BE294972	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	1.6
15	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	1.6
	127569	AI765107	Hs.274422	hypothetical protein FLJ20550	1.6
	113302	T66919	Hs.268575	ESTs	1.6
	119705	AI984203	Hs.57874	ESTs	1.6
	127226	AL036559	Hs.3463	ribosomal protein S23	1.6
20	123489	AA599708		gb:ag11a10.s1 Gessler Wilms tumor Homo s	1.6
	107468	AA740979	Hs.91389	ESTs	1.6
	115916	AI052731	Hs.91910	ESTs	1.6
	127815	AA743490	Hs.255015	ESTs	1.6
	100364	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.6
25	125568	AW615396	Hs.105613	ESTs	1.6
	105260	N81201	Hs.31755	ESTs	1.6
	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	1.6
	111275	N70970	Hs.35006	ESTs	1.6
	106542	AA339541	Hs.24956	hypothetical protein FLJ22056	1.6
30	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.6
	124770	AA984414	Hs.120429	ESTs	1.6
	117936	AI382904	Hs.47213	ESTs	1.6
	134385	M14660	Hs.169274	ESTs, Highly similar to IFT2_HUMAN INTER	1.6
	108367	AW410478	Hs.104019	transforming, acidic coiled-coil contain	1.6
35	131143	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	1.6
	105441	N28522	Hs.8935	quinolinate phosphoribosyltransferase (n	1.6
	128215	AA973310		gb:op91e06.s1 Soares_NFL_T_GBC_S1 Homo s	1.6
	127344	AI003929	Hs.80624	hypothetical protein MGC2560	1.6
	126478	BE541249	Hs.109697	ESTs	1.6
40	122053	AI637498	Hs.98745	ESTs	1.5
	111760	BE551929	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE	1.5
	112401	R61279	Hs.237536	ESTs, Weakly similar to AF151067 1 HSPC2	1.5
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	1.5
	125575	H14983		gb:ym19h09.r1 Soares infant brain 1NIB H	1.5
45	128765	AF073310	Hs.143648	insulin receptor substrate 2	1.5
	108935	AA147848	Hs.67991	hypothetical protein DKFZp434G0522	1.5
	121221	AI140708	Hs.97461	ESTs	1.5
	120091	AW024672	Hs.59558	EST	1.5
	107375	BE011845	Hs.251064	high-mobility group (nonhistone chromoso	1.5
50	125803	AW876115	Hs.29852	ESTs	1.5
	115132	AA811762	Hs.71433	ESTs	1.5
	113346	AF143876	Hs.14318	Homo sapiens clone IMAGE:113399 mRNA seq	1.5
	107357	U63973	Hs.103501	rhodopsin kinase	1.5
	125443	BE251057	Hs.177592	ribosomal protein, large, P1	1.5
55	133803	M24461	Hs.76305	surfactant, pulmonary-associated protein	1.5
	113378	T80738	Hs.14757	ESTs	1.5
	105540	BE391690	Hs.9265	hypothetical protein FLJ20917	1.5
	127446	F13008		gb:HSC3HE011 normalized infant brain cDN	1.5
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	1.5
60	127585	AA604144	Hs.190632	ESTs	1.5
	125824	Z45258	Hs.286013	short coiled-coil protein	1.5
	127606	AA621135	Hs.136552	ESTs	1.5
	125585	AW298113	Hs.92909	SON DNA binding protein	1.5
	107757	BE621721	Hs.280792	hypothetical protein FLJ12387 similar to	1.5
	109978	H09356	Hs.22528	ESTs	1.5
65	132297	BE272446	Hs.265317	hypothetical protein MGC2562	1.5
	115784	AW402151	Hs.54673	tumor necrosis factor (ligand) superfami	1.5
	127880	W39735	Hs.73818	ubiquinol-cytochrome c reductase hinge p	1.5
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	1.5
70	102868	X02419	Hs.77274	plasminogen activator, urokinase	1.5
	133457	J04948	Hs.333509	alkaline phosphatase, placental-like 2	1.5
	130339	AA435746		gb:zt79e03.s1 Soares_testis_NHT Homo sap	1.5
	125444	N28476	Hs.159161	Rho GDP dissociation inhibitor (GDI) alp	1.5
	123470	AW303285	Hs.303632	Human DNA sequence from clone RP11-110H4	1.5
	100025				1.5
75	127063	AI276526	Hs.331564	Homo sapiens mRNA; cDNA DKFZp434H1215 (f	1.5
	127945	AA815031	Hs.123598	ESTs	1.5
	111557	R09510	Hs.20373	EST	1.5
	116009	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	1.5
80	119858	W01370	Hs.46824	ESTs	1.5
	106509	AI042309	Hs.64552	hypothetical protein MGC15563	1.5
	124124	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clone HE	1.5
	126713	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypothe	1.5
	126475	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	1.5

	126851	R40611	Hs.137565	ESTs	1.5
	104820	AW162768	Hs.22620	ESTs	1.5
	127235	AI817309	Hs.225583	ESTs, Weakly similar to 2004399A chromos	1.5
5	126552	AF168711	Hs.159397	x 010 protein	1.5
	127523	AA617637		gb:np34h12.s1 NCI_CGAP_Lu1 Homo sapiens	1.5
	131692	BE559681	Hs.30736	KIAA0124 protein	1.5
	112974	AL353965	Hs.101174	microtubule-associated protein tau	1.5
	118921	N91914	Hs.54751	ESTs	1.5
10	100676	X02761	Hs.287820	fibronectin 1	1.5
	127721	T59578	Hs.188440	ESTs, Weakly similar to ALUF_HUMAN !!!!	1.5
	115254	AA279024	Hs.269316	ESTs, Weakly similar to S65657 alpha-1C	1.5
	128173	AI457242	Hs.127024	ESTs	1.5
	126846	AA663527	Hs.116910	ESTs	1.5
15	125294	R40025	Hs.106551	ESTs	1.5
	127494	AW978730	Hs.291956	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.5
	134191	W26632	Hs.7979	KIAA0736 gene product	1.5
	107394	AA864798	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	1.5
	131562	NM_003512	Hs.28777	H2A histone family, member L	1.5
20	127310	AW450671	Hs.189284	ESTs	1.5
	122359	AA523486		gb:ni67f11.s1 NCI_CGAP_Pr12 Homo sapiens	1.5
	100524	M80902	Hs.183704	ubiquitin C	1.5
	128422	T77794		gb:yd20d09.r1 Soares fetal liver spleen	1.5
	129902	AA076278	Hs.13277	hypothetical protein FLJ22054	1.5
25	126784	T81887	Hs.108854	HSPC163 protein	1.5
	123343	AI761902	Hs.99597	ESTs	1.5
	105458	AW954377	Hs.26412	ring finger protein 26	1.5
	112266	AI652534	Hs.25934	ESTs, Weakly similar to HSHU11 histone H	1.5
	127622	AA628222	Hs.97883	ESTs	1.5
30	113659	R06545	Hs.189781	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.5
	116892	AI573283	Hs.38458	ESTs	1.5
	126995	NM_014351	Hs.189810	sulforanferase family 4A, member 1	1.5
	111657	R07364	Hs.268667	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
	100243	AB028125	Hs.77854	regucalcin (senescence marker protein-30	1.5
35	116153	AF107203	Hs.57937	ataxin 2-binding protein 1	1.5
	108892	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	1.5
	113294	AI037922	Hs.11000	leptin receptor overlapping transcript-l	1.5
	126691	W03046	Hs.283664	aspartate beta-hydroxylase	1.5
	106979	AW015227	Hs.289053	hypothetical protein FLJ14733	1.5
40	125546	H09950		gb:ym01d12.r1 Soares infant brain 1NIB H	1.5
	113990	AI497945	Hs.83097	hypothetical protein FLJ22955	1.5
	129295	U63127	Hs.110121	SEC7 homolog	1.5
	125431	AW851639	Hs.75584	polymyositis/scleroderma autoantigen 2 (1.5
	112558	AK001621	Hs.15921	hypothetical protein FLJ10759	1.5
45	122046	AI560456	Hs.107319	ESTs	1.5
	122472	AA448509	Hs.128652	ESTs	1.5
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	1.5
	131714	AA642831	Hs.31016	putative DNA binding protein	1.5
	101233	AL135173	Hs.878	sorbitol dehydrogenase	1.5
50	109501	AF047437	Hs.90436	sperm associated antigen 7	1.5
	126984	AA213820	Hs.256533	ESTs, Weakly similar to S11998 finger pr	1.5
	125765	BE243877	Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly	1.5
	127693	AA676727		gb:zj68b11.s1 Soares fetal liver spleen_	1.5
	128453	X02761	Hs.287820	fibronectin 1	1.5
55	119418	T97590	Hs.221711	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr	1.5
	116708	F10528	Hs.70001	ESTs, Moderately similar to JC6169 nucl	1.5
	122420	AA446971		gb:zw85f11.s1 Soares_total_fetus_Nb2HF8_	1.5
	100238	L24959	Hs.348	calcium/calmodulin-dependent protein kin	1.5
60	109710	D20044	Hs.12929	hypothetical protein FLJ20721	1.5
	105704	AI282341	Hs.75431	fibrinogen, gamma polypeptide	1.5
	112712	R91060	Hs.330761	ESTs	1.5
	100098	AF003743		gb:Homo sapiens delayed rectifier potass	1.5
	114122	R46128	Hs.12751	ESTs	1.5
65	132397	AA021160	Hs.4750	hypothetical protein DKFZp564K0822	1.5
	107881	AI568350	Hs.61273	hypothetical protein MGC2650	1.5
	106302	AA398859	Hs.18397	hypothetical protein FLJ23221	1.5
	125898	AK001823	Hs.92287	Homo sapiens mRNA; cDNA DKFZp564C2478 (f	1.5
	104957	AI359009	Hs.10026	mitochondrial ribosomal protein L17	1.5
70	102909	NM_005269	Hs.2693	glioma-associated oncogene homolog (zinc	1.5
	125559	BE297488	Hs.279877	cell division protein FtsJ	1.5
	109634	H17063	Hs.183646	ESTs	1.5
	116607	W05238	Hs.94316	ESTs, Weakly similar to T31613 hypotheti	1.5
	127175	R11937		gb:yf54b08.r1 Soares infant brain 1NIB H	1.5
75	110617	W93231	Hs.285901	Homo sapiens, clone IMAGE:3948563, mRNA,	1.5
	125988	W27648		gb:37e10 Human retina cDNA randomly prim	1.5
	115093	AI241932	Hs.3542	hypothetical protein FLJ11273	1.5
	121207	AA705799	Hs.183714	ESTs	1.5
80	112652	BE269699	Hs.235782	solute carrier family 21 (organic anion	1.5
	125213	AB014554	Hs.109299	protein tyrosine phosphatase, receptor t	1.5
	125912	AW867467	Hs.278712	eukaryotic translation initiation factor	1.5
	133046	R96881	Hs.63609	Hpal1 tiny fragments locus 9C	1.5
	122791	AL122055	Hs.129836	KIAA1028 protein	1.5

Table 26B

5	Pkey:		Unique Eos probeset identifier number
	CAT number:	Accession:	Gene cluster number Genbank accession numbers
	Pkey	CAT number	Accession
10	108451	13766_27	AA079195 AA084955 AA126308 AA084956
	124195	2606_3	H83034 H52379
	123619	371681_1	AA602964 AA609200
	125165	1852047_1	W45350 W45406
	125324	1692163_1	R07785 T85948 T86972
15	126053	1601238_1	H64450 H64464
	126086	1606216_1	H75681 H70975
	126098	1629789_1	M79088 N88221
	125464	168460_1	N71807 AA203399
	125499	1562851_1	H10543 R11878
20	126127	1205826_1	N95428 W24040 AW751366 H81987
	125546	356478_1	H09950 R18413 AA570553 AW973425
	125549	1702179_1	R20215 R18767
	125558	1703083_1	R59305 R19748
	125575	1566885_1	H14983 R21554
25	125743	5025_5	H17151 H11956
	125761	1744008_1	R68351 R68364
	126426	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
	127155	200358_1	AA284993 AA478122 AA477923
30	127175	1695805_1	R11937 Z45532
	126528	1276201_1	Z24895 AW891336 R01294
	125957	1583542_1	H41694 H45213
	125976	296453_1	AA436760 AW237453 BE327496 N47347 N56967
	125982	1766315_1	R98091 W92898
35	125988	1365728_1	W27648 R99193 BE090398
	127245	226662_1	AA323958 AA370268
	127248	227560_1	AA364195 AA325029 AW962050
	127262	231725_1	AA828125 AA834883 AA330555
	126659	1541209_1	T16245 R19694 F13545 H10299 T66048 T65279 H18006
40	126693	87363_1	C05723 AA018342
	127315	37938_1	AF116622 AI114507 AA640834 AA377999
	126730	297653_1	AA442429 T19477
	103898	187213_-3	AA248884
	127446	16001_2	F13008 T75435
45	126826	127356_1	AA099764 AA112950
	126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073, BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
	128132	177108_1	AA225632 AI820970 AI820952 AA226472 AI732140 AI732059 AA226307 AA225500
50	127523	351071_1	AA617637 AA554963
	126982	171753_1	AA211419 AA211566
	128215	530345_-1	AA973310
	127704	405690_1	AA679609 AA694592
	127705	966283_2	AJ003322 AJ003324
55	128422	1811283_1	T77794 T85681
	127897	446527_1	AA773681 AA773857
	120734	208882_1	AA299948 AA299949
	100098	25117_-13	AF003743
	114620	32062_8	AA642974 AA084223
60	122652		26401_-30 AA454641
	100842		tigr_HT4398 U05597
	123783		genbank_AA610112
	125032		genbank_T74884
	123808		genbank_AA620552
65	123864		genbank_AA620882
	118049		genbank_N53145
	102406		entrez_U43177
	116962		genbank_H79677
	134076	40321_1	AF066215 W02702 AA284288 W25655
70	125888	266863_1	H18298 H46830
	127271	321389_1	H96820 H79463
	113119		genbank_T47910 T47910
	104799		genbank_AA029703 AA029703
	127693	790317_1	AA676727 AA704704
75	120415		genbank_AA235810 AA235810
	127964	135151_1	F06298 R18057
	122359		681003_1 AA523486 AW026780 AI821660 AA443898
	122420		genbank_AA446971
	124276		genbank_H83465
80	101447		entrez_M21305
	124540		genbank_N63232
	124554		genbank_N65961
	117357		genbank_N24829
	103305		entrez_X82279

103392 entrez_X94563
 119416 genbank_T97186
 105225 genbank_AA211777
 121292 genbank_AA401807
 112853 genbank_T02843
 121387 genbank_AA405854
 114601 genbank_AA075566
 100221 entrez_D28383
 130339 genbank_AA435746
 100554 tigr_HT2241
 123423 genbank_AA598484
 123474 genbank_AA599209
 123489 genbank_AA599708

TABLE 27A: ABOUT 895 GENES UP-REGULATED IN COMBINED LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 27A lists about 895 genes that are upregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with the normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90th percentile amongst fibrosis samples. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of fibrosis to normal body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	56.0
424917	AI636208	Hs.96901	Homo sapiens cDNA: FLJ23049 fis, clone L	26.5
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	25.5
457200	U33749	Hs.197764	thyroid transcription factor 1	22.2
414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	21.1
429272	W25140	Hs.110667	ESTs	19.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	19.1
442006	AW975183	Hs.292663	ESTs	18.8
445885	AI734009	Hs.127699	KIAA1603 protein	18.0
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	17.8
422426	W79117	Hs.58559	ESTs, Weakly similar to rholekin [M.musc	17.4
444929	AI685841	Hs.161354	ESTs	16.5
440807	AW269421	Hs.128093	ESTs	16.3
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	14.2
446967	AI699629	Hs.156781	ESTs	13.3
417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	12.3
437119	AI379921	Hs.177043	ESTs	12.3
451103	R52804	Hs.25956	DKFZP564D206 protein	11.5
443450	N66045	Hs.133529	ESTs	11.4
411880	AW872477		gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens	11.3
432519	AI221311	Hs.130704	ESTs	11.3
414142	AW368397	Hs.150042	ESTs	11.0
433283	BE041135	Hs.175622	ESTs	10.1
441082	AW444804	Hs.202655	ESTs	10.1
452039	AI922988	Hs.172510	ESTs	10.0
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	9.9
421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	9.8
412372	R65998	Hs.118615	ESTs	9.8
426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfam	9.7
431007	AF039564	Hs.248211	retinoblastoma-binding protein 9	9.4
443709	AI082692	Hs.134662	ESTs	9.3
446232	AI281848	Hs.165547	ESTs	9.2
448253	H25899	Hs.201591	ESTs	9.2
432133	AB033088	Hs.272567	KIAA1262 protein	9.1
409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	9.0
431353	AA828032	Hs.189076	ESTs	8.8
450050	AI681268	Hs.257883	ESTs	8.8
458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	8.8
414968	C16096	Hs.297777	ESTs	8.7
425664	AJ006276	Hs.159003	transient receptor potential channel 6	8.7
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	8.6
453672	U73531	Hs.34526	G protein-coupled receptor	8.5
429420	AK001679	Hs.202289	hypothetical protein FLJ10376	8.5
421478	AI683243	Hs.97258	ESTs	8.4
404916				8.4
444396	T65213	Hs.4257	ESTs	8.3
442275	AW449467	Hs.54795	ESTs	8.3
437479	R61866	Hs.101277	ESTs	8.2
432203	AA305746	Hs.49	macrophage scavenger receptor 1	8.2
431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	7.9
406747	AI925153	Hs.217493	annexin A2	7.8

	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	7.7
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	7.6
	421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	7.5
5	421155	H87879	Hs.102267	lysyl oxidase	7.5
	446917	AI347863	Hs.156672	ESTs	7.5
	422798	R92347	Hs.34574	ESTs	7.4
	426830	AA385751	Hs.160392	ESTs	7.4
	437157	BE048860	Hs.120655	ESTs	7.4
10	433231	AB040926	Hs.143552	KIAA1493 protein	7.3
	451561	N52812	Hs.177403	ESTs	7.1
	430656	AA482900	Hs.162080	ESTs	7.1
	448206	BE622585	Hs.3731	ESTs	7.1
	420209	AA256444	Hs.32295	Homo sapiens cDNA FLJ12604 fis, clone NT	7.0
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	6.9
15	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.9
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	6.8
	443324	R44013	Hs.164225	ESTs	6.8
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	6.8
20	427356	AW023482	Hs.97849	ESTs	6.7
	418735	N48769	Hs.44609	ESTs	6.7
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	6.6
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.6
	430099	AW194988	Hs.20537	Homo sapiens cDNA FLJ13942 fis, clone Y7	6.6
25	441835	AB036432	Hs.184	advanced glycosylation end product-speci	6.5
	428508	BE252383	Hs.184668	SBBI31 protein	6.5
	438202	AW169287	Hs.22588	ESTs	6.5
	441233	AA972965	Hs.135568	ESTs	6.4
	433384	AI021992	Hs.124244	ESTs	6.3
	427043	AA397679	Hs.298460	ESTs	6.3
30	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	6.3
	438909	AF085839		gb:Homo sapiens full length insert cDNA	6.3
	433365	AF026944	Hs.293797	ESTs	6.3
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.2
35	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.2
	431337	N48107	Hs.292593	ESTs	6.1
	434819	AA650099	Hs.291541	ESTs	6.0
	458219	H22195	Hs.31874	ESTs	6.0
	434377	AW137148	Hs.136348	osteoblast specific factor 2 (fasciclin	5.9
40	435933	AA805520	Hs.192075	ESTs	5.9
	436954	AA740151	Hs.130425	ESTs	5.9
	445424	AB028945	Hs.12696	coractin SH3 domain-binding protein	5.8
	449108	AI140683	Hs.98328	ESTs	5.8
	410334	AW979261	Hs.291993	ESTs	5.7
	447112	H17800	Hs.7154	ESTs	5.7
45	447700	AI420183	Hs.171077	ESTs, Weakly similar to similar to serin	5.7
	449208	AW263635	Hs.48643	ESTs	5.7
	445657	AW612141	Hs.279575	ESTs	5.7
	421554	AW137676	Hs.97775	ESTs, Weakly similar to Testis-specific	5.7
	435299	AI745458	Hs.122614	ESTs, Weakly similar to apoptotic protea	5.6
50	416769	AI339257	Hs.115436	ESTs	5.6
	433527	AW235613	Hs.133020	ESTs	5.6
	452771	T05477		gb:EST03366 Fetal brain, Stratagene (cat	5.6
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	5.5
55	411514	AW850178	Hs.18995	KIAA1304 protein	5.5
	424084	AI940675	Hs.20914	Homo sapiens cDNA: FLJ23056 fis, clone L	5.5
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.4
	429710	AI337113	Hs.146025	Homo sapiens cDNA: FLJ23594 fis, clone L	5.4
	432113	AA935065	Hs.152385	ESTs	5.4
	447997	H00656	Hs.29792	ESTs	5.4
60	449328	AI962493	Hs.197647	ESTs	5.3
	416575	W02414	Hs.38383	ESTs	5.3
	432009	AL137424		gb:Homo sapiens mRNA; cDNA DKFZp761G2123	5.3
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	5.3
65	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	5.2
	414299	AA142989	Hs.71730	ESTs	5.2
	431041	AA490967	Hs.105276	ESTs	5.2
	448104	AI674818	Hs.178391	ribosomal protein L44	5.2
	445279	R41900	Hs.22245	ESTs	5.1
70	408978	AL133617	Hs.49421	Homo sapiens mRNA; cDNA DKFZp434M0728 (f	5.1
	415094	D59513		gb:HUM042H10B Clontech human fetal brain	5.1
	428244	AI564123	Hs.42500	ADP-ribosylation factor-like 5	5.1
	452784	BE463857	Hs.151258	Homo sapiens cDNA: FLJ21062 fis, clone C	5.1
	455431	AW938484	Hs.80738	sialophorin (gpl115, leukosialin, CD43)	5.1
75	449416	AI651016	Hs.246311	ESTs	5.1
	421659	NM_014459	Hs.106511	protocadherin 17	5.1
	407638	AJ404672	Hs.288693	Homo sapiens cDNA FLJ11667 fis, clone HE	5.0
	446164	AW273539	Hs.199329	Homo sapiens cDNA: FLJ23577 fis, clone L	5.0
	413048	M93221	Hs.75182	mannose receptor, C type 1	5.0
80	446608	N75217	Hs.257846	ESTs	4.9
	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo	4.9
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	4.9
	442652	AI005163	Hs.201378	ESTs, Weakly similar to KIAA0944 protein	4.9
	429496	AA453800	Hs.192793	ESTs	4.8

	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	4.8
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	4.8
	425509	AF079363	Hs.158213	sperm associated antigen 6	4.8
5	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.8
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	4.8
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	4.7
	453382	AA709285	Hs.5997	Homo sapiens cDNA FLJ13078 fis, clone NT	4.7
	447033	AI357412	Hs.157601	ESTs	4.7
10	417235	AA810278	Hs.24250	ESTs	4.7
	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	4.7
	427652	AI673025	Hs.43874	ESTs	4.7
	431255	AA497043	Hs.115685	ESTs	4.7
	441143	AI027604	Hs.159650	ESTs	4.7
15	452293	AI871833		gb:wm51h09.x1 NCI_CGAP_UI2 Homo sapiens	4.7
	443903	AI220547	Hs.135223	ESTs	4.7
	422352	AA766296	Hs.99200	ESTs	4.7
	424105	AI142336	Hs.43977	ESTs	4.6
	439759	AI359055	Hs.67709	Homo sapiens mRNA full length insert cDN	4.6
20	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.6
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.6
	425804	BE501698	Hs.258189	ESTs	4.6
	435347	AW014873	Hs.116963	ESTs	4.6
	446002	AI346468	Hs.145789	ESTs	4.6
25	452883	X80031	Hs.150318	ESTs	4.6
	442176	AA983764	Hs.128910	ESTs	4.6
	443253	AI041212	Hs.132117	ESTs	4.5
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	4.5
	439920	H05430	Hs.144455	ESTs	4.5
30	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	4.5
	434424	AI811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone L	4.4
	408625	AW243323	Hs.266785	ESTs	4.4
	449299	AA299919		gb:EST12592 Uterus tumor I Homo sapiens	4.4
	450656	AA010539	Hs.18912	ESTs	4.4
35	433815	AI696602	Hs.112757	ESTs	4.4
	416879	H98899	Hs.42599	ESTs	4.3
	432182	AW607789	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.3
	445386	AI422005	Hs.160380	ESTs	4.3
	450478	AW451709	Hs.271200	ESTs	4.3
40	453080	AI423056	Hs.23921	Homo sapiens cDNA FLJ12482 fis, clone NT	4.3
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	4.3
	443257	AI334040	Hs.11614	Homo sapiens cDNA: FLJ23555 fis, clone L	4.3
	453921	AI824009	Hs.44577	ESTs	4.3
	419721	NM_001650	Hs.288650	aquaporin 4	4.2
45	432316	AW973235	Hs.293697	ESTs	4.2
	435202	AI971313	Hs.170204	KIAA0551 protein	4.2
	440320	AA879294		gb:nw86e09.s1 NCI_CGAP_Pr12 Homo sapiens	4.2
	438796	W67821	Hs.109590	genethonin 1	4.2
	400269				4.2
50	447724	AW298375	Hs.24477	ESTs	4.1
	446509	AF169693	Hs.132892	protocadherin 20	4.1
	451620	AW449888	Hs.257224	ESTs	4.1
	451963	AI825440	Hs.224952	ESTs	4.1
	456408	AI288348	Hs.23450	mRNA for FLJ00023 protein	4.1
55	425895	AI269484	Hs.161427	zinc finger protein 215	4.1
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	4.1
	454024	AA993527	Hs.16281	hypothetical protein FLJ23403	4.0
	415929	AA724373	Hs.295306	ESTs, Highly similar to unnamed protein	4.0
	426625	T78300	Hs.171409	serologically defined colon cancer antig	4.0
60	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	4.0
	437138	AI935622	Hs.271245	ESTs	4.0
	455024	AW851309		gb:IL3-CT0220-170200-067-C11 CT0220 Homo	4.0
	436246	AW450963	Hs.119991	ESTs	4.0
	416030	H15261	Hs.21948	ESTs	4.0
65	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA	3.9
	445122	AW241632	Hs.147377	Homo sapiens cDNA: FLJ23598 fis, clone L	3.9
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.9
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	3.9
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.9
70	429208	AA447990	Hs.190478	ESTs	3.9
	442957	AI949952	Hs.49397	ESTs	3.9
	444050	AW138295	Hs.135024	ESTs	3.9
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.9
	451024	AA442176		gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_	3.9
75	442832	AW206560	Hs.253569	ESTs	3.9
	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	3.9
	451895	T93573	Hs.16970	ESTs	3.9
	442353	BE379594	Hs.49136	ESTs	3.8
	421464	AA291553	Hs.190086	ESTs	3.8
80	404043				3.8
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	3.8
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	3.8
	410247	AF181721	Hs.61345	RU2S	3.8
	417461	R38403	Hs.13305	ESTs	3.8

	423609	AA328348	Hs.218289	ESTs	3.8
	440444	AA885221	Hs.156984	ESTs	3.8
	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone NT	3.8
5	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	3.8
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	3.8
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	3.8
	444271	AW452569	Hs.149804	ESTs	3.8
	434217	AW014795	Hs.23349	ESTs	3.8
10	452571	W31518	Hs.34665	ESTs	3.7
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	3.7
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	3.7
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	3.7
	445034	AW293376	Hs.160323	ESTs	3.7
15	438842	AA827176	Hs.124316	ESTs	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	415025	AW207091	Hs.72307	ESTs	3.7
	420313	AB023230	Hs.96427	KIAA1013 protein	3.7
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone CO	3.7
20	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo	3.7
	434636	AA083764	Hs.241334	ESTs	3.7
	435747	AI079519	Hs.134398	ESTs	3.7
	458158	AW296778	Hs.300357	ESTs, Highly similar to dJ416F21.2 [H.sa	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
25	410060	NM_001448	Hs.58367	glypican 4	3.7
	426116	AA868729	Hs.144694	ESTs	3.7
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	3.7
	414259	W44633	Hs.25044	Homo sapiens cDNA: FLJ23131 fis, clone L	3.7
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	3.6
30	431889	AA521277	Hs.124946	ESTs	3.6
	430414	AW365665	Hs.120388	ESTs	3.6
	433426	H69125	Hs.133525	ESTs	3.6
	421764	AI681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN CALCI	3.6
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	3.6
35	455235	AW875951		gb:CM1-PT0013-131299-067-f09 PT0013 Homo	3.6
	408399	NM_005426	Hs.44585	tumor protein p53-binding protein, 2	3.6
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	3.6
	432231	AA339977	Hs.274127	CLST 11240 protein	3.6
40	432837	AA310693	Hs.279512	HSPC072 protein	3.6
	452166	AI948607	Hs.264680	ESTs	3.5
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234 Homo	3.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	3.5
	424202	BE350295	Hs.15032	ESTs, Weakly similar to RAN binding prot	3.5
45	410658	AW105231	Hs.192035	ESTs	3.5
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	419503	AA243642	Hs.137422	ESTs	3.5
	439479	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.5
50	424268	AA397653	Hs.144339	Human DNA sequence from clone 495010 on	3.5
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	3.5
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.5
	428927	AA441837	Hs.90250	ESTs	3.5
	422544	AB018259	Hs.118140	KIAA0716 gene product	3.4
55	431207	AA495925	Hs.9394	ESTs	3.4
	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13658 fis, clone PL	3.4
	441484	AA935481	Hs.58972	ESTs	3.4
	425916	NM_006786	Hs.162200	urotensin 2	3.4
	401793				3.4
60	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	3.4
	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	3.4
	439619	AW975998	Hs.58595	ESTs	3.4
	446577	AB040933	Hs.15420	KIAA1500 protein	3.4
	450445	AW974636	Hs.194563	ESTs	3.4
65	459482	AA625339	Hs.237052	EST, Weakly similar to ALU1_HUMAN ALU SU	3.4
	445495	BE622641	Hs.38489	ESTs	3.4
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.4
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.4
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	3.3
70	419235	AW470411	Hs.288433	neurotrimin	3.3
	429703	T93154	Hs.28705	ESTs	3.3
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	3.3
	406182				3.3
	417307	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ	3.3
75	430140	AW296771	Hs.221999	ESTs	3.3
	436111	AI803082	Hs.157212	ESTs	3.3
	449729	R72032	Hs.29235	ESTs	3.3
	457620	AA602711		gb:np03h06.s1 NCI_CGAP_Pr2 Homo sapiens	3.3
80	428434	AW363590	Hs.65551	ESTs, Weakly similar to AF172993 1 PLUNC	3.3
	406554				3.3
	451381	BE241831		gb:TCAAP2E0011 Pediatric acute myelogeno	3.3
	443113	AI040686	Hs.132908	ESTs	3.3
	421470	R27496	Hs.1378	annexin A3	3.3
	446428	AW082270	Hs.210617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3

	435031	AI632091	Hs.116877	ESTs	3.3
	413136	BE066941		gb:PMO-BT0340-091299-002-a11 BT0340 Homo	3.2
	429228	AI553633	Hs.104985	ESTs	3.2
5	420252	AW270404	Hs.193161	ESTs	3.2
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.2
	444339	T96555	Hs.31562	ESTs	3.2
	434164	AW207019	Hs.148135	ESTs	3.2
	404599				3.2
10	426920	AA393351	Hs.132121	ESTs	3.2
	453736	AL118674	Hs.34871	KIAA0569 gene product	3.2
	408923	H73881	Hs.255436	ESTs	3.2
	430919	AA489041	Hs.295448	ESTs	3.2
	431622	AW979271	Hs.293184	ESTs	3.2
15	433584	AW295399		gb:UI-H-BI2-ahv-h-03-0-UI.s1 NCL_CGAP_Su	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
	438394	BE379623	Hs.27693	CGI-124 protein	3.2
	446242	N66336	Hs.7360	ESTs	3.2
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	3.2
20	454009	AW015927	Hs.233071	ESTs	3.2
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN AL	3.2
	415652	T79213	Hs.272073	ESTs	3.2
	453931	AL121278	Hs.25144	ESTs	3.2
	439382	BE247684	Hs.103070	ESTs	3.2
25	420077	AW512260	Hs.87767	ESTs	3.2
	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.2
	446745	AW118189	Hs.156400	ESTs	3.1
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	3.1
	450320	AW291775	Hs.213793	ESTs	3.1
30	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.1
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.1
	451110	AI955040	Hs.301584	ESTs	3.1
	431745	AW972448	Hs.163425	ESTs	3.1
	410781	AI375672	Hs.165028	ESTs	3.1
35	419546	AA244199		gb:nc06c05.s1 NCL_CGAP_Pr1 Homo sapiens	3.1
	444330	AI597655	Hs.49265	ESTs	3.1
	408761	AA057264	Hs.238936	ESTs	3.1
	409026	AL137554	Hs.49927	Homo sapiens mRNA; cDNA DKFZp434H1720 (f	3.1
	432055	AW972359	Hs.293334	ESTs	3.1
40	432441	AW292425	Hs.163484	ESTs	3.1
	408045	AW138959	Hs.245123	ESTs	3.1
	427191	BE221825	Hs.97691	ESTs	3.1
	416965	N26223	Hs.160436	ESTs	3.1
	441594	AL041080	Hs.208765	ESTs	3.1
45	406992	S82472		gb:beta-pol=DNA polymerase beta [exon a	3.0
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.0
	438323	AI985394	Hs.123369	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	424296	AI631874	Hs.169391	ESTs	3.0
50	450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.0
	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	3.0
	417991	AA731452	Hs.190008	ESTs	3.0
	422589	AA312735	Hs.179725	ESTs	3.0
	437583	AA761190	Hs.244627	ESTs	3.0
55	452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.0
	449494	AW237014	Hs.288650	aquaporin 4	3.0
	444188	AI393165	Hs.19175	ESTs	3.0
	400297	AI127076	Hs.288381	hypothetical protein DKFZp564O1278	3.0
	410811	AW805687	Hs.300648	ESTs	3.0
60	450584	AA040403	Hs.60371	ESTs	3.0
	428043	T92248	Hs.2240	uteroglobin	3.0
	436120	AI248193	Hs.119860	ESTs	3.0
	442324	R63578	Hs.28426	ESTs	2.9
	448693	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	2.9
65	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.9
	431385	BE178536	Hs.11090	high affinity immunoglobulin epsilon rec	2.9
	408427	AW194270	Hs.177236	ESTs	2.9
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to U4/U6 small nucl	2.9
70	408938	AA059013	Hs.22607	ESTs	2.9
	419276	BE165909	Hs.134682	Homo sapiens cDNA: FLJ23161 fis, clone L	2.9
	422022	AA302420	Hs.200442	ESTs	2.9
	426890	AA393167	Hs.41294	ESTs	2.9
	427374	AI150033	Hs.143686	ESTs	2.9
75	434208	T92641	Hs.127648	hypothetical protein PRO2176	2.9
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	2.9
	451229	AW967707	Hs.48473	ESTs	2.9
	415511	AI732617	Hs.182362	ESTs	2.9
	408776	AA057365	Hs.63356	ESTs	2.9
80	421110	AJ250717	Hs.1355	cathepsin E	2.9
	453636	R67837	Hs.169872	ESTs	2.9
	436578	AI091435	Hs.134859	ESTs	2.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	2.9
	419231	AL046294	Hs.136245	ESTs, Weakly similar to dJ202121.4 [H.sa	2.8

	408171	AA301228	Hs.43299	Homo sapiens cDNA FLJ12890 fis, clone NT	2.8
	445189	AI936450	Hs.147482	ESTs	2.8
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.8
5	427457	AW779105	Hs.164682	ESTs, Weakly similar to ORF2 consensus s	2.8
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	2.8
	446932	AA961459	Hs.125644	ESTs	2.8
	439140	W85737	Hs.290830	ESTs	2.8
	405041				2.8
10	421306	AA806207	Hs.125889	ESTs	2.8
	427514	AA640773	Hs.209224	ESTs	2.8
	427939	T92459	Hs.16886	ESTs	2.8
	429127	AA749382	Hs.107233	ESTs	2.8
	429590	AI219490	Hs.44445	ESTs, Weakly similar to Kelch motif cont	2.8
15	433163	R40468	Hs.163582	ESTs	2.8
	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone H	2.8
	448015	AI458065	Hs.23196	ESTs	2.8
	456761	D59899	Hs.127842	CGI-142	2.8
	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
20	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	2.8
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	2.8
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.8
	433515	AA595800	Hs.190246	ESTs	2.8
	424450	AL137526	Hs.147472	dynein intermediate chain 2	2.8
25	438122	AI620270	Hs.129837	ESTs	2.8
	424086	AI351010	Hs.102267	lysyl oxidase	2.8
	438885	AI886558	Hs.184987	ESTs	2.8
	412903	BE007967	Hs.155795	ESTs	2.8
	454111	AW081681	Hs.269064	ESTs	2.8
30	439398	AA284267	Hs.221504	ESTs	2.8
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	2.8
	434812	AA649860	Hs.189496	ESTs	2.8
	432583	AW023624	Hs.162282	ESTs	2.8
	428104	AA421350	Hs.191604	ESTs	2.8
35	408217	AI433201	Hs.279860	hypothetical protein FLJ20030	2.8
	438016	AI949638	Hs.109150	SH3-domain binding protein 5 (BTK-associ	2.8
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	2.7
	430887	N66801	Hs.260287	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
	446311	AW007294	Hs.149795	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
40	416185	AW975861	Hs.291995	ESTs	2.7
	408613	AW242086	Hs.253967	ESTs	2.7
	442510	AF150179	Hs.249890	ESTs	2.7
	433293	AF007835	Hs.32417	ESTs	2.7
	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.7
	404488				2.7
45	408936	AL138043	Hs.293549	ESTs	2.7
	431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fis, clone C	2.7
	436738	AW102613	Hs.152913	ESTs	2.7
	451797	AW663858	Hs.56120	ESTs	2.7
50	452163	AI863140		gb:tz43h12.x1 NCL_CGAP_Brn52 Homo sapien	2.7
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.7
	459366	AA129703		gb:zn92b05.r1 Stratagene lung carcinoma	2.7
	431448	AL137517	Hs.288381	hypothetical protein DKFZp564O1278	2.7
	430733	AW975920	Hs.283361	ESTs	2.7
55	453652	AW009640	Hs.28368	ESTs	2.7
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	2.7
	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	2.7
	408729	AA195764	Hs.72639	ESTs	2.7
	450726	AW204600	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.7
60	447720	AL038765	Hs.161304	ESTs	2.7
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	2.7
	442074	C17511	Hs.128430	ESTs	2.7
	424115	AA335497	Hs.293965	ESTs	2.7
	417728	AW138437	Hs.24790	KIAA1573 protein	2.7
65	433803	AI823593	Hs.27688	ESTs	2.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	2.7
	424310	AA338648	Hs.50334	ESTs	2.6
	438504	AW665281	Hs.224625	ESTs	2.6
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	2.6
70	430417	AA461045	Hs.50701	ESTs	2.6
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	422505	AL120862	Hs.124165	ESTs	2.6
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-tyr	2.6
	428667	AI375550	Hs.74407	nucleolar protein p40; homolog of yeast	2.6
75	431750	AA514986	Hs.283705	ESTs	2.6
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.6
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.6
	403903				2.6
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.6
80	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	2.6
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	2.6
	436645	AW023424	Hs.156520	ESTs	2.6
	408380	AF123050	Hs.44532	diubiquitin	2.6
	402629				2.6

	406594			2.6
	415122	D60708	Hs.22245	ESTs
	416747	AW876523	Hs.15929	Homo sapiens cDNA FLJ12910 fis, clone NT
5	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C
	444361	W76027	Hs.23920	Homo sapiens cDNA FLJ13124 fis, clone NT
	446609	BE395090	Hs.15535	Human gene from PAC 886K2, chromosome 1
	449260	AA741180	Hs.29879	ESTs
	452311	AW304029	Hs.252744	ESTs
10	413802	AW964490	Hs.32241	ESTs
	417318	AW953937	Hs.12891	ESTs
	440028	AW473675	Hs.125843	ESTs
	437960	AI669586	Hs.222194	ESTs
	433687	AA743391		gb:ny57g01.s1 NCLCGAP_Pr18 Homo sapiens
15	430573	AA744550	Hs.136345	ESTs
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN
	453204	R10799	Hs.191990	ESTs
	436751	AA732217	Hs.294054	ESTs
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f
20	431120	AA492588		gb:ng99c08.s1 NCLCGAP_Thy1 Homo sapiens
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f
	438458	AW975186	Hs.162875	ESTs, Weakly similar to ALU1_HUMAN ALU S
	446063	AI720140	Hs.151079	ESTs
	430499	AW969408	Hs.231991	ESTs
25	450496	AW449251	Hs.257131	ESTs
	441330	AI692984	Hs.129354	ESTs
	424433	H04607	Hs.9218	ESTs
	434677	AW444575	Hs.130834	ESTs
	445779	AI253104	Hs.189267	ESTs
30	444649	AW207523	Hs.197628	ESTs
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1
	404288			
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A
35	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912
	410095	AW589638	Hs.258947	ESTs
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298
	418343	AA216372	Hs.159501	ESTs
40	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto
	428637	AW979268		gb:EST391378 MAGE resequences, MAGP Homo
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy
	432507	BE391093		gb:601286042F1 NIH_MGC_44 Homo sapiens c
	433858	N69243	Hs.192974	Homo sapiens cDNA FLJ12735 fis, clone NT
45	438651	H64500	Hs.123646	ESTs
	443830	AI142095	Hs.143273	ESTs
	446800	AI341635	Hs.156486	ESTs
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN A
	451343	AW975057	Hs.293353	ESTs
50	451539	AA059467	Hs.218933	ESTs
	452412	AA029608	Hs.61373	ESTs
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap
	445745	AB007924	Hs.13245	KIAA0455 gene product
	424943	AI077260	Hs.153924	death-associated protein kinase 1
55	440106	AA864968	Hs.127699	KIAA1603 protein
	458429	AV646559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C
	415261	T40928	Hs.8346	ESTs
	420026	AI831190	Hs.166676	ESTs
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam
60	458722	AA741545	Hs.282832	ESTs
	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S
	433644	AW342028	Hs.256112	ESTs
	419172	AW338625	Hs.22120	ESTs
65	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti
	443348	AW873596	Hs.57572	ESTs
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE
	448030	N30714	Hs.20161	HDCME31P protein
70	417203	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE
	449275	AW450848	Hs.205457	KIAA1620 protein
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL
	442191	W95186	Hs.8136	endothelial PAS domain protein 1
75	428571	NM_006531	Hs.2291	Probe hTg737 polycystic kidney disease,
	453142	AA033648	Hs.7473	ESTs
	425657	T89839	Hs.119471	ESTs
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone H
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf
80	458332	AI000341	Hs.220491	ESTs
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor
	459644			
	429125	AA446854	Hs.271004	ESTs
	448337	AW206453	Hs.3782	ESTs

	427778	AA412323	Hs.105323	ESTs	2.4
	425371	D49441	Hs.155981	mesothelin	2.4
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.4
5	447610	AW296286	Hs.255534	ESTs	2.4
	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.4
	441006	AW605267	Hs.7627	CGI-60 protein	2.4
	440817	AI341423	Hs.270165	ESTs	2.4
	420020	BE295866	Hs.94382	adenosine kinase	2.4
10	435395	AA729235	Hs.117907	ESTs	2.4
	424144	AA454033	Hs.41644	Homo sapiens cDNA: FLJ23003 fis, clone L	2.4
	405494				2.4
	458145	AI239457	Hs.130794	ESTs	2.4
	408547	AA574291	Hs.57837	ESTs	2.4
15	408941	AI452469	Hs.165221	ESTs	2.4
	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276 Homo	2.4
	417137	U46265	Hs.81281	hypothetical protein	2.4
	418950	T78517	Hs.13941	ESTs	2.4
	420756	AA411800	Hs.189900	ESTs	2.4
20	428316	AI860775	Hs.98506	ESTs	2.4
	432896	NM_014097	Hs.279778	PRO1693 protein	2.4
	436148	BE005252		gb:CM1-BN0116-030400-171-g02 BN0116 Homo	2.4
	436284	AA708016	Hs.190389	ESTs	2.4
	437327	AL353942		gb:Homo sapiens mRNA; cDNA DKFZp761L2312	2.4
25	442611	BE077155	Hs.177537	ESTs	2.4
	456062	AI866286	Hs.71962	ESTs	2.4
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.4
	401335				2.4
	428771	AB028992	Hs.193143	KIAA1069 protein	2.4
30	419140	AI982647	Hs.215725	ESTs	2.4
	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	2.4
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.4
	407339	AA777542	Hs.132670	ESTs	2.4
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	2.4
35	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	2.4
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.4
	452561	AI692181	Hs.49169	KIAA1634 protein	2.4
	427878	C05766	Hs.181022	CGI-07 protein	2.4
	419752	AA249573	Hs.152618	ESTs	2.4
40	430073	U86136	Hs.232070	telomerase-associated protein 1	2.4
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	2.4
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.3
	407905	AW103655	Hs.252905	ESTs	2.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.3
45	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3 (G	2.3
	453049	BE537217	Hs.30343	ESTs	2.3
	438568	R98865	Hs.11135	major histocompatibility complex, class	2.3
	453445	AL036532	Hs.91453	ESTs	2.3
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.3
50	446346	AI290205		gb:q179g06.x1 Soares_NhHMPu_S1 Homo sapi	2.3
	441974	AI683782	Hs.128245	ESTs	2.3
	444805	AB007899	Hs.12017	KIAA0439 protein; homolog of yeast ubiqu	2.3
	424027	AW337575	Hs.201591	ESTs	2.3
	419606	AW294795	Hs.198529	ESTs, Weakly similar to similar to acyl-	2.3
55	428613	AB037749	Hs.186928	KIAA1328 protein	2.3
	434340	AI193043	Hs.128685	ESTs	2.3
	450297	AW901347	Hs.38592	Homo sapiens cDNA: FLJ23342 fis, clone H	2.3
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.3
	433650	AA603472	Hs.28456	ESTs	2.3
60	419086	NM_000216	Hs.89591	Kalimann syndrome 1 sequence	2.3
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PL	2.3
	430153	AW968128		gb:EST380338 MAGE resequences, MAGJ Homo	2.3
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.3
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	2.3
65	400610				2.3
	402222				2.3
	407162	N63855	Hs.142634	zinc finger protein	2.3
	415250	F02614	Hs.27319	ESTs	2.3
70	421751	AW813731	Hs.159153	ESTs	2.3
	428552	AW274560	Hs.129520	ESTs	2.3
	432658	AW973769	Hs.162319	ESTs	2.3
	434742	AA648302	Hs.291695	ESTs	2.3
	436586	AI308862	Hs.167028	ESTs	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
75	442039	AW276240	Hs.128352	ESTs, Weakly similar to p80 [R.norvegicu	2.3
	443160	AI467915	Hs.36053	ESTs	2.3
	448764	AI568607	Hs.182112	ESTs	2.3
	449579	AW207260	Hs.134014	prostate cancer associated protein 6	2.3
	439810	AL109710	Hs.85568	EST	2.3
80	413714	AI560944	Hs.71428	ESTs	2.3
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	2.3
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	2.3
	438670	AI275803	Hs.123428	ESTs	2.3
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	2.3

	459702				2.3
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	2.3
	438474	AW865818	Hs.6232	KIAA0764 gene product	2.3
5	453037	AA045175	Hs.177552	ESTs	2.3
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	2.3
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	2.3
	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	2.3
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	2.3
10	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.3
	406506				2.3
	448330	AL036449	Hs.207163	ESTs	2.3
	409719	AI769160	Hs.108681	ESTs	2.3
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.3
15	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.3
	427961	AW293165	Hs.143134	ESTs	2.3
	447357	AI375922	Hs.159367	ESTs	2.3
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	2.3
	453716	AA037675	Hs.152675	ESTs	2.3
20	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.3
	407949	W21874	Hs.247057	ESTs	2.2
	427972	AA864870	Hs.181304	putative gene product	2.2
	453313	BE005771	Hs.153746	Homo sapiens cDNA: FLJ22490 fis, clone H	2.2
	426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	2.2
25	424238	AA337401	Hs.137635	ESTs	2.2
	452930	AW195285	Hs.194097	ESTs	2.2
	424527	AW138558	Hs.267158	ESTs	2.2
	453095	AW295660	Hs.252756	ESTs	2.2
	449161	N53431	Hs.47647	ESTs, Weakly similar to KIAA0423 [H.sapi	2.2
30	429586	T73510	Hs.209153	angiotensin-like 3	2.2
	423782	AI472209	Hs.288369	ESTs	2.2
	458124	AW005548	Hs.124590	ESTs	2.2
	450109	AI539295	Hs.17967	ESTs	2.2
	421461	AW291023	Hs.97255	ESTs	2.2
35	412222	AA528283	Hs.292737	ESTs	2.2
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	441736	AW292779	Hs.169799	ESTs	2.2
	401049				2.2
	440727	AI073991	Hs.134268	ESTs	2.2
40	419751	AW195581	Hs.93121	KIAA0761 protein	2.2
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.2
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.2
	410292	AA843087	Hs.124194	ESTs	2.2
45	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	2.2
	449695	AA164569	Hs.34550	ESTs	2.2
	429399	AA452244	Hs.16727	ESTs	2.2
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	2.2
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.2
50	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	2.2
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.2
	445268	AI218358	Hs.175048	ESTs	2.2
	402481				2.2
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.2
55	416521	H60929	Hs.44197	hypothetical protein DKFZp564D0462	2.2
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
	421211	AA284966	Hs.266308	ESTs, Weakly similar to AF216312 1 type	2.2
	427541	AI798983	Hs.97961	ESTs	2.2
60	432013	AI796879	Hs.162102	ESTs	2.2
	436461	AW511956	Hs.293261	ESTs	2.2
	438002	AI560246	Hs.201648	ESTs, Weakly similar to ZN42_HUMAN ZINC	2.2
	440312	AW614597	Hs.72475	ESTs	2.2
	440479	AA886461	Hs.208161	ESTs	2.2
65	441178	W90789	Hs.153976	ESTs	2.2
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	2.2
	443314	AW771701	Hs.54646	ESTs	2.2
	422165	AL041199	Hs.1481	histidine decarboxylase	2.2
70	450696	AI654223	Hs.16026	Homo sapiens cDNA: FLJ23191 fis, clone L	2.2
	432974	BE348793		gb:ht70g02.x1 NCI_CGAP_Lu24 Homo sapiens	2.2
	404200				2.2
	435990	AI015862	Hs.131793	ESTs	2.2
	421309	AI222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.2
75	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.2
	416642	T96118	Hs.226313	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	406672	M26041	Hs.198253	major histocompatibility complex, class	2.2
	417819	AI253112	Hs.133540	ESTs	2.2
	417355	D13168	Hs.82002	endothelin receptor type B	2.2
80	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	2.2
	404274				2.2
	415086	AI597963	Hs.118726	ESTs	2.2
	418210	R54575	Hs.13337	ESTs, Weakly similar to unnamed protein	2.2
	419220	AA811938	Hs.291759	ESTs	2.2
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.2

	451050	AW937420	Hs.69662	ESTs	2.2
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	2.2
	428414	AL049980	Hs.184216	DKFZP564C152 protein	2.2
5	412925	AI089319	Hs.179243	ESTs	2.2
	438192	AI859065	Hs.16808	ESTs, Weakly similar to paraplegin-like	2.2
	410976	R36207	Hs.25092	ESTs	2.2
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.2
	449677	AA002071		gb:zh85d01.s1 Soares_fetal_liver_spleen_	2.2
10	449321	AA001150	Hs.132937	ESTs	2.2
	418557	BE140602	Hs.246645	ESTs	2.2
	416320	H47867	Hs.34024	ESTs	2.2
	426384	AI472078		gb:tj85h03.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.2
	414140	AA281279	Hs.23317	ESTs	2.2
	419520	AB009303	Hs.297790	Human clone 23734 mRNA sequence	2.2
15	446999	AA151520	Hs.279525	hypothetical protein PRO2605	2.2
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	2.2
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.1
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	2.1
20	410048	W76467	Hs.274550	proline oxidase homolog	2.1
	400880				2.1
	418092	R45154	Hs.106604	ESTs	2.1
	428780	AI478578	Hs.50636	ESTs	2.1
	431067	AW574823	Hs.200413	ESTs	2.1
25	432803	AA565398		gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	2.1
	412104	AW205197	Hs.240951	ESTs	2.1
	422819	AL122084	Hs.121073	hypothetical protein FLJ10466	2.1
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	2.1
	424806	AA382523	Hs.105689	ESTs	2.1
30	434445	AI349306	Hs.11782	ESTs	2.1
	442994	AI026718	Hs.16954	ESTs	2.1
	410371	AA084482	Hs.115850	ESTs	2.1
	450232	BE300815	Hs.201326	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.1
35	430899	BE018217	Hs.183528	ESTs, Weakly similar to Bem46-like prote	2.1
	431814	BE256242	Hs.270847	delta-tubulin	2.1
	417543	AA203620	Hs.110153	ESTs, Weakly similar to BCGF_HUMAN B-CEL	2.1
	444542	AI161293	Hs.146862	ESTs, Weakly similar to KIAA0525 protein	2.1
	404593				2.1
40	434803	AW974640		gb:EST386744 MAGE resequences, MAGM Homo	2.1
	451623	H77818	Hs.268991	ESTs	2.1
	452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on	2.1
	402046				2.1
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.1
45	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ21317 fis, clone L	2.1
	401987				2.1
	423119	AA322201	Hs.131976	EST	2.1
	427112	Z32887	Hs.290951	ESTs	2.1
	414464	AI870175	Hs.13957	ESTs	2.1
50	447829	AI433029	Hs.164104	ESTs	2.1
	449679	AI823951	Hs.296668	Homo sapiens cDNA FLJ11846 fis, clone HE	2.1
	405472				2.1
	413621	AI808648	Hs.184156	ESTs	2.1
	432212	AW137742	Hs.293451	ESTs	2.1
55	404289				2.1
	415362	F06735		gb:HSC1JB091 normalized infant brain cDN	2.1
	427739	AW196755	Hs.98105	ESTs	2.1
	427772	AA412289	Hs.98123	ESTs	2.1
60	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.1
	434335	AA630107	Hs.213220	ESTs	2.1
	436052	AI021983	Hs.271432	ESTs	2.1
	442773	AB037722	Hs.8707	Homo sapiens mRNA; cDNA DKFZp434N1131 (f	2.1
	446799	AW978373	Hs.49221	ESTs, Weakly similar to zinc finger prot	2.1
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.1
65	455673	BE065939		gb:RC3-BT0319-100100-012-c11 BT0319 Homo	2.1
	458624	AI362790	Hs.181801	ESTs	2.1
	405095				2.1
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	2.1
	433589	AA886530	Hs.188912	ESTs	2.1
70	438398	AA806526	Hs.130277	ESTs	2.1
	447233	AW246333	Hs.17901	Homo sapiens cDNA: FLJ21974 fis, clone H	2.1
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.1
	431087	H12723	Hs.290791	ESTs	2.1
	409064	AA062954	Hs.141883	ESTs	2.1
75	427558	D49493	Hs.2171	growth differentiation factor 10	2.1
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	2.1
	438118	AW753311	Hs.259415	ESTs	2.1
	427621	BE621182	Hs.179882	Homo sapiens cDNA FLJ12437 fis, clone NT	2.1
	452114	N22687	Hs.8236	ESTs	2.1
80	448782	AL050295	Hs.301550	KIAA0758 protein	2.1
	403937				2.1
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	2.1
	452416	AA026115	Hs.114777	ESTs	2.1
	451609	AL046019	Hs.209276	ESTs	2.1

	435934	R19382	Hs.117869	ESTs	2.1
	445158	AI992108	Hs.127206	ESTs	2.1
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.1
5	439335	AA742697	Hs.62492	ESTs, Weakly similar to S59856 collagen	2.1
	443949	AW827419	Hs.235070	ESTs	2.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.1
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	2.1
	438676	AA813745	Hs.123446	ESTs	2.1
10	405848				2.1
	416940	N75620	Hs.43157	ESTs	2.1
	442381	AI185136	Hs.48650	ESTs	2.1
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586i1823 (f	2.1
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	2.1
15	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	2.1
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	2.1
	439425	AF086244	Hs.114659	ESTs	2.1
	421168	AF182277	Hs.1360	cytochrome P450, subfamily IIB (phenobar	2.1
	449611	AI970394	Hs.197075	ESTs	2.1
	404548				2.1
20	416734	H81213	Hs.14825	ESTs	2.1
	435865	AA883552	Hs.16810	ESTs	2.1
	439072	AF085930	Hs.269123	ESTs	2.1
	447482	AB033059	Hs.18705	KIAA1233 protein	2.1
25	457292	AI921270	Hs.214178	Homo sapiens cDNA FLJ14251 fis, clone OV	2.1
	444974	AI203500	Hs.151612	ESTs	2.1
	456034	AW450979		gb:U1-H-BI3-ata-a-12-0-UI.s1 NCI_CGAP_Su	2.1
	430634	AI860651	Hs.26685	ESTs	2.1
	426782	R14614	Hs.191254	ESTs	2.0
30	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.0
	445326	AI220072	Hs.165893	ESTs	2.0
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.0
	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	2.0
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.0
35	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.0
	417321	N68722	Hs.191368	ESTs	2.0
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.0
	404323				2.0
40	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
	421047	AW514772	Hs.104473	ESTs	2.0
	425497	AA524596	Hs.188844	ESTs	2.0
	444623	AI183829	Hs.202111	ESTs	2.0
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.0
	433563	AI732637	Hs.277901	ESTs	2.0
45	406485				2.0
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.0
	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.0
	425465	L18964	Hs.1904	protein kinase C, iota	2.0
	449424	AW448937	Hs.197030	ESTs	2.0
50	427940	AA417812	Hs.38775	ESTs	2.0
	411502	AW946605	Hs.250154	Homo sapiens cDNA FLJ12973 fis, clone NT	2.0
	411365	M76477	Hs.278242	tubulin, alpha, ubiquitous	2.0
	412369	H80456	Hs.285243	Homo sapiens cDNA: FLJ22029 fis, clone H	2.0
	452959	AI933416	Hs.189674	ESTs	2.0
55	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.0
	428775	AA434579	Hs.143691	ESTs	2.0
	420000	AB036063	Hs.180726	Homo sapiens cDNA FLJ13543 fis, clone PL	2.0
	408321	AW405882	Hs.44205	cortistatin	2.0
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	2.0
60	411050	AW814902		gb:MR1-ST0206-120400-022-f08 ST0206 Homo	2.0
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.0
	428978	AA442784	Hs.125445	ESTs	2.0
	458562	N34128	Hs.145268	ESTs	2.0
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	2.0
65	403760				2.0
	424368	AB037766	Hs.146085	KIAA1345 protein	2.0
	421229	AI056590	Hs.7086	Homo sapiens cDNA: FLJ23000 fis, clone L	2.0
	436304	AA339622	Hs.108887	ESTs	2.0
	453498	BE181412	Hs.23245	Homo sapiens cDNA FLJ11767 fis, clone HE	2.0
70	439018	AW300887	Hs.26638	ESTs, Weakly similar to unnamed protein	2.0
	453280	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFZp761C082 (fr	2.0
	420193	AI460080	Hs.202869	ESTs	2.0
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.0
	401575				2.0
75	419092	J05581	Hs.89603	mucin 1, transmembrane	2.0
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.0
	410763	AF279145	Hs.8966	tumor endothelial marker 8	2.0
	414783	AW069569	Hs.75839	zinc finger protein 6 (CMPX1)	2.0
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.0
80	405963				2.0
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.0
	420831	AA280824	Hs.190035	ESTs	2.0
	424152	AL133591	Hs.301405	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.0
	424641	AB001106	Hs.151413	glia maturation factor, beta	2.0

	427616	AI698684	Hs.98028	ESTs	2.0
	435115	AI821726	Hs.116603	ESTs	2.0
	437636	AA764781	Hs.291844	ESTs	2.0
5	438295	AI394151	Hs.37932	ESTs	2.0
	439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	2.0
	445388	AI925280	Hs.236842	EST	2.0
	447101	N72185	Hs.44189	ESTs	2.0
	448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.0
10	449623	C00719	Hs.120440	ESTs	2.0
	450159	AI702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN CALPA	2.0
	456613	R19992	Hs.106620	Homo sapiens clone 23950 mRNA sequence	2.0
	457233	AI355009	Hs.221698	ESTs	2.0
	457384	AA501760	Hs.18075	chromosome 9 open reading frame 3	2.0
15	457471	AW971364		gb:EST383453 MAGE resequenes, MAGL Homo	2.0

TABLE 27B

20	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
25	Pkey	CAT number	Accession		
	409457	1132521_1	AW818081 AW392887 AW514700 AW392881		
	409519	113722_1	AA075368 AA075369		
	410008	116812_1	AA079552 BE142525 BE142527		
	410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803395 AW803334 AW803355		
	411050	1230330_1	AW814902 BE156656 BE156667 BE156590 BE156441 BE156447		
30	411880	1263110_1	AW872477 BE088101 T05990		
	411905	1265181_1	BE265067 BE264978 AW875420		
	412303	1288130_1	AW936336 AW936339		
	413136	1350379_1	BE066941 BE066911 BE066979 BE066929 BE066925		
	413499	1373910_1	BE144884 H97942		
35	413875	1396766_1	BE176776 H85072		
	415094	1522103_1	D59513 D59515 D80174 D59514		
	415362	1534980_1	F06735 R55896 R12110 H08697		
	416624	1604694_1	H69044 T47567 H75691 T50292		
40	418378	174656_1	AW962081 AA218925 AA354237		
	419546	185766_1	AA244199 AA244272 H57440		
	419807	188252_1	R77402 AA262462 AA250988 R06794		
	420637	195241_1	AW976153 AA278945 AA747691		
	422429	216469_1	AA310527 AW962295 Z44865 H06641		
	423377	22769_1	AL049377 AL079930 AL047223 AW885968 AA385235		
45	426384	266211_1	AI472078 AA377209 AA865807		
	428637	293660_1	AW979268 AA878419 AA431342 AA431628		
	430153	313709_1	AW968128 AA468102 AA468165		
	430844	324570_1	T94960 AA487679 T95013		
50	431120	328264_1	AA492588 AA492498 AA492571		
	431169	328799_1	AW971240 AA493843 AA493723		
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188		
	432009	34025_1	AL137424 BE007148 T52277		
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756		
55	432507	348711_1	BE391093 AA551334 BE389643		
	432779	354024_1	AW979241 AA565006 AA847102		
	432803	354267_1	AA565398 AW894072 H97930		
	432869	355475_1	AW974094 AA569074 AA602574		
	432974	356950_1	BE348793 AA573118 N79366		
60	433492	367934_1	AW605849 AW262898 N41060 AA594852		
	433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832		
	433687	373061_1	AA743991 AA604852 AW272737		
	434803	393471_1	AW974640 AA649516 N75626		
	436148	41500_1	BE005252 AK000786		
	437327	43610_1	AL353942 AW994305		
65	438909	46684_1	AF085839 R69137 AW188788 R69254		
	440320	491930_1	AA879294 N67538 AI474541		
	444314	600667_1	AI140497 AW749625 AW749626 AW749644		
	444610	612257_1	AI174783 R83569 R12271		
70	446346	673545_1	AI290205 AW235762 AI651268		
	447197	711623_1	R36075 AI366546 R36167		
	448404	761515_1	BE089973 AI498612 AW805032		
	449299	80436_1	AA299919 AW957012 AA001107 T83631 BE156389		
	449540	80945_2	AA001713 H63836		
75	449677	81270_1	AA002071 AA002232 T99209		
	450522	837264_1	AI698839 AI909260 AI909259		
	451024	85565_1	AA442176 AA259181		
	451381	867770_1	BE241831 AW249135 BE548847 AW250245		
	452163	902067_1	AI863140 W80703 R43474		
80	452293	909195_1	AI871833		
	452453	918300_1	AI902519 AI902518 AI902516		
	452542	921410_1	AW812256 AW812257 AI906423 AI906422		
	452771	930983_1	T05477 T07855 AI917711		
	454359	1130674_1	N71277 AW390764		

454693 1229132_1 AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
 455024 1249196_1 AW851309 AW850888 AW851419 AW851412 AW851299
 455226 1262534_1 AW902103 AW869012 AW869139
 455235 1265634_1 AW875951 AW875950 AW875936 AW875948 AW875939 AW875957
 455673 1349656_1 BE065939 BE066079 BE065956
 455807 1370914_1 BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
 456034 142696_1 AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
 BE011368 BE011362 BE011215 BE011365 BE011363
 457471 340916_1 AW971364 AA525021 AA570759
 457620 371514_1 AA602711 BE078290
 458154 491768_1 AW816379 AA888282 AA879046 AA879195
 459267 966605_1 AJ003631 AJ003650 AJ003651

TABLE 27C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source: 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400610	9887671	Minus	117606-117928,124040-124147
400880	9931121	Plus	29235-29336,36363-36580
401049	7232177	Plus	149157-150692
401335	9884881	Plus	15736-16352
401575	7229804	Minus	76253-76364
401793	7263888	Minus	102945-103083
401987	4406829	Minus	72893-73021,76938-77049
402046	8072415	Plus	166394-166556,168167-168395
402222	9958106	Plus	3261-3834,3939-4269
402481	9797406	Plus	87891-88991
402629	9931216	Plus	33641-33775,34182-34372,36003-36084,40343-40612
403760	7712202	Minus	45910-46260,47563-47824
403903	7710671	Minus	101165-102597
403937	7711761	Minus	12609-12773
404043	9558573	Plus	29042-29135,46597-46699
404200	6010176	Minus	7066-7210
404274	9885189	Plus	104127-104318
404288	2769644	Plus	3512-3691
404289	2769644	Plus	15049-15286,30267-30457
404323	9719753	Minus	31913-32219
404488	8113286	Minus	64835-64994
404548	8570305	Minus	83896-84162
404593	9944086	Minus	74922-75788
404599	8705107	Plus	110443-110733
404916	7341826	Plus	91057-91188
405041	7547195	Plus	121230-121714
405095	8072599	Plus	138877-139066
405472	8439781	Plus	106297-106447,108462-108596
405494	8050952	Minus	70284-70518
405848	7651809	Minus	28135-28244
405963	8247786	Plus	4056-4699
406182	5923650	Minus	28256-28935
406485	7711305	Plus	125036-125422
406506	7711374	Minus	6843-8077
406554	7711566	Plus	106956-107121
406594	8248611	Minus	35543-35845

TABLE 28A: ABOUT 796 GENES DOWN-REGULATED IN LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 28A lists of about 796 genes that are downregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues sample expression was less than or equal to 0.1. The "average" normal lung tissue level was set to the 75th percentile amongst normal lung tissues. The "average" fibrosis expression level was set to the 95th percentile amongst fibrosis samples. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of normal lung to fibrosis

Pkey	ExAccn	Unigene ID	Unigene Title	R1
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	18.18
421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	9.39
404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	8.30
404795				5.56

	403211				5.46
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	5.43
	400489				5.19
5	425571	AJ007292	Hs.158306	ephrin-A2	5.19
	406357				5.08
	407979	AA046306	Hs.62927	ESTs	5.08
	452378	AA025855	Hs.19597	ESTs	4.78
	408053	AW139474	Hs.246862	ESTs	4.62
10	421770	AA374192	Hs.108124	ribosomal protein L41	4.52
	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	4.49
	402386				4.39
	402448				4.37
	448245	AI923551	Hs.170843	ESTs	4.31
15	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	4.29
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	4.24
	447768	X86400	Hs.19520	FXFD domain-containing ion transport reg	4.21
	405163				4.19
	437120	AI356125	Hs.157767	ESTs, Weakly similar to human HOXA2 [H.s	4.19
20	409020	AA062549	Hs.21162	ESTs	4.09
	431073	BE254470	Hs.249186	cone-rod homeobox	4.07
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	4.05
	403716				3.99
	424969	AW950928	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.94
25	404348				3.90
	407070	Y10209		gb:H.sapiens mRNA for CD30L protein	3.82
	412919	AI368680	Hs.816	SRY (sex determining region Y)-box 2	3.81
	402409				3.80
	456150	Z42308		gb:HSC0FB121 normalized infant brain cDN	3.79
30	427030	AA397600	Hs.97531	ESTs	3.76
	426328	AW631296		gb:hh83c09.y1 NCL_CGAP_GU1 Homo sapiens	3.74
	429307	AU076592	Hs.198951	jun B proto-oncogene	3.71
	400172				3.70
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	3.68
35	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 proline-r	3.68
	446850	R71245	Hs.174303	ESTs	3.67
	405147				3.64
	406821	AA977896	Hs.128873	ESTs, Highly similar to ALFA_HUMAN FRUCT	3.57
	402762				3.55
40	401496				3.50
	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	3.50
	402911				3.49
	425330	D25216	Hs.155650	KIAA0014 gene product	3.49
	438004	AA774984	Hs.220649	ESTs, Weakly similar to FCE2 MOUSE LOW A	3.46
45	448185	AI633040	Hs.172730	ESTs	3.46
	433367	AA584930	Hs.269451	ESTs, Weakly similar to XAP-5-like prote	3.43
	416596	H67669	Hs.38564	ESTs	3.41
	400545				3.39
	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB5	3.37
50	426507	AA380285		gb:EST93491 Supt cells Homo sapiens cDNA	3.35
	403479				3.34
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (iso	3.34
	401919				3.33
	449031	AI867502	Hs.271462	ESTs	3.33
55	400116				3.31
	401590				3.29
	401007				3.28
	404610	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	3.25
	408641	AW245207	Hs.5555	Homo sapiens cDNA FLJ13170 fis, clone NT	3.25
60	407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma viru	3.23
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-bi	3.23
	433232	AI658621	Hs.127769	ESTs	3.23
	457937	AW976930	Hs.128760	ESTs	3.23
	406101				3.18
65	407080	Z38133	Hs.113973	myosin, heavy polypeptide 8, skeletal mu	3.18
	419947	AW298744	Hs.118894	ESTs	3.16
	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H	3.16
	454019	D31846	Hs.37025	aquaporin 2 (collecting duct)	3.16
	428674	AA431734	Hs.104915	ESTs	3.14
70	402056				3.06
	425182	AF041259	Hs.155040	zinc finger protein 217	3.06
	425393	NM_000218	Hs.156115	potassium voltage-gated channel, KQT-IIk	3.06
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	3.05
	402158				3.03
75	404938				3.02
	403376				3.01
	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-ty	3.00
	402423				2.99
	416253	BE250659	Hs.15463	ESTs	2.99
80	435265	AA779958	Hs.185932	ESTs	2.99
	425655	BE614551	Hs.158675	ribosomal protein L14	2.98
	428704	AA432007	Hs.249484	ESTs	2.98
	425439	D38024	Hs.157425	double homeobox, 2	2.97
	445613	BE550889	Hs.158491	ESTs	2.97

	402714			2.96	
	403526			2.96	
	403605			2.95	
5	441852	AB028968	Hs.7989	KIAA1045 protein	2.95
	417629	T76945	Hs.64211	ESTs, Weakly similar to similar to acyl-	2.94
	447744	AA313230	Hs.19413	S100 calcium-binding protein A12 (calgr	2.91
	419821	AW967486	Hs.189119	ESTs	2.90
	446993	AI570964	Hs.164257	ESTs	2.89
10	414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	2.88
	423379	AI985349	Hs.157492	Homo sapiens cDNA FLJ14079 fis, clone HE	2.88
	440206	AI762232	Hs.46794	ESTs	2.88
	402212	AW502761	Hs.30909	KIAA0430 gene product	2.87
	406059				2.86
15	423548	AF007194	Hs.129782	mucin 3A, intestinal	2.86
	402051				2.85
	415196	AK000150	Hs.78185	MAX-like bHLHZIP protein	2.85
	455446	AW947749		gb:RC0-MT0005-130300-031-b01 MT0005 Homo	2.85
	442428	BE464988	Hs.298302	ESTs	2.84
20	403247				2.83
	404825				2.83
	459184	L35001	Hs.95669	ESTs	2.83
	402968				2.82
	417575	R00382	Hs.191199	ESTs	2.82
25	404668				2.81
	420619	AF130255	Hs.99430	testis zinc finger protein	2.81
	447241	BE382838	Hs.19322	ESTs	2.80
	448793	AI864581	Hs.215477	ESTs	2.79
	453014	AI937242	Hs.176590	ESTs	2.79
30	446775	AI792836	Hs.232273	ESTs	2.78
	455075	AW854850		gb:QV2-CT0261-201099-011-h03 CT0261 Homo	2.78
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	2.75
	457546	AA568484	Hs.153632	ESTs	2.75
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.74
35	433677	AI791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN A	2.74
	405703				2.73
	408840	AW277132	Hs.254880	ESTs	2.73
	413958	BE277913	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	2.73
	454421	BE409759	Hs.59563	Homo sapiens mRNA for FLJ00007 protein,	2.73
40	406702	Z20656	Hs.278432	myosin, heavy polypeptide 6, cardiac mus	2.72
	408664	R56362		gb:y93c07.r1 Soares infant brain 1N1B H	2.72
	402457				2.71
	403612				2.71
	407049	X72632		(NONE)	2.71
45	415423	AA164743	Hs.187617	Homo sapiens cDNA FLJ13941 fis, clone Y7	2.70
	402862				2.69
	403540				2.69
	431465	AW293178	Hs.180086	ESTs	2.69
50	406563				2.68
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.68
	426220	AI383475	Hs.171697	ESTs, Weakly similar to immunoglobulin s	2.68
	446707	AI591214	Hs.156336	ESTs	2.68
	447557	AW028809	Hs.229570	ESTs	2.68
	413529	U11874	Hs.846	interleukin 8 receptor, beta	2.67
55	403997				2.66
	408704	AA056635	Hs.5366	Homo sapiens cDNA: FLJ21522 fis, clone C	2.66
	407005	U20230		gb:Human guanyl cyclase C gene, partial	2.65
	405075				2.64
	430728	AW968522		gb:EST380598 MAGE resequences, MAGJ Homo	2.64
60	405327				2.63
	409419	BE207219	Hs.20474	ESTs, Highly similar to S17112 interfero	2.63
	434300	AA740944	Hs.116295	ESTs	2.63
	405895				2.62
	431929	AW294163	Hs.146127	ESTs	2.61
65	405217				2.60
	437569	AA760849	Hs.294052	ESTs	2.60
	419822	AW966864	Hs.255780	ESTs	2.59
	445918	AW014139	Hs.145656	ESTs	2.59
	446149	BE242960	Hs.203181	ESTs	2.59
70	457829	AI742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [H.sa	2.58
	404282				2.53
	409778	AW499705		gb:UI-HF-BR0p-ajk-b-05-0-UI.r1 NIH_MGC_5	2.53
	445353	BE551465	Hs.175211	ESTs	2.53
	458764	BE619386		gb:601473204F1 NIH_MGC_68 Homo sapiens c	2.53
75	402195				2.52
	404247				2.52
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.52
	402588				2.50
	432301	U34249	Hs.167075	ring finger protein 9	2.50
80	424958	AA984420	Hs.283659	ESTs	2.49
	442197	AW837912		gb:QV3-LT0048-260100-068-c02 LT0048 Homo	2.49
	415003	M11437	Hs.77741	kininogen	2.48
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	2.48
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1	2.47

	440424	AI991125	Hs.189109	Homo sapiens cDNA: FLJ21458 fis, clone C	2.47
	402153				2.46
	432152	AK000245	Hs.272790	Homo sapiens cDNA FLJ20238 fis, clone CO	2.46
5	454414	R55574	Hs.164675	ESTs	2.45
	401603				2.44
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.44
	408513	AW206468	Hs.103118	ESTs	2.43
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	2.42
10	400672				2.41
	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	2.41
	449748	H23963	Hs.32043	ESTs	2.41
	453756	AW139415	Hs.61906	ESTs	2.41
	400624				2.40
	403125				2.40
15	406118				2.39
	402165				2.38
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	2.38
	425515	W26609		gb:35f12 Human retina cDNA randomly prim	2.38
	402951				2.37
20	427886	AA417083	Hs.104789	ESTs	2.37
	447173	AW449385	Hs.157294	ESTs	2.37
	448703	BE613942	Hs.170890	Homo sapiens cDNA: FLJ21129 fis, clone C	2.37
	426344	H41821	Hs.169393	transcriptional activator of the c-fos p	2.36
25	401840				2.35
	403731				2.34
	405378				2.34
	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	2.34
	416559	AI039195	Hs.128060	ESTs, Weakly similar to cDNA EST yk481g5	2.34
30	438216	Z83952	Hs.252815	ESTs	2.34
	448427	BE395260		gb:601311130F1 NIH_MGC_44 Homo sapiens c	2.34
	451588	AW072057		gb:ws58g05.x1 NCL_CGAP_Brn25 Homo sapien	2.34
	423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA	2.33
	451172	AW206465	Hs.207423	ESTs	2.33
	401015				2.32
35	414705	BE464157	Hs.281455	ESTs	2.32
	439894	AA853077		gb:NHTBCae03a05f1 Normal Human Trabecula	2.31
	446305	AW270149	Hs.254515	ESTs, Moderately similar to AF248953 1 g	2.31
	453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker pr	2.29
40	418556	T02850		gb:FB12A9 Fetal brain, Stralagene Homo s	2.28
	457197	AB016092	Hs.197114	RNA binding protein; AT-rich element bin	2.28
	457275	AA463422	Hs.209431	ESTs	2.28
	458766	AW183618	Hs.188417	ESTs, Weakly similar to ZnT-3 [H.sapiens	2.28
	414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	2.27
45	430210	AL157426	Hs.235390	Homo sapiens mRNA; cDNA DKFZp761B101 (fr	2.27
	442614	AI269030		gb:qj73c12.x1 NCL_CGAP_Kid3 Homo sapiens	2.27
	402538				2.26
	439891	AL389940	Hs.109968	ESTs	2.26
	440056	BE294828	Hs.13323	hypothetical protein FLJ22059	2.26
50	406150				2.25
	426880	AA453482		gb:zx47a11.r1 Soares_testis_NHT Homo sap	2.25
	447129	AW014123	Hs.161402	ESTs	2.25
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.25
	456778	AI458309	Hs.117406	ESTs	2.24
55	401728				2.23
	404139				2.23
	414095	BE293546		gb:601186671F1 NIH_MGC_15 Homo sapiens c	2.23
	432037	AW450592	Hs.300459	ESTs	2.23
	451965	AA021163	Hs.22287	ESTs	2.23
60	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	2.22
	427586	AA609661	Hs.190592	ESTs	2.22
	454108	AA161071	Hs.71465	squalene epoxidase	2.22
	429749	AI685174	Hs.22293	ESTs	2.21
	434507	AW511138	Hs.256581	ESTs	2.21
65	436652	AA724543	Hs.168824	ESTs	2.21
	437433	R74016	Hs.121581	ESTs	2.21
	401688				2.20
	441748	R14439	Hs.209194	ESTs	2.19
	453072	BE251845	Hs.221516	ESTs, Weakly similar to tetraspan TM4SF	2.19
70	400635				2.18
	417176	AW974475	Hs.143467	ESTs	2.18
	427858	NM_001971	Hs.21	elastase 1, pancreatic	2.18
	454886	AW837063		gb:QV1-LT0037-150200-069-g08 LT0037 Homo	2.18
	458232	BE217872	Hs.279537	ESTs	2.18
75	408922	R87388		gb:ym88g04.r1 Soares adult brain N2b4HB5	2.17
	423668	Y10148	Hs.131138	neurotensin receptor 2	2.17
	440338	R62431	Hs.12758	ESTs	2.17
	403115				2.16
	409125	R17268	Hs.301560	ESTs	2.16
80	426887	AI971975	Hs.212892	ESTs	2.16
	413811	BE168828		gb:QV1-HT0517-020400-145-f04 HT0517 Homo	2.15
	442962	AI025315	Hs.131615	ESTs	2.15
	403921				2.14
	413140	T06607	Hs.6846	hypothetical protein FLJ13055	2.14

	421996	AW583807	Hs.1460	glucagon	2.14
	436130	AA341497	Hs.31408	ESTs	2.14
	407243	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	2.13
5	407708	AF019968	Hs.37936	suppressor of variegation 3-9 (Drosophil	2.13
	442792	AI352340	Hs.131194	ESTs	2.12
	454406	AA213605	Hs.267861	ESTs	2.12
	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	2.11
	433963	AI218808	Hs.187778	ESTs	2.11
10	400736				2.10
	406343				2.10
	409702	AI752244	Hs.285749	Human DNA from chromosome 19-specific co	2.10
	432092	AF135026		gb:Homo sapiens kallikrein-like protein	2.10
	441915	AI566116	Hs.207066	ESTs, Weakly similar to FOG [M.musculus]	2.10
15	453147	AA733098	Hs.279909	CGI-05 protein	2.10
	415604	Z44177	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.08
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.08
	401211	AJ004832	Hs.5038	neuropathy target esterase	2.07
	413808	J00287	Hs.182183	caldesmon 1	2.07
20	414433	BE407755	Hs.169100	Homo sapiens cDNA FLJ12529 fis, clone NT	2.07
	421978	AJ243662	Hs.110196	NICE-1 protein	2.07
	431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	2.07
	433605	AI378012	Hs.147953	ESTs	2.06
	449383	AW444712	Hs.196573	ESTs	2.06
25	455652	BE064675		gb:RC1-BT0313-301299-012-h11 BT0313 Homo	2.05
	402382				2.04
	407282	AI345597	Hs.254727	ESTs	2.04
	457273	AI167145	Hs.165538	ESTs	2.04
	459073	AW968616	Hs.296234	ESTs, Highly similar to mitogen-activate	2.04
	402394				2.03
30	428875	AW451624	Hs.178202	ESTs	2.03
	456634	AA609911	Hs.109012	ESTs	2.03
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.02
	439281	AA100768	Hs.48485	ESTs	2.02
35	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	2.02
	401122				2.01
	444340	AI143198	Hs.143561	ESTs	2.01
	455104	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	2.01
	415011	AW963085		gb:EST375158 MAGE resequences, MAGH Homo	2.00
40	440144	AW082297	Hs.88523	ESTs	2.00
	403183				1.99
	409802	AW500732		gb:UI-HF-BN0-akm-h-07-0-UI.r1 NIH_MGC_50	1.98
	430144	AI732722	Hs.187694	ESTs	1.98
	444580	AI168365	Hs.268663	ESTs	1.98
45	401704				1.97
	401810				1.97
	424473	AK001405	Hs.148584	Homo sapiens cDNA FLJ10543 fis, clone NT	1.97
	438573	AW135084	Hs.299865	ESTs	1.97
	412921	BE009345	Hs.128942	ESTs	1.96
50	422233	AB002058	Hs.113275	purinergic receptor P2X-like 1, orphan r	1.96
	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin	1.96
	410285	AA083609		gb:zm63d05.r1 Stratagene fibroblast (937	1.95
	414323	NM_014759	Hs.239500	KIAA0273 gene product	1.94
	428119	AW298211	Hs.255737	ESTs	1.94
55	424510	AK001841	Hs.149797	hypothetical protein FLJ10979	1.92
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	1.92
	429785	H82114	Hs.301769	ESTs	1.92
	437344	R90921	Hs.6846	hypothetical protein FLJ13055	1.92
	451819	AI819096	Hs.249260	ESTs	1.92
60	459060	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein	1.92
	422664	AA315933	Hs.120879	ESTs	1.91
	432247	AA531287	Hs.105805	ESTs	1.91
	453820	R77494	Hs.75416	DAZ associated protein 2	1.91
	400675				1.90
65	405556	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	1.90
	407099	M94891	Hs.278423	pregnancy specific beta-1-glycoprotein 4	1.90
	440297	BE560553	Hs.205450	Homo sapiens cDNA: FLJ22570 fis, clone H	1.90
	443104	AA088470	Hs.83135	p53-responsive gene 6	1.90
	444329	W73753	Hs.58330	ESTs	1.90
	402690				1.89
70	432354	AW137262	Hs.192713	ESTs	1.89
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.88
	443322	AI825817	Hs.143272	ESTs	1.88
	458185	AI762757	Hs.129869	ESTs, Weakly similar to AF113685 1 PRO09	1.88
75	459072	AI815978	Hs.160427	ESTs	1.88
	402534				1.87
	409689	AA078492		gb:7P04D11 Chromosome 7 Placental cDNA L	1.87
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	1.87
	430176	AL161995	Hs.234775	neurturin	1.87
80	430631	AJ003147	Hs.278464	olfactory receptor, family 1, subfamily	1.87
	433114	AA121579		gb:zn77f02.r1 Stratagene NT2 neuronal pr	1.87
	439254	U57352	Hs.6517	amiloride-sensitive cation channel 1, ne	1.87
	448461	AW166358	Hs.124979	ESTs	1.87
	450675	AA010662	Hs.188639	ESTs	1.87

	401767				1.86
	449891	N64867	Hs.37848	ESTs	1.85
	400527				1.84
5	428581	AA430570	Hs.104881	ESTs	1.84
	443647	AV653846	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	1.84
	444785	AV651441	Hs.282475	ESTs	1.84
	449566	AA001778	Hs.288156	Homo sapiens cDNA: FLJ21819 fis, clone H	1.84
	436752	AW298529	Hs.255774	ESTs	1.83
10	437405	AA338837	Hs.42547	Homo sapiens cDNA FLJ13975 fis, clone Y7	1.83
	449174	T66136	Hs.12880	ESTs	1.83
	449887	AW080843	Hs.200275	ESTs	1.83
	453261	AA034116	Hs.118494	ESTs	1.83
	454243	AW241901	Hs.250683	ESTs	1.83
15	459188	AA216382	Hs.30002	SH3-containing protein SH3GLB2	1.83
	424334	AA393460		gb:zt71e05.r1 Soares_testis_NHT Homo sap	1.82
	432150	AK000224	Hs.272769	hypothetical protein FLJ20217	1.82
	408123	AW163377		gb:au94e02.y1 Schneider fetal brain 0000	1.81
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	1.80
20	442196	AI902646	Hs.31844	Homo sapiens cDNA FLJ12586 fis, clone NT	1.80
	421419	M99587	Hs.104134	homeo box (H6 family) 1	1.79
	405420				1.78
	405737				1.78
	414016	AA134594	Hs.71528	ESTs	1.78
25	415744	AW964850	Hs.279307	ESTs	1.78
	420375	AF182077	Hs.97244	glioma tumor suppressor candidate region	1.78
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	1.78
	421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila) homolog 1	1.77
	401743				1.75
	405187				1.75
30	442763	AI017037	Hs.131121	ESTs	1.75
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	1.75
	413248	T64858	Hs.21433	ESTs	1.74
	423913	NM_016436	Hs.301055	hepatocellular carcinoma-associated anti	1.74
35	439999	AA115811	Hs.6838	ras homolog gene family, member E	1.74
	440185	AW104546	Hs.270929	ESTs	1.74
	450482	AI697844	Hs.221720	ESTs	1.74
	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYD	1.73
	420476	AW575863	Hs.136232	ESTs	1.73
40	428748	AW593206	Hs.98785	ESTs	1.73
	431148	AA502653	Hs.28621	ESTs	1.73
	447205	BE617015	Hs.11006	ESTs	1.73
	455994	BE179190		gb:RC0-HT0613-210300-032-f07 HT0613 Homo	1.73
	401039				1.72
	403251				1.72
45	409762	AW498884	Hs.257970	ESTs	1.72
	440914	AA909552	Hs.143884	ESTs	1.72
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	1.72
	409605	AW444477	Hs.258507	ESTs	1.71
50	441212	AW242447	Hs.146182	ESTs, Weakly similar to lactase phlorizi	1.71
	445624	AW140103	Hs.78880	ilvB (bacterial acetolactate synthase)-I	1.71
	458619	AA872064	Hs.301218	ESTs, Weakly similar to Unknown gene pro	1.71
	401969				1.70
	403327				1.70
55	407245	X90568	Hs.172004	titin	1.70
	417361	NM_000275	Hs.82027	oculocutaneous albinism II (pink-eye dil	1.70
	436034	AF282693	Hs.150185	inflammation-related G protein-coupled r	1.70
	442682	AI014545	Hs.231027	EST	1.70
	458494	AI380906	Hs.158436	ESTs	1.70
	404682				1.69
60	407402	AF035303		gb:Homo sapiens clone 23943 mRNA sequenc	1.69
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	1.69
	440362	AA883812	Hs.125508	ESTs	1.69
	448866	BE297743	Hs.284203	myogenic factor 3	1.69
	402201				1.68
65	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.68
	403186				1.67
	409543	AW410200		gb:fh05b12.x1 NIH_MGC_17 Homo sapiens cD	1.67
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.67
70	450391	AI694522	Hs.202280	ESTs	1.67
	408919	AW295352	Hs.251836	ESTs	1.66
	416136	H45027	Hs.181770	ESTs	1.66
	416865	H97863	Hs.42456	ESTs	1.66
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	1.66
75	437237	BE513073		gb:601171435F1 NIH_MGC_15 Homo sapiens c	1.66
	429134	AA446953	Hs.99004	ESTs	1.65
	445041	T64183	Hs.11398	ESTs	1.65
	453240	AI969564	Hs.284249	Homo sapiens cDNA: FLJ22334 fis, clone H	1.65
	405243				1.64
80	426039	BE265133	Hs.217493	annexin A2	1.64
	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate	1.64
	435942	R06285	Hs.191215	ESTs	1.64
	448106	AI800470	Hs.171941	ESTs	1.64
	408591	AF015224	Hs.46452	mammaglobin 1	1.63

	410881	AW809157		gb:RC0-ST0118-041099-031-c07_1 ST0118 Ho	1.63
	417743	R14738	Hs.8312	ESTs, Weakly similar to AF170723 1 prote	1.62
	430632	AC004597	Hs.248088	olfactory receptor, family 10, subfamily	1.62
	448651	BE246440	Hs.93728	pre-B-cell leukemia transcription factor	1.62
5	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, c	1.62
	459499	AW402653	Hs.28355	Homo sapiens cDNA: FLJ22402 fis, clone H	1.62
	412374	X01388	Hs.73849	apolipoprotein C-III	1.61
	419113	AI446586	Hs.21835	ESTs	1.61
	426795	AI810474	Hs.196945	ESTs	1.61
10	426998	BE274360		gb:601121068F1 NIH_MGC_20 Homo sapiens c	1.61
	428407	NM_003963	Hs.184194	transmembrane 4 superfamily member 5	1.61
	444475	C75571		gb:C75571 Human pancreatic islet Homo sa	1.61
	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	1.61
	456275	AW976183	Hs.88414	ESTs, Weakly similar to dJ512E2.1 [H.sap	1.61
15	414060	BE246327		gb:TCBAP1E1967 Pediatric pre-B cell acut	1.60
	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	1.60
	428651	AF196478	Hs.188401	annexin A10	1.60
	443853	AI089064	Hs.250644	ESTs	1.60
	407007	U22961		gb:Human mRNA clone with similarity to L	1.59
20	412067	N45697		gb:yy78d01.r1 Soares_multiple_sclerosis_	1.59
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	1.59
	448619	AI867182	Hs.202255	ESTs	1.59
	403665				1.58
25	407524	X64985		gb:H.sapiens mRNA HTPCRX11 for olfactory	1.58
	424286	AA338285	Hs.90744	proteasome (prosome, macropain) 26S subu	1.58
	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	1.57
	430218	AW998865	Hs.186703	ESTs	1.57
	431882	NM_001426	Hs.271977	engrailed homolog 1	1.57
30	450797	AI761930	Hs.205127	ESTs	1.57
	455366	AW947563		gb:RC0-MT0004-140300-031-g11 MT0004 Homo	1.57
	408421	AW193734	Hs.253067	ESTs	1.56
	421907	BE018556	Hs.109358	ATPase, Class V, type 10B	1.56
	432742	AA564453	Hs.162339	ESTs	1.56
35	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	1.56
	439543	W75935	Hs.146083	ESTs	1.56
	443317	AI051601	Hs.200191	ESTs	1.56
	449097	BE271708	Hs.95110	ESTs, Weakly similar to PIP6_HUMAN 1-PHO	1.56
	457127	AA194554	Hs.183434	ATPase, H+ transporting, lysosomal (vacu	1.56
40	407387	AB000895		gb:Homo sapiens mRNA for cadherin FIB1,	1.55
	418837	U48263	Hs.89040	prepronociceptin	1.55
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.55
	458475	AI650322	Hs.143249	ESTs	1.55
	402561				1.54
45	411187	AW821291		gb:PM3-ST0307-241299-002-f03 ST0307 Homo	1.54
	419224	NM_012189	Hs.252716	fibrousheathin II	1.54
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	1.53
	415426	Z41991	Hs.23197	ESTs	1.53
	421428	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	1.53
50	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.53
	428489	AI807459	Hs.98582	ESTs	1.53
	437728	AA766719		gb:aa39c09.s1 NCL_CGAP_GCB1 Homo sapiens	1.53
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.52
	414932	C14577	Hs.194517	ESTs	1.52
55	433500	AF064255	Hs.111401	very long-chain acyl-CoA synthetase homo	1.52
	439688	AW445181	Hs.209637	Homo sapiens cDNA FLJ12921 fis, clone NT	1.52
	453391	AW600302	Hs.232655	ESTs	1.52
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	1.51
	436895	AF037335	Hs.5338	carbonic anhydrase XII	1.51
60	443012	AI566813	Hs.132278	ESTs	1.51
	415824	D42039	Hs.78871	mesoderm development candidate 2	1.50
	445152	AI214667	Hs.283597	ESTs	1.50
	455941	BE160011	Hs.129998	Homo sapiens cDNA FLJ14267 fis, clone PL	1.50
	457889	AL035964	Hs.69517	ESTs, Highly similar to differentially e	1.50
65	458503	AL133933	Hs.64310	interleukin 11 receptor, alpha	1.50
	400694				1.49
	420937	AW966719	Hs.1340	collpase, pancreatic	1.49
	426752	X69490	Hs.172004	titin	1.49
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.49
70	428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis t	1.49
	444287	AI033077	Hs.10755	dihydropyrimidinase	1.49
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.49
	425747	AI457620	Hs.205360	ESTs	1.48
	432378	AI493046	Hs.146133	ESTs	1.48
75	447999	AW138840	Hs.201778	ESTs	1.48
	453888	AW450670	Hs.252819	ESTs	1.48
	406667	M12523	Hs.75442	albumin	1.47
	418129	X52997	Hs.1144	glycoprotein IX (platelet)	1.47
	426309	AI912555	Hs.157195	peptide YY, 2 (seminalplasmin)	1.47
80	426755	BE253469		gb:601108143F1 NIH_MGC_16 Homo sapiens c	1.47
	414258	AA203285	Hs.294141	ESTs, Weakly similar to dJ733D15.1 [H.sa	1.46
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	1.46
	420562	AI345569	Hs.190046	ESTs	1.46
	425011	T51986	Hs.283108	hemoglobin, gamma G	1.46

	443050	AI612788	Hs.132348	ESTs, Weakly similar to diaphanous 1 [H.	1.46
	411074	XG0435	Hs.68137	adenylate cyclase activating polypeptide	1.45
	434680	T11738	Hs.127574	ESTs	1.45
5	454771	AW819939	Hs.273629	ESTs	1.45
	415672	N53097	Hs.193579	ESTs	1.44
	418141	AW845738	Hs.171118	Homo sapiens mRNA for FLJ00026 protein,	1.44
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.43
	418197	AA214253		gb:zn58g02.r1 Stratagene muscle 937209 H	1.43
10	431821	AW452256	Hs.271221	hypothetical protein FLJ20064	1.43
	455433	AW939463		gb:QV1-DT0072-310100-056-g02 DT0072 Homo	1.43
	407743	AW814118		gb:MR3-ST0203-151199-011-d09 ST0203 Homo	1.42
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	1.42
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	1.42
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.42
15	452456	BE080763		gb:QV1-BT0631-150200-071-f09 BT0631 Homo	1.42
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit Vb	1.42
	408349	BE546947	Hs.44276	homeo box C10	1.41
	420391	AA456891	Hs.79123	KIAA0084 protein	1.41
20	421126	M74587	Hs.102122	insulin-like growth factor binding prote	1.41
	449329	AW752783		gb:IL3-CT0219-221199-029-F03 CT0219 Homo	1.41
	453615	AA195712	Hs.132696	ESTs	1.41
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	1.40
	420287	AA740907	Hs.88297	ESTs	1.40
25	427583	M82962	Hs.179704	meprin A, alpha (PABA peptide hydrolase)	1.40
	418787	AW296134	Hs.86999	ESTs	1.39
	422072	AB018255	Hs.111138	KIAA0712 gene product	1.39
	425988	BE045897	Hs.274454	ESTs	1.39
	428087	AA100573	Hs.182421	troponin C2, fast	1.39
30	438136	NM_002390	Hs.6088	a disintegrin and metalloproteinase doma	1.39
	455579	BE011320		gb:PM3-BN0218-090500-002-d09 BN0218 Homo	1.39
	402316				1.38
	417084	H08370	Hs.33067	ESTs	1.38
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	1.38
35	433787	AI472951	Hs.173688	ESTs	1.38
	413830	BE263439	Hs.13144	HSPC160 protein	1.37
	423576	NM_000383	Hs.129829	autoimmune regulator (autommune polyen	1.37
	401886				1.36
	412688	AW583062	Hs.74502	chymotrypsinogen B1	1.36
40	401238				1.34
	421511	AA488940	Hs.105216	hypothetical protein FLJ11125	1.34
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11	1.34
	425450	U14755	Hs.157449	LIM homeobox protein 1	1.34
	427333	AF067797	Hs.176658	aquaporin 8	1.34
45	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	1.34
	445204	AW135523	Hs.245853	ESTs	1.34
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (f	1.34
	456379	W22206		gb:63E10 Human retina cDNA Tsp5091-cleav	1.34
	457416	BE142052		gb:CM3-HT0137-150999-011-b05 HT0137 Homo	1.34
50	415741	AI902761	Hs.272087	ESTs	1.33
	422260	AA315993	Hs.105484	ESTs, Weakly similar to LITB_HUMAN LITHO	1.33
	429188	AB011171	Hs.198037	KIAA0599 protein	1.33
	442776	AW959498	Hs.8709	chymotrypsin C (caldecrin)	1.33
	454748	AW862014		gb:RC3-CT0347-160200-013-d09 CT0347 Homo	1.33
55	437744	AW290905	Hs.300288	ESTs, Weakly similar to CGHU2E collagen	1.32
	451997	AA021351	Hs.158497	KIAA0724 gene product	1.32
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	1.32
	411879	BE145354	Hs.273758	Homo sapiens cDNA: FLJ23112 fis, clone L	1.31
	424304	NM_001395	Hs.144879	dual specificity phosphatase 9	1.31
60	401442				1.30
	403942				1.30
	443687	F13040	Hs.182937	peptidylprolyl isomerase A (cyclophilin	1.30
	401624				1.29
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	1.29
65	418575	AA225313	Hs.222886	ESTs	1.29
	419818	AI657122	Hs.301931	ESTs	1.29
	429845	AB020337	Hs.225943	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	1.29
	447586	AI081980	Hs.285829	solute carrier family 25 (mitochondrial	1.29
	407013	U35637		gb:Human nebulin mRNA, partial cds	1.28
70	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	1.28
	429780	AL137518	Hs.300388	ESTs	1.28
	453539	AW731886	Hs.95196	ESTs, Weakly similar to T20B12.3 [C.eleg	1.28
	400846				1.27
	420257	AA257035	Hs.190042	ESTs	1.27
75	429184	AF095735	Hs.198003	sarcosine dehydrogenase	1.27
	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	1.27
	444412	AI147652	Hs.216381	Homo sapiens clone HH409 unknown mRNA	1.27
	451139	AW293316	Hs.205558	ESTs	1.27
	431284	AA570148	Hs.126783	Homo sapiens cDNA: FLJ22610 fis, clone H	1.26
80	431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	1.26
	406158				1.25
	419648	T73661	Hs.91877	ESTs, Highly similar to THIH_HUMAN THYRO	1.25
	430681	AW969675	Hs.291232	ESTs	1.25
	434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.25

	436217	T53925	Hs.107	fibrinogen-like 1	1.25
	440089	AA864468	Hs.135646	ESTs	1.25
	446787	U67167	Hs.315	mucin 2, intestinal/tracheal	1.25
5	448207	AI475490	Hs.170577	ESTs	1.25
	454869	AW836004		gb:PM0-LT0019-170200-001-d11 LT0019 Homo	1.25
	413271	AA127873	Hs.114949	ESTs	1.24
	422619	AA313322		gb:EST185218 Colon carcinoma (HCC) cell	1.24
	422796	AW897265		gb:CM0-NN0057-150400-335-a04 NN0057 Homo	1.24
10	427530	AA405093	Hs.126519	ESTs	1.24
	437727	AA766707	Hs.153039	ESTs	1.24
	426435	AI827946	Hs.189118	ESTs	1.23
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	1.22
	407964	AW130334	Hs.281111	ESTs	1.21
	430828	AI763257	Hs.86327	Homo sapiens cDNA: FLJ22431 fis, clone H	1.21
15	432029	D31628	Hs.2899	4-hydroxyphenylpyruvate dioxygenase	1.21
	457843	AW138211	Hs.128746	ESTs	1.21
	413242	BE074165		gb:PM3-BT0564-030300-002-e12 BT0564 Homo	1.20
	446057	AI420227	Hs.149358	ESTs	1.20
	447198	D61523	Hs.283435	ESTs	1.20
20	449513	AI653232	Hs.195059	EST	1.20
	415566	F12119		gb:HSC35H091 normalized infant brain cDN	1.19
	423315	R54109	Hs.26096	ESTs	1.19
	455817	BE142384		gb:CM2-HT0144-210999-011-d04 HT0144 Homo	1.19
25	459354	BE514778		gb:601317094F1 NIH_MGC_9 Homo sapiens cD	1.19
	408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	1.18
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.18
	419251	NM_001486	Hs.89771	glucokinase (hexokinase 4) regulatory pr	1.18
	456702	AI684534		gb:wa72f10.x1 Soares_NFL_T_GBC_S1 Homo s	1.18
	458009	AI221409	Hs.144983	ESTs	1.18
30	410193	AJ132592	Hs.59757	zinc finger protein 281	1.17
	417779	AA829526	Hs.124977	ESTs	1.17
	435101	AI743156	Hs.131064	ESTs	1.17
	445360	AI798776	Hs.156029	ESTs	1.17
	414160	BE257021		gb:601117426F1 NIH_MGC_16 Homo sapiens c	1.15
35	418078	AA521268	Hs.86508	ESTs	1.15
	425133	NM_002613	Hs.154729	3-phosphoinositide dependent protein kin	1.15
	437935	AW939591	Hs.5940	hypothetical protein FLJ20063	1.15
	446377	AW014022	Hs.170953	ESTs	1.15
40	420097	AA700127	Hs.190504	ESTs	1.13
	446591	H44186	Hs.15456	PDZ domain containing 1	1.13
	451477	AI798425	Hs.42710	ESTs	1.13
	459197	BE244587		gb:TCBAP2E0851 Pediatric pre-B cell acut	1.13
	428934	AF039401	Hs.194659	chloride channel, calcium activated, fam	1.12
45	431191	AW972118	Hs.100002	HSPC162 protein	1.12
	424403	F05183	Hs.1799	CD1D antigen, d polypeptide	1.11
	433546	AI075877	Hs.125461	Homo sapiens cDNA FLJ11539 fis, clone HE	1.11
	451179	W05469	Hs.31818	ESTs	1.11
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	1.10
50	420774	AA280209	Hs.165270	ESTs	1.10
	428887	AA437009	Hs.98984	ESTs	1.10
	430582	AI215509	Hs.143964	ESTs	1.10
	453642	AI370936	Hs.34074	diptidylpeptidase VI	1.10
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.09
55	417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo	1.09
	456387	W28876		gb:52h7 Human retina cDNA randomly prime	1.09
	427965	D00306	Hs.183864	elastase 3B	1.08
	447388	AW630534	Hs.76277	ESTs, Weakly similar to TB2 [H.sapiens]	1.08
	413841	M34276	Hs.75576	plasminogen	1.07
60	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.07
	433313	W20128	Hs.296039	ESTs	1.07
	439450	R51613	Hs.125304	ESTs	1.07
	458963	AI701393	Hs.278728	Rad and Gem-related 2 (rat homolog)	1.07
	405161				1.06
65	406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	1.06
	424294	BE299311		gb:601119256F1 NIH_MGC_17 Homo sapiens c	1.06
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.06
	444687	AW972109	Hs.135107	ESTs	1.06
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	1.06
70	421243	AW873803	Hs.102876	pancreatic lipase	1.05
	444290	AA262496	Hs.29280	ESTs	1.05
	407984	AW134708	Hs.243569	ESTs	1.04
	439706	AW872527	Hs.59761	ESTs	1.04
	402194				1.03
75	427506	AK000134	Hs.179100	hypothetical protein FLJ20127	1.03
	428819	AL135623	Hs.193914	KIAA0575 gene product	1.03
	434590	T47232		gb:yb64b08.s1 StrataGene ovary (937217)	1.03
	416378	AW044467	Hs.73708	ESTs, Weakly similar to A57291 cytokine	1.02
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	1.02
80	443316	AI478463	Hs.18443	ESTs	1.02
	428585	AB007863	Hs.185140	KIAA0403 protein	1.01
	400440	X83957	Hs.83870	nebulin	1.00
	404619	BE514535	Hs.77171	minichromosome maintenance deficient (S.	1.00
	407168	R45175		gb:yg40f01.s1 Soares infant brain 1N1B H	1.00

	408052	AW501117	Hs.283585	ESTs	1.00
	409187	AF154830	Hs.50966	carbarnoyl-phosphate synthetase 1, mitoch	1.00
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	1.00
5	410234	NM_003837	Hs.61255	fructose-1,6-bisphosphatase 2	1.00
	410319	R23413	Hs.71935	putative zinc finger protein from EUOIM	1.00
	411000	N40449	Hs.201619	ESTs, Weakly similar to SEB4B [H.sapiens	1.00
	412098	AI493054	Hs.158968	ESTs	1.00
	412446	AI768015	Hs.92127	ESTs	1.00
10	412637	AA115097	Hs.261313	ESTs	1.00
	413147	BE067271		gb:PM2-BT0349-161299-001-b05 BT0349 Homo	1.00
	413597	AW302885	Hs.117183	ESTs	1.00
	414117	W88559	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	1.00
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	1.00
15	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	1.00
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	1.00
	419768	T72104	Hs.93194	apolipoprotein A-I	1.00
	420182	Z44245	Hs.22999	ESTs	1.00
	420923	AF097021	Hs.273321	differentially expressed in hematopiet	1.00
20	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.00
	421204	AW081587	Hs.165051	ESTs	1.00
	422189	AF252292	Hs.112933	Tax interaction protein 40	1.00
	422792	AI951548	Hs.135163	ESTs	1.00
	423371	AU076819	Hs.1650	solute carrier family 26, member 3	1.00
25	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.00
	424922	BE386547	Hs.217112	ESTs, Weakly similar to Similarity to Ye	1.00
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	1.00
	425545	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	1.00
	425983	AK000226	Hs.165619	mucin and cadherin-like	1.00
30	426004	AW600300	Hs.124123	ESTs, Weakly similar to syncollin [R.nor	1.00
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	1.00
	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	1.00
	429027	AL022314	Hs.194750	Human DNA sequence from clone 1170K4 on	1.00
	429231	AA813214		gb:aj32e09.s1 Soares_testis_NHT Homo sap	1.00
35	429441	AJ224172	Hs.204096	lipophilin B (uterglobin family member)	1.00
	429930	AI580809	Hs.99569	ESTs	1.00
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1.00
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	1.00
	431845	AA516469	Hs.270554	ESTs	1.00
40	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	1.00
	433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00
	434452	AA634333	Hs.116822	ESTs	1.00
	435499	R89344	Hs.14148	ESTs	1.00
	438433	AB018274	Hs.6214	KIAA0731 protein	1.00
45	442403	AW207724	Hs.129516	ESTs	1.00
	442803	AI675298	Hs.199917	ESTs	1.00
	443266	AI277101	Hs.25890	ESTs, Weakly similar to transducin [H.sa	1.00
	444656	AI277924	Hs.145199	ESTs	1.00
	445573	AI439646	Hs.157494	ESTs, Weakly similar to KIAA0676 protein	1.00
50	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00
	447359	NM_012093	Hs.18268	adenylate kinase 5	1.00
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac mus	1.00
	448657	BE147857	Hs.293841	ESTs, Weakly similar to KIAA0672 protein	1.00
	449238	AA428229	Hs.85524	muscle-specific RING-finger protein homo	1.00
55	450085	AW293791	Hs.60162	Homo sapiens cDNA: FLJ21528 fis, clone C	1.00
	450390	N93227	Hs.98403	ESTs	1.00
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	1.00
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	1.00
	452528	AA742457	Hs.291479	ESTs	1.00
60	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	1.00
	453754	AW972580	Hs.172753	ESTs	1.00
	453991	AW014915	Hs.273741	ESTs	1.00
	454517	AW803340		gb:IL2-UM0079-090300-050-D02 UM0079 Homo	1.00
	459367	BE148877		gb:CM4-HT0244-111199-040-h12 HT0244 Homo	1.00
65	408021	AW137133	Hs.245867	ESTs	0.99
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	0.99
	437206	AW975934	Hs.283382	ESTs, Weakly similar to Protein sequence	0.99
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial	0.98
	425878	AW964806	Hs.38085	ESTs, Weakly similar to putative glycine	0.98
70	441888	AI733306	Hs.128071	hypothetical protein FLJ21302	0.98
	423068	M25629	Hs.123107	kallikrein 1, renal/pancreas/salivary	0.97
	453534	NM_014796	Hs.33187	KIAA0748 gene product	0.97
	457787	AA683268		gb:ae92b04.s1 Stratagene schizo brain S1	0.97
75	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	0.96
	422069	AJ010063	Hs.111110	titin-cap (telethonin)	0.96
	425260	L47726	Hs.1870	phenylalanine hydroxylase	0.96
	418406	X73501	Hs.84905	cytokeratin 20	0.95
	425670	AW968536	Hs.190146	ESTs	0.95
	416373	AA195845	Hs.73680	ESTs, Weakly similar to AF198455 1 epith	0.94
80	452243	AL355715	Hs.28555	programmed cell death 9	0.94
	411908	L27943	Hs.72924	cytidine deaminase	0.93
	415067	AI264969	Hs.929	myosin, heavy polypeptide 7, cardiac mus	0.93
	437156	AI916600	Hs.121194	Homo sapiens cDNA: FLJ21569 fis, clone C	0.93
	450685	L15533	Hs.423	pancreatitis-associated protein	0.92

	427450	AB014526	Hs.178121	KIAA0626 gene product	0.91
	432440	X63597	Hs.2996	sucrase-isomaltase	0.91
	426651	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.90
5	414910	X12662	Hs.29679	cofactor required for Sp1 transcriptiona	0.89
	423317	AJ272204	Hs.64616	chromosome 12 open reading frame 3	0.89
	424735	U31875	Hs.152677	Homo sapiens cDNA FLJ20338 fis, clone HE	0.89
	439751	AA196090	Hs.50794	Homo sapiens mRNA full length insert cDN	0.89
	452689	F33868	Hs.284176	transferrin	0.89
10	446240	AI535736	Hs.170165	ESTs	0.88
	449110	H56112	Hs.277053	ESTs	0.88
	453817	AW755253	Hs.61920	ESTs	0.88
	428221	U96781	Hs.183075	ESTs, Highly similar to Ca2+ ATPase of f	0.87
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	0.87
15	446525	AW967069	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone H	0.87
	453341	AI758912	Hs.296341	adenylyl cyclase-associated protein 2	0.87
	403740				0.86
	420156	AW449258	Hs.6187	ESTs	0.86
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.86
20	421142	AW503944	Hs.130822	ESTs	0.85
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	0.85
	419415	AW451692	Hs.192036	ESTs	0.84
	423321	AB013885	Hs.126926	beta-ureidopropionase	0.84
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	0.84
25	433447	U29195	Hs.3281	neuronal pentraxin II	0.84
	403047				0.83
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	0.81
	407782	AA608956	Hs.112619	ESTs, Weakly similar to PQ0109 Purkinje	0.81
	405232				0.80
30	437776	AA768037	Hs.291671	ESTs	0.80
	415505	R39870	Hs.12548	ESTs	0.79
	444436	N25871	Hs.177337	ESTs	0.78
	409096	AA194412	Hs.50550	sarcomeric muscle protein	0.77
	432134	AI816782	Hs.122583	Homo sapiens cDNA: FLJ21934 fis, clone H	0.76
35	437066	AA743570	Hs.200935	ESTs	0.76
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	0.75
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	0.73
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	0.71
	420567	AK000812	Hs.98874	similar to proline-rich protein 48	0.71
40	447145	AA761073	Hs.192943	ESTs	0.71
	452103	R42764	Hs.3248	mutS (E. coli) homolog 6	0.71
	410929	H47233	Hs.30643	ESTs	0.70
	400301	X03635	Hs.1657	estrogen receptor 1	0.69
	415702	F28877		gb:HSPD18414 HM3 Homo sapiens cDNA clone	0.67
45	411396	C04646	Hs.85428	ESTs	0.65
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	0.65

TABLE 28B

50	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
55	Pkey	CAT number
	407743	1012151_1
	408123	1040435_1
	408432	1058667_1
60	408664	1073340_1
	408922	109017_1
	409368	112377_1
	409543	1138723_1
	409689	114833_1
65	409778	1154206_1
	409802	1155179_1
	410285	119128_1
	410881	1225682_1
	411187	1235092_1
70	412067	1275641_1
	413147	1350637_1
	413242	1355323_1
	413811	1391117_1
	414060	1413697_1
75	414095	1416521_1
	414160	1422273_1
	414580	1463848_1
	415011	151328_1
	415566	1539861_1
80	415702	1547874_1
	417998	171375_1
	418197	172864_1
	418464	1759038_-2
	418556	1767866_-1

	422619	218670_1	AA313322 BE408282 AA465612 BE073382
	422796	221500_1	AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361 T06241 AA326794 AL138130
5	424294	237907_1	BE299311 AA338954 AA338468 AW960907
	424334	238221_1	AA393460 AA338940 AW966277 AA419006
	424648	241947_1	AA344576 AA732430 AA344601
	425515	252721_1	W26609 W27360 AA358818
	426328	264901_1	AW631296 AA375484
10	426507	268382_1	AA380285 AW934727 AW934914
	426755	271382_1	BE253469 BE176417 BE176415 AA384133
	426880	273277_2	AA453482 AF012388
	426998	274259_1	BE274360
	429231	301463_1	AA813214 AI936567 AI743529 AA448279 AA994476 AI807452 AI218180 AA972858
15	430728	322706_1	AW968522 AA485112 AA485162 AW968698
	432092	34124_1	AF135026 AA583908
	433114	35904_1	AA121579 AB005217
	434590	38931_1	T47232 AF147365 T47231
	437237	43506_2	BE513073
20	437728	441520_1	AA766719 AA767041 AW977440
	439894	478738_1	AA853077 AA852175
	442197	535550_1	AW837912 AW837934 AA984475 AW997490
	442614	547073_1	AI269030 AI204085 AI004047
	444475	607874_1	C75571 AI150469 T10778
25	448427	762970_1	BE395260 AW291036 AI500420
	449329	80484_1	AW752783 H38266 AA001166
	451588	87667_1	AW072057 AI225096 AA018702
	452456	918391_1	BE080763 T96699 BE081135 AI902630 H49182 AI904021 AI902697
	454517	1221063_1	AW803340 AW803280 AW803275 AW803415 AW803343 AW803422
30	454748	1233013_1	AW862014 AW858740 AW858735 AW818542 AW858765 AW862027 AW858771 AW858773
	454869	1238137_1	AW836004 AW836087 AW836163 AW836162 AW836085 AW836084 AW836079 AW836083 AW836086 AW836088 AW836166 AW836164
			AW836002 AW836078 AW836161 AW862135 AW836165 AW836003
	454886	1238987_1	AW837063 AW935882 AW935957
	455075	1252389_1	AW854850 AW854848
35	455104	1253737_1	BE064863 BE153698 AW856751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AW856622 BE155079 BE064651 BE153665
			BE064650 BE064691
	455366	1284685_1	AW947563 AW947543 AW947553 AW947549 AW947717 AW902859 AW902927 BE011032
	455433	1290311_1	AW939463 AW939484 AW939480 AW939459 AW939546 AW939593 AW939548 AW939595 AW939106
	455446	1291969_1	AW947749 AW947746 AW947754 AW946636 AW946674
40	455579	1333944_1	BE011320 BE006381 BE006361 BE011180 BE011328 BE011325 BE011157 BE006384 BE006387 BE006385 BE011160 BE011319 BE011346
			BE006370 BE006386 BE011173 BE006389 BE006376 BE006375 BE006364 BE011321 BE006379
	455652	1348736_1	BE064675 BE064761 BE064809 BE064673 BE064672 BE064674
	455817	1371986_1	BE142384 BE142387
	455994	1398737_1	BE179190 BE179206 BE179182 BE179185 BE179186 BE179194
45	456150	1574395_1	Z42308 H23514
	456379	1839113_2	W22206 W22498 W26922
	456387	1842730_1	W28876 W26158
	456702	219191_1	AI684534 BE262411 AA314031 AW752724
	457416	334503_1	BE142052 AW265588 AA506741
50	457787	407235_1	AA683268 BE002903 BE002672
	458764	73207_1	BE619386 AA300887
	459197	924229_1	BE244587 AW938684 AW176490 AI940102 AW844995 AW938670 AI909850 AI909885 AI940079 AI909873
55	TABLE 28C		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.	
60	Strand:	Indicates DNA strand from which exons were predicted.	
	Nt_position:	Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand
65	400489	8954013	Plus
	400527	9796886	Plus
	400545	9800107	Minus
	400624	7228177	Minus
	400635	8567750	Minus
70	400672	8118724	Minus
	400675	8118750	Plus
	400694	8118802	Plus
	400736	8118985	Plus
	400846	9188605	Plus
75	401007	8117333	Minus
	401015	8117441	Plus
	401039	7232177	Plus
	401122	8570296	Plus
	401238	9954455	Minus
80	401442	8346725	Minus
	401496	7381769	Minus
	401590	9966320	Minus
	401603	7689963	Minus
	401624	8575907	Plus

	401688	2347081	Plus	22016-22624
	401704	3097841	Plus	24712-25374
	401728	8134856	Minus	82117-82920
5	401743	2865207	Plus	115475-115640
	401767	9958312	Plus	156823-156921,157364-157554
	401810	7342191	Plus	129063-129476
	401840	7684597	Plus	56283-56439
	401886	7229913	Minus	79215-79393
10	401919	9502466	Plus	67536-67666
	401969	3126777	Plus	44863-45366
	402051	8082020	Minus	19346-19480,20041-20119
	402056	8084234	Plus	207002-207288
	402153	8247879	Minus	122580-122987
15	402158	8516165	Minus	148298-148429,148566-148677
	402165	8569830	Minus	65064-65979
	402194	8576113	Plus	70917-71191
	402195	7689778	Minus	147901-148884
	402201	8576119	Plus	655-951
20	402316	7527774	Minus	10751-10919,18817-19052,22131-22328
	402382	9690314	Minus	155331-155528
	402386	9799769	Plus	22069-22303
	402394	9929690	Plus	33308-33482
	402409	9796255	Minus	8571-10061
25	402423	9796344	Minus	62487-62664
	402448	9796640	Plus	112942-113069,114303-114521
	402457	9796782	Minus	16513-16577,16838-16926
	402534	9801061	Plus	58989-59457
	402538	9801137	Minus	96314-96539
30	402561	9864675	Plus	72967-73163
	402588	9908948	Minus	33027-33183,59060-59198
	402690	8348058	Plus	13368-13998
	402714	8969253	Minus	18811-18886,19105-19328,19525-19764
	402762	9230904	Minus	123298-124035
35	402862	2956660	Minus	18518-18656
	402911	7263904	Plus	142689-142979
	402951	9408717	Plus	73252-73329,73718-73877,76217-76299,78195-78401
	402968	9581763	Minus	58658-58924
	403047	3540153	Minus	59793-59968
40	403115	7331404	Minus	142952-143094,145474-145653,146269-146445,152816-152998
	403125	9180936	Minus	197548-197712
	403183	9838273	Plus	109930-110074
	403186	9838287	Minus	117513-117856
	403211	7630841	Minus	159211-159369
45	403247	7656833	Minus	76626-77140
	403251	7677983	Plus	100391-100652
	403327	8440025	Minus	174311-174451,174587-174705,175523-175592
	403376	9369545	Minus	108698-108830
	403479	7329292	Minus	148369-148533,150678-150809
50	403526	8017144	Plus	55367-55483
	403540	8077057	Minus	56315-56450
	403605	6862654	Plus	91614-91718
	403612	8469060	Minus	94723-94859
	403665	7249278	Plus	69027-69375
55	403716	7239669	Plus	86899-87122
	403731	7543752	Minus	144000-144618
	403740	7630882	Plus	86504-87227
	403921	7711590	Minus	3297-3536
	403942	7711825	Minus	99606-99757
60	403997	7708819	Plus	134427-134593
	404139	9838113	Plus	76707-76891
	404247	7406725	Minus	83949-84214,84312-84415,84499-84677,84878-85114
	404282	2276311	Plus	61503-62205
	404348	7630858	Minus	28895-29062
65	404668	9797204	Minus	11332-11546,12584-12718
	404682	9797231	Minus	40977-41150
	404795	4826439	Plus	147501-147780
	404825	6478944	Plus	210382-210494
	404938	7381808	Minus	165838-165950
70	405075	7770506	Minus	124680-125321
	405147	9438278	Minus	158996-159557
	405161	9966260	Plus	157607-157785
	405163	9966267	Minus	161171-161299
	405187	7229826	Plus	117025-117170,118567-118736
75	405217	7239551	Plus	32646-33138
	405232	7249042	Plus	125904-126063
	405243	7249201	Minus	22312-23197
	405327	6094661	Minus	120550-120750
	405378	6491714	Plus	91139-91440
80	405420	7211837	Minus	13428-13582
	405703	4240388	Minus	15850-16061
	405737	9943984	Minus	104275-104508,104755-104877
	405895	7677903	Minus	66990-67484
	406059	9103984	Minus	13856-14004

406101	9124019	Plus	125325-125831
406118	9143818	Plus	53997-54629
406150	9886026	Minus	59331-59701
406158	7144874	Plus	62393-63016,65012-65578
406343	9255974	Plus	17284-17440,18489-18646,18917-19004,19384-19538
406357	9256093	Minus	77181-77415
406563	7711604	Plus	34401-34538

TABLE 29A: 2286 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO NORMAL BODY

Table 29A lists about 2286 genes that are up regulated in idiopathic pulmonary fibrosis samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis expression level to "average" normal adult tissues sample expression was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of IPF to normal body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	211.8
442275	AW449467	Hs.54795	ESTs	189.7
431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	134.1
441835	AB036432	Hs.184	advanced glycosylation end product-speci	130.4
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	116.8
421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	92.1
406964	M21305		gb:Human alpha satellite and satellite 3	80.7
443709	AI082692	Hs.134662	ESTs	67.1
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	61.4
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	57.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	54.6
457200	U33749	Hs.197764	thyroid transcription factor 1	44.9
432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	42.7
443324	R44013	Hs.164225	ESTs	39.8
414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	27.3
442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypotheti	27.1
444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	27.1
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	26.9
424084	AI940675	Hs.20914	hypothetical protein FLJ23056	22.2
421659	NM_014459	Hs.106511	protocadherin 17	21.0
450478	AW451709	Hs.271200	ESTs	20.2
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	19.7
447033	AI357412	Hs.157601	ESTs	19.4
445885	AI734009	Hs.127699	KIAA1603 protein	18.9
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	17.9
432437	W07088	Hs.293685	ESTs	17.8
424105	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1	17.3
431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	17.2
440807	AW269421	Hs.128093	ESTs	16.7
424917	AI636208	Hs.96901	hypothetical protein FLJ23049	16.4
433365	AF026944	Hs.293797	ESTs	16.4
445279	R41900	Hs.22245	ESTs	16.4
417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	16.4
405654				16.1
449328	AI962493	Hs.197647	ESTs	16.1
449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	15.7
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	15.5
417728	AW138437	Hs.24790	KIAA1573 protein	15.0
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	14.8
452039	AI922988	Hs.172510	ESTs	14.4
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	14.3
421464	AA291553	Hs.190086	ESTs	14.1
421554	AW137676	Hs.97775	ESTs	13.8
431889	AA521277	Hs.124946	ESTs, Weakly similar to A46010 X-linked	13.2
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	13.2
431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	12.9
459702				12.7
421110	AJ250717	Hs.1355	cathepsin E	12.6
407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	12.6
423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	12.5
423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	12.2
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	12.1
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	12.1
451561	N52812	Hs.177403	ESTs	12.0
424086	AI351010	Hs.102267	lysyl oxidase	12.0
435299	AI745458	Hs.122614	ESTs, Weakly similar to T20593 hypotheti	12.0
429496	AA453800	Hs.192793	ESTs	11.9

	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
	403637				11.2
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	11.2
5	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	10.9
	421470	R27496	Hs.1378	annexin A3	10.8
	440209	H05049	Hs.22269	neurexin 3	10.8
	428927	AA441837	Hs.90250	ESTs	10.7
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	10.5
10	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	10.4
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	10.4
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.4
	442176	AA983764	Hs.128910	ESTs	10.4
	439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
15	452883	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture	10.3
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	10.3
	422022	AA302420	Hs.200442	ESTs	10.3
	447724	AW298375	Hs.24477	ESTs	10.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	10.0
20	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	9.9
	446232	AI281848	Hs.194691	retinoic acid induced 3	9.9
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	9.9
	453382	AA709285	Hs.5997	hypothetical protein FLJ13078	9.8
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	9.8
25	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H	9.8
	407568	AA740964	Hs.62699	ESTs	9.8
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	9.6
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	9.5
	441484	AA935481	Hs.58972	ESTs	9.5
30	422426	W79117	Hs.58559	ESTs	9.4
	406747	AI925153	Hs.217493	annexin A2	9.4
	450050	AI681268	Hs.257883	ESTs	9.4
	431337	N48107	Hs.292593	ESTs	9.3
	408427	AW194270	Hs.177236	ESTs	9.3
35	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	9.3
	453636	R67837	Hs.169872	ESTs	9.3
	443450	N66045	Hs.133529	ESTs	9.2
	418735	N48769	Hs.44609	ESTs	9.2
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	9.1
40	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	9.1
	441233	AA972965	Hs.135568	ESTs	9.1
	459587	AA031956		gb:zkl5e04.s1 Soares_pregnant_uterus_NbH	9.0
	436246	AW450963	Hs.119991	ESTs	9.0
	445189	AI936450	Hs.147482	ESTs	8.9
45	410781	AI375672	Hs.165028	ESTs	8.9
	446868	AV660737	Hs.135100	ESTs	8.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	8.8
	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	8.8
50	410334	AW979261	Hs.291993	ESTs	8.8
	442510	AF150179	Hs.249890	ESTs	8.8
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	8.7
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	8.7
	444929	AI685841	Hs.161354	ESTs	8.7
55	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	8.6
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	8.6
	412719	AW016610	Hs.129911	ESTs	8.6
	453445	AL036532	Hs.91453	ESTs	8.5
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	8.5
60	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	8.5
	433815	AI696602	Hs.112757	ESTs	8.3
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	8.3
	451103	R52804	Hs.25956	DKFZP564D206 protein	8.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	8.3
65	424989	AA985520	Hs.23575	ESTs	8.3
	433231	AB040926	Hs.143552	KIAA1493 protein	8.2
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	8.1
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	8.1
	436751	AA732217	Hs.294054	ESTs	8.0
70	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	8.0
	413048	M93221	Hs.75182	mannose receptor, C type 1	8.0
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	7.9
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	7.8
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	7.8
75	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.7
	421013	M62397	Hs.1345	mutated in colorectal cancers	7.7
	437479	R61866	Hs.101277	ESTs	7.6
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	7.6
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	7.6
80	444396	T65213	Hs.4257	ESTs	7.6
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	7.6
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.6
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	7.6
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	7.6

	449108	AI140683	Hs.98328	hypothetical protein MGC13040	7.5
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.5
	416030	H15261	Hs.21948	ESTs	7.5
5	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	7.4
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	7.4
	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	7.3
	432133	AB033088	Hs.272567	KIAA1262 protein	7.3
	447112	H17800	Hs.7154	ESTs	7.3
10	446917	AI347863	Hs.156672	ESTs	7.3
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.3
	431761	AW002846	Hs.105468	hypothetical protein FLJ22690	7.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	7.2
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	7.2
15	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	7.2
	438122	AI620270	Hs.129837	ESTs, Weakly similar to Z263_HUMAN ZINC	7.2
	449611	AI970394	Hs.197075	ESTs	7.2
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	7.2
	410060	NM_001448	Hs.58367	glypican 4	7.2
20	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
	452571	W31518	Hs.34665	ESTs	7.2
	453736	AL118674	Hs.34871	zinc finger homeobox 1B	7.2
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	7.2
	405494				7.2
25	442832	AW206560	Hs.253569	ESTs	7.1
	420193	AI460080	Hs.202869	ESTs	7.1
	434217	AW014795	Hs.23349	ESTs	7.0
	427356	AW023482	Hs.97849	ESTs	7.0
30	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.9
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	6.9
	442377	AA993807	Hs.167367	ESTs	6.9
	441143	AI027604	Hs.159650	ESTs	6.9
	445122	AW241632	Hs.147377	hypothetical protein FLJ23598	6.9
	431353	AA828032	Hs.189076	ESTs	6.9
35	407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.8
	426753	T89832	Hs.170278	ESTs	6.8
	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.8
	451963	AI825440	Hs.224952	ESTs	6.8
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	6.8
40	433426	H69125	Hs.133525	ESTs	6.8
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	6.8
	416236	R41400		gb:yr94b12.s1 Soares infant brain 1NIB H	6.8
	409031	AA376836	Hs.76728	ESTs	6.7
	427558	D49493	Hs.2171	growth differentiation factor 10	6.7
45	437259	AI377755	Hs.120695	ESTs	6.7
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	6.7
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	6.7
	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	6.7
	422475	AL359938	Hs.117313	Meis (mouse) homolog 3	6.7
50	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.7
	424750	D29956	Hs.152818	ubiquitin specific protease 8	6.6
	403574				6.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	6.6
	415025	AW207091	Hs.72307	ESTs	6.5
55	448104	AI674818	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HE	6.5
	444271	AW452569	Hs.149804	ESTs	6.5
	437157	BE048860	Hs.120655	ESTs	6.5
	444050	AW138295	Hs.135024	ESTs	6.5
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	6.5
60	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	6.5
	424433	H04607	Hs.9218	ESTs	6.4
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	6.4
	445424	AB028945	Hs.12696	coractin SH3 domain-binding protein	6.4
	422544	AB018259	Hs.118140	KIAA0716 gene product	6.4
65	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	6.3
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	6.3
	417246	AI760098	Hs.21411	ESTs	6.3
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	6.3
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	6.3
70	438909	AF085839		gb:Homo sapiens full length insert cDNA	6.3
	446002	AI346468	Hs.145789	ESTs	6.3
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	6.3
	424202	BE350295	Hs.15032	RAN binding protein 17	6.3
75	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	6.2
	415511	AI732617	Hs.182362	ESTs	6.2
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.2
	416879	H98899	Hs.42599	ESTs	6.2
	432803	AA566398		gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	6.2
80	442862	BE080429	Hs.15738	ESTs	6.2
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	6.2
	441082	AW444804	Hs.202655	ESTs	6.2
	404599				6.1
	453931	AL121278	Hs.25144	ESTs	6.1

	420252	AW270404	Hs.193161	ESTs	6.1
	431622	AW979271	Hs.293184	ESTs	6.1
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.1
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.0
	424693	BE169810	Hs.47557	ESTs	6.0
	419172	AW338625	Hs.22120	ESTs	6.0
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.0
	453037	AA045175	Hs.177552	ESTs	6.0
10	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	6.0
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	6.0
	422352	AA766296	Hs.99200	ESTs	5.9
	433527	AW235613	Hs.133020	ESTs	5.9
	420077	AW512260	Hs.87767	ESTs	5.9
15	429703	T93154	Hs.28705	ESTs	5.9
	433098	AW190593	Hs.151143	ESTs	5.9
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	5.9
	449416	AI651016	Hs.246311	ESTs	5.9
	459023	AW968226	Hs.60798	ESTs	5.9
20	450584	AA040403	Hs.60371	ESTs	5.9
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	5.9
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	5.9
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	5.9
	433479	AW511459	Hs.249972	ESTs	5.8
25	443113	AI040686	Hs.132908	ESTs	5.8
	430414	AW365665	Hs.120388	ESTs	5.8
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	5.8
	435420	AI928513	Hs.59203	ESTs	5.8
	404916				5.8
30	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.8
	448253	H25899	Hs.201591	ESTs	5.8
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.8
	446967	AI699629	Hs.156781	ESTs	5.8
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	5.7
35	438842	AA827176	Hs.124316	ESTs	5.7
	437260	AA747807	Hs.149500	ESTs	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	428043	T92248	Hs.2240	uteroglobin	5.7
	408045	AW138959	Hs.245123	ESTs	5.7
40	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	5.7
	428508	BE252383	Hs.184668	SBB131 protein	5.7
	453393	AW956392	Hs.110376	ESTs	5.6
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	5.6
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.6
45	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	5.6
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	5.6
	416575	W02414	Hs.38383	ESTs	5.5
	404043				5.5
	415094	D59513	Hs.330778	ESTs	5.5
50	453049	BE537217	Hs.30343	ESTs	5.5
	430153	AW968128	Hs.336679	ESTs	5.5
	410811	AW805687	Hs.300648	ESTs	5.5
	443903	AI220547	Hs.135223	ESTs	5.5
	429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	5.5
55	444471	AB020684	Hs.11217	KIAA0877 protein	5.5
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	5.5
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	5.5
	432113	AA935065	Hs.152385	ESTs	5.5
	446608	N75217	Hs.257846	ESTs	5.5
60	419945	AW290975	Hs.118923	ESTs	5.5
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	5.4
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	5.4
	439382	BE247684	Hs.103070	ESTs	5.4
	428895	AA437124	Hs.187247	ESTs	5.4
65	446577	AB040933	Hs.15420	KIAA1500 protein	5.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	427778	AA412323	Hs.105323	ESTs	5.4
	437138	AI935622	Hs.271245	ESTs	5.4
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	5.4
70	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	5.4
	435202	AI971313	Hs.170204	KIAA0551 protein	5.4
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	5.3
	434992	AA658501	Hs.283358	ESTs	5.3
	454039	AW079064	Hs.245540	ESTs	5.3
75	456408	AI288348	Hs.23450	mitochondrial ribosomal protein S25	5.3
	406554				5.3
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	5.3
	416769	AI339257	Hs.115436	ESTs, Moderately similar to I54374 gene	5.3
	414299	AA142989	Hs.71730	ESTs	5.3
80	420362	U79734	Hs.97206	huntingtin interacting protein 1	5.3
	459664				5.3
	425509	AF079363	Hs.158213	sperm associated antigen 6	5.3
	401497				5.3
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	5.2

	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.2
	408776	AA057365	Hs.63356	ESTs, Weakly similar to I38022 hypotheti	5.2
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	5.2
	451050	AW937420	Hs.69662	ESTs	5.2
5	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	5.2
	404957				5.2
	452771	T05477	Hs.333265	ESTs	5.2
	438885	AI886558	Hs.184987	ESTs	5.2
10	428244	AI564123	Hs.42500	ADP-ribosylation factor-like 5	5.2
	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	5.2
	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.2
	408729	AA195764	Hs.72639	ESTs	5.1
	457100	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A	5.1
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.1
15	417154	AI674701	Hs.21388	ESTs	5.1
	411869	W20027	Hs.23439	ESTs	5.1
	427043	AA397679	Hs.3991	ESTs	5.1
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	5.1
20	422063	BE156476		gb:QV0-HT0368-040100-082-c05 HT0368 Homo	5.1
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	5.1
	408677	AI279892	Hs.46801	sorting nexin 14	5.0
	404097				5.0
25	437636	AA764781	Hs.291844	ESTs	5.0
	452822	X85689	Hs.288617	hypothetical protein FLJ22621	5.0
	410733	D84284	Hs.66052	CD38 antigen (p45)	5.0
	439140	W85737	Hs.290830	ESTs	5.0
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	5.0
	405547				5.0
30	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	5.0
	449168	NM_016206	Hs.23142	colon carcinoma related protein	5.0
	455431	AW938484		gb:CM0-DT0057-290200-253-d06 DT0057 Homo	5.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.0
	411149	N68715	Hs.269128	ESTs	5.0
35	432441	AW292425	Hs.163484	ESTs	5.0
	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
	450109	AI539295	Hs.115740	KIAA0210 gene product	5.0
	449695	AA164569	Hs.34550	ESTs	5.0
40	421764	AI681535	Hs.148135	serine/threonine kinase 33	4.9
	404593				4.9
	423607	AA328329	Hs.6591	ESTs	4.9
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (f	4.9
	419235	AW470411	Hs.288433	neurotrimin	4.9
45	436304	AA339622	Hs.108887	ESTs	4.9
	434613	AI821826		gb:ms92b10.x5 NCL_CGAP_Pr3 Homo sapiens	4.9
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	4.9
	415245	N59650	Hs.27252	ESTs	4.9
	428780	AI478578	Hs.50636	ESTs	4.9
50	406333				4.9
	445034	AW293376	Hs.143659	ESTs	4.8
	440202	AW516211	Hs.125300	ring finger protein 21, interferon-respo	4.8
	424638	AI472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HE	4.8
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	4.8
55	427652	AI673025	Hs.43874	ESTs, Moderately similar to I54374 gene	4.8
	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.8
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
	415261	T40928	Hs.8346	ESTs	4.8
60	453543	AA485425	Hs.48919	Homo sapiens cDNA FLJ11508 fis, clone HE	4.8
	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HE	4.8
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	4.8
	441006	AW605267	Hs.7627	CGI-60 protein	4.8
	412222	AA528283	Hs.292737	ESTs	4.8
65	424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypotheti	4.8
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	4.8
	439398	AA284267	Hs.221504	ESTs	4.8
	436397	AA715013	Hs.169835	ESTs	4.8
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	4.8
70	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	425916	NM_006786	Hs.162200	urotensin 2	4.8
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	4.8
	427457	AW779105	Hs.164682	ESTs	4.7
75	451620	AW449888	Hs.257224	ESTs	4.7
	408938	AA059013	Hs.22607	ESTs	4.7
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	4.7
	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13658 fis, clone PL	4.7
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	4.7
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	4.7
80	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	435347	AW014873	Hs.116963	ESTs	4.7
	425458	H89317	Hs.182889	ESTs	4.7
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	4.7

	436594	AI419982	Hs.156189	ESTs	4.7
	421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	4.7
	432731	R31178	Hs.287820	fibronectin 1	4.7
5	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	4.7
	426320	W47595	Hs.169300	transforming growth factor, beta 2	4.7
	419751	AW195581	Hs.93121	KIAA0761 protein	4.6
	433515	AA595800	Hs.190246	ESTs	4.6
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	4.6
10	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	4.6
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	4.6
	406992	S82472		gb:beta-pol=DNA polymerase beta [exon a	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	435933	AA805520	Hs.192075	ESTs	4.6
	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	4.6
15	445657	AW612141	Hs.279575	Homo sapiens G-protein coupled receptor	4.6
	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypotheti	4.6
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapi	4.6
20	424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.6
	416258	N45661	Hs.90011	adenylosuccinate synthase	4.6
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	4.6
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	4.5
	422977	AA631498		gb:np83h04.s1 NCL_CGAP_Thy1 Homo sapiens	4.5
25	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
	450192	AA263143	Hs.24596	RAD51-interacting protein	4.5
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	4.5
	407266	AI235664		gb:Homo sapiens mRNA for immunoglobulin	4.5
	409041	AB033025	Hs.50081	KIAA1199 protein	4.5
30	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.5
	452526	W38537	Hs.280740	hypothetical protein MGC3040	4.5
	403271				4.5
	450656	AA010539	Hs.18912	ESTs	4.5
	446096	AI276454		gb:q171a12.x1 Soares_NhHMPu_S1 Homo sapi	4.5
35	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.5
	437960	AI669586	Hs.222194	ESTs	4.5
	440862	H39048	Hs.127432	ESTs	4.5
	410615	AW772721		gb:hl95c01.x1 NCL_CGAP_Thy8 Homo sapiens	4.5
	413583	AL120806	Hs.5888	ESTs	4.5
40	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL	4.5
	442324	R63578	Hs.28426	ESTs	4.4
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	4.4
	435747	AI079519	Hs.134398	ESTs	4.4
	446509	AF169693	Hs.132892	protocadherin 20	4.4
45	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.4
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	4.4
	448089	AI467945	Hs.173696	ESTs	4.4
	434367	AB020700	Hs.3830	KIAA0893 protein	4.4
	434757	AI038997	Hs.132921	ESTs	4.4
50	413453	AA129640	Hs.128065	ESTs	4.4
	454438	AA224053	Hs.172405	cell division cycle 27	4.4
	458154	AW816379	Hs.335018	ESTs	4.4
	430417	AA461045	Hs.50701	ESTs	4.4
	434819	AA650099	Hs.291541	ESTs, Weakly similar to ALUB_HUMAN !!!!	4.4
55	438796	W67821	Hs.109590	genethonin 1	4.4
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.4
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.4
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.4
	451895	T93573	Hs.16970	ESTs	4.4
60	435434	AA680387	Hs.187850	ESTs	4.4
	449623	C00719	Hs.120440	EST	4.4
	433563	AI732637	Hs.277901	ESTs	4.3
	444649	AW207523	Hs.197628	ESTs	4.3
	441594	AL041080	Hs.208765	ESTs, Moderately similar to ALU7_HUMAN A	4.3
65	443314	AW771701	Hs.54646	ESTs	4.3
	400292	AA250737	Hs.72472	ESTs	4.3
	427972	AA864870	Hs.181304	putative gene product	4.3
	446932	AA961459	Hs.125644	ESTs	4.3
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.3
70	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	4.3
	400608				4.3
	411156	AW819939	Hs.273629	ESTs	4.3
	435772	AA700019	Hs.132992	ATP-binding cassette, sub-family G (WHIT	4.3
75	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	4.3
	455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	4.3
	443257	AI334040	Hs.11614	HSPC065 protein	4.3
	436033	H75391	Hs.255748	ESTs	4.3
	420214	AI146375	Hs.286073	ESTs, Moderately similar to ALU5_HUMAN A	4.3
80	410519	AW612264	Hs.131705	ESTs	4.3
	401189				4.3
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3

	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	4.3
	434677	AW444575	Hs.130834	ESTs	4.3
	403310				4.3
5	451830	H18433	Hs.21542	KIAA1035 protein	4.3
	422222	AI699372	Hs.193247	hypothetical protein DKFZp434A171	4.3
	435627	W88774	Hs.118370	ESTs	4.3
	436461	AW511956	Hs.293261	ESTs	4.3
	452166	AI948607	Hs.264680	ESTs	4.3
10	413998	AW103807	Hs.243933	ESTs	4.2
	416642	T96118	Hs.226313	ESTs	4.2
	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	4.2
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypotheti	4.2
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.2
15	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	4.2
	424641	AB001106	Hs.151413	glia maturation factor, beta	4.2
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.2
	409629	AW449589	Hs.279724	ESTs	4.2
	458771	AW295151	Hs.163612	ESTs	4.2
20	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	4.2
	436645	AW023424	Hs.156520	ESTs	4.2
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	4.2
	445268	AI218358	Hs.175048	ESTs	4.2
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.2
25	431917	D16181	Hs.2868	peripheral myelin protein 2	4.2
	443348	AW873596	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	4.2
	443151	AI827193	Hs.132714	ESTs	4.2
	419255	AA235672	Hs.87491	ESTs	4.2
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	4.2
30	452561	AI692181	Hs.49169	KIAA1634 protein	4.2
	421106	AA877124	Hs.172844	ESTs	4.2
	424268	AA397653	Hs.307438	Human DNA sequence from clone 495010 on	4.2
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.2
	421515	Y11339	Hs.105352	GallNAc alpha-2, 6-sialyltransferase I, I	4.2
35	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	4.2
	428771	AB028992	Hs.193143	KIAA1069 protein	4.1
	445745	AB007924	Hs.13245	KIAA0455 gene product	4.1
	417009	AA191719	Hs.314714	ESTs	4.1
	436517	BE080932	Hs.135225	ESTs	4.1
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.1
	414083	AL121282	Hs.257786	ESTs	4.1
	452728	AI915676	Hs.239708	ESTs	4.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	4.1
	441802	AA968636	Hs.127877	ESTs	4.1
45	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	4.1
	413875	BE176776		gb:RC3-HT0586;110300-011-g09 HT0586 Homo	4.1
	444009	AI380792	Hs.135104	ESTs	4.1
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	4.1
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	4.1
50	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	435256	AF193766	Hs.13872	cytokine-like protein C17	4.1
	428104	AA421350	Hs.191604	ESTs	4.1
	439648	AW780192	Hs.267596	ESTs	4.1
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	4.1
55	446364	AB006624	Hs.14912	KIAA0286 protein	4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	4.0
	404561				4.0
60	401575				4.0
	419296	AA236115	Hs.120785	ESTs	4.0
	432055	AW972359	Hs.293334	ESTs	4.0
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	4.0
	450320	AW291775	Hs.213793	ESTs	4.0
65	447350	AI375572	Hs.172634	ESTs	4.0
	441974	AI683782	Hs.128245	ESTs	4.0
	453142	AA033648	Hs.7473	ESTs	4.0
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.0
	410292	AA843087	Hs.124194	ESTs	4.0
70	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	4.0
	420218	AW958037	Hs.286	ribosomal protein L4	4.0
	426625	T78300	Hs.300642	serologically defined colon cancer antig	4.0
	417708	N74392	Hs.50495	ESTs	4.0
75	451024	AA442176		gb:zw63b08.r1 Soares_tota1_fetus_Nb2HF8_	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0
	422058	AA862231	Hs.334443	ESTs	4.0
	439479	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	4.0
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.0
80	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.0
	453096	AW294631	Hs.11325	ESTs	4.0
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	4.0
	421002	AF116030	Hs.100932	transcription factor 17	4.0
	445414	AV653692	Hs.146105	ESTs	4.0

	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.0
	451353	N21043	Hs.42932	ESTs	4.0
	437075	AA743748	Hs.40758	ESTs	3.9
5	410505	AW752139	Hs.314323	ESTs	3.9
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	3.9
	426116	AA868729	Hs.144694	ESTs	3.9
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
10	417718	T86540	Hs.193981	ESTs	3.9
	436772	AW975688	Hs.74170	metallothionein 1E (functional)	3.9
	401045				3.9
	408767	AA057279	Hs.211928	ESTs	3.9
	407303	AA016296	Hs.165200	ESTs, Weakly similar to A56194 thromboxa	3.9
15	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	3.9
	451623	H77818	Hs.268991	ESTs	3.9
	450063	AI681509	Hs.277133	ESTs	3.9
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.9
	419276	BE165909	Hs.306881	MSTP043 protein	3.9
20	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
	436149	AI754308	Hs.159452	ESTs	3.9
	422667	H25642	Hs.133471	ESTs	3.9
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	3.9
	458219	H22195	Hs.31874	ESTs	3.9
25	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.9
	439810	AL109710	Hs.85568	EST	3.9
	436578	AI091435	Hs.134859	ESTs	3.9
	415598	AI433165	Hs.9856	ESTs	3.9
	425087	R62424	Hs.126059	ESTs	3.9
30	454111	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	3.9
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	3.9
	452466	N84635	Hs.29664	hypothetical protein DKFZp564B052	3.9
	424962	NM_012288	Hs.153954	TRAM-like protein	3.9
	435823	R07856	Hs.16355	ESTs	3.9
35	440633	AI140686	Hs.263320	ESTs	3.9
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	3.9
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.9
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.9
	417461	R38403	Hs.13305	ESTs	3.9
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.8
	419140	AI982647	Hs.215725	ESTs	3.8
	415652	T79213	Hs.272073	ESTs	3.8
	430140	AW296771	Hs.221999	ESTs	3.8
45	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	3.8
	422165	AL041199	Hs.1481	histidine decarboxylase	3.8
	417706	T90797	Hs.268623	ESTs	3.8
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.8
	450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.8
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.8
50	449729	R72032	Hs.29235	ESTs	3.8
	414700	H63202	Hs.38163	ESTs	3.8
	440899	AW449445	Hs.120021	DKFZP434I092 protein	3.8
	439335	AA742697	Hs.62492	ESTs, Weakly similar to B39066 proline-r	3.8
	408625	AW243323	Hs.266785	ESTs	3.8
55	421987	AI133161	Hs.286131	CGI-101 protein	3.8
	418915	AI474778	Hs.118977	ESTs	3.8
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.8
	442849	R10099	Hs.269805	ESTs	3.8
60	427191	BE221825	Hs.97691	ESTs	3.8
	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	3.8
	437030	AA742577	Hs.303781	EST	3.8
	427940	AA417812	Hs.38775	ESTs	3.7
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.7
65	449679	AI823951	Hs.129700	toll-like 1	3.7
	425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3.7
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	439957	AI453184	Hs.66357	ESTs	3.7
70	446999	AA151520	Hs.334822	hypothetical protein MGC4485	3.7
	428414	AL049980	Hs.184216	DKFZP564C152 protein	3.7
	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.7
	418379	AA218940	Hs.137516	fidgellin-like 1	3.7
	419720	AA249131	Hs.337778	hypothetical protein FLJ11068	3.7
75	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	3.7
	416185	AW975861	Hs.47367	KIAA1785 protein	3.7
	417235	AA810278	Hs.24250	ESTs	3.7
	441720	AI346487	Hs.28739	ESTs	3.7
80	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
	417355	D13168	Hs.82002	endothelin receptor type B	3.7
	449321	AA001150	Hs.132937	ESTs	3.7
	424806	AA382523	Hs.105689	MSTP031 protein	3.7
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	3.7
	409248	AB033035	Hs.51965	KIAA1209 protein	3.7

	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	3.7
	420026	AI831190	Hs.166676	ESTs	3.7
5	429419	AB023226	Hs.202276	KIAA1009 protein	3.7
	447410	AI470235	Hs.172698	EST	3.7
	404274				3.7
	416320	H47867	Hs.34024	ESTs	3.7
10	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	3.7
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.7
	446025	AW305075	Hs.180948	KIAA0729 protein	3.7
	450458	AA009926		gb:zi07e05.r1 Soares_fetal_liver_spleen_	3.6
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor 1	3.6
15	438257	AW474419	Hs.224794	ESTs	3.6
	440887	AI799488	Hs.135905	ESTs	3.6
	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.6
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	408687	AL110280	Hs.301152	Homo sapiens mRNA; cDNA DKFZp434F053 (fr	3.6
	407726	AA435679	Hs.88594	ESTs	3.6
20	436026	AI349764	Hs.217081	ESTs	3.6
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
	452293	AI871833	Hs.304609	ESTs	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.6
25	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.6
	429208	AA447990	Hs.190478	ESTs	3.6
	458429	AV646559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C	3.6
	404476				3.6
	405848				3.6
30	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	3.6
	403937				3.6
	437918	AI761449	Hs.121629	ESTs	3.6
	432408	N39127	Hs.332557	ESTs, Weakly similar to A46010 X-linked	3.6
	437641	AA811452	Hs.291911	ESTs	3.6
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.6
35	446102	AW168067	Hs.252956	ESTs	3.6
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	432030	AI908400	Hs.143789	ESTs	3.6
40	446453	AV658469	Hs.188646	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	3.6
	440801	AA906366	Hs.190535	ESTs	3.6
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	440886	AW511032	Hs.190516	ESTs	3.6
	401049				3.6
45	449424	AW448937	Hs.197030	ESTs	3.6
	418076	R61388	Hs.6724	ESTs	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	3.6
50	438016	AI949638	Hs.336846	EST	3.6
	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	3.5
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	3.5
	455536	AW135986	Hs.257859	ESTs	3.5
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	3.5
55	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	435344	AA700326	Hs.190599	ESTs	3.5
	445056	AB014530	Hs.12259	KIAA0630 protein	3.5
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	3.5
	442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	3.5
60	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	3.5
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.5
	428409	AW117207	Hs.98523	ESTs	3.5
	431087	H12723	Hs.290791	ESTs	3.5
65	426920	AA393351	Hs.132121	ESTs	3.5
	427687	AW003867	Hs.1570	histamine receptor H1	3.5
	437583	AA761190	Hs.244627	ESTs	3.5
	421599	AA293655	Hs.97293	ESTs	3.5
	433687	AA743991		gb:ny57g01.s1 NCL_CGAP_Pr18 Homo sapiens	3.5
70	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	3.5
	430499	AW969408	Hs.231991	ESTs	3.5
	451531	AA018311	Hs.114762	ESTs	3.5
	457620	AA602711	Hs.336753	EST	3.5
	410658	AW105231	Hs.192035	ESTs	3.5
75	427865	AA416931	Hs.126065	ESTs	3.5
	453390	AA862496	Hs.28482	ESTs	3.5
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	3.5
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
80	427718	AI798680	Hs.25933	ESTs	3.5
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.5
	420381	D50640	Hs.337616	phosphodiesterase 3B, cGMP-inhibited	3.5
	410908	AA121686	Hs.10592	ESTs	3.5
	442080	AW444761	Hs.44565	ESTs	3.5
	406685	M18728		gb:Human nonspecific crossreacting antig	3.5

	404200				3.5
	417976	BE565892	Hs.83077	interleukin 18 (interferon-gamma-inducin	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	432868	AW974093	Hs.292775	ESTs	3.5
5	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo	3.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.4
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	3.4
	428775	AA434579	Hs.143691	ESTs	3.4
10	410004	AI298027	Hs.5057	carboxypeptidase D	3.4
	422093	AF151852	Hs.111449	CGI-94 protein	3.4
	441736	AW292779	Hs.169799	ESTs	3.4
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	3.4
	405970				3.4
15	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
	459482	AA625339	Hs.237052	EST, Weakly similar to I38022 hypothetical	3.4
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	3.4
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.4
	402230				3.4
20	436120	AI248193	Hs.119860	ESTs	3.4
	405336				3.4
	434374	AA631439		gb:np85d02.s1 NCI_CGAP_Thy1 Homo sapiens	3.4
	428911	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	3.4
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.4
25	416057	AI927382	Hs.29857	ESTs	3.4
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	3.4
	436088	AA704687	Hs.191294	ESTs	3.4
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.4
	454076	AW204712	Hs.61957	ESTs	3.4
30	431733	AW298410	Hs.21475	ESTs	3.4
	432974	BE348793	Hs.233331	ESTs	3.4
	412576	AA447718	Hs.107057	ESTs	3.4
	446142	AI754693	Hs.145968	ESTs	3.4
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	3.4
35	433384	AI021992	Hs.124244	ESTs	3.4
	413621	AI808648	Hs.184156	ESTs	3.4
	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	3.4
	436111	AI803082	Hs.157212	ESTs	3.4
	421236	AI287622	Hs.151956	ESTs	3.4
40	433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D1	3.4
	403515				3.4
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	3.4
	453375	AI990114	Hs.240091	ESTs	3.4
45	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	3.4
	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	3.4
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	3.4
	409642	AW450809	Hs.257347	ESTs	3.4
	420092	AA814043	Hs.88045	ESTs	3.4
	453365	AA035211	Hs.17404	ESTs	3.3
50	437007	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypotheti	3.3
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	3.3
	439024	R96696	Hs.35598	ESTs	3.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.3
	417991	AA731452	Hs.190008	ESTs	3.3
55	403356				3.3
	433650	AA603472	Hs.28456	ESTs	3.3
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviri	3.3
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	3.3
	413714	AI560944	Hs.71428	ESTs	3.3
60	430887	N66801	Hs.260287	KIAA1841 protein	3.3
	413618	BE154078		gb:PM0-HT0339-200400-010-F04 HT0339 Homo	3.3
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	405692				3.3
65	432809	AA565509	Hs.131703	ESTs	3.3
	433805	AA706910	Hs.112742	ESTs	3.3
	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	3.3
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-hergulin	3.3
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	3.3
70	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.3
	410434	AF051152	Hs.63668	toll-like receptor 2	3.3
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.3
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	3.3
	444301	AK000136	Hs.10760	asporin (LRR class 1)	3.3
75	428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyl	3.3
	458924	BE242158	Hs.24427	DKFZP566O1646 protein	3.3
	435934	R19382	Hs.117869	ESTs	3.3
	400269				3.3
80	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.3
	412903	BE007967	Hs.155795	ESTs	3.3
	400889				3.3
	449585	AI655321	Hs.197693	ESTs	3.3
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.3
	418557	BE140602	Hs.246645	ESTs	3.3

5	453204	R10799	Hs.191990	ESTs	3.3
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	3.3
	427374	AI150033	Hs.143686	ESTs	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
10	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.3
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	3.3
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.3
	403895				3.2
	414899	AW975433	Hs.36288	ESTs	3.2
15	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.2
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
	427119	AW880562	Hs.114574	ESTs	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
20	443830	AI142095	Hs.143273	ESTs	3.2
	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_UI2 Homo sapiens	3.2
	417561	AW974345		gb:EST386449 MAGE resequences, MAGM Homo	3.2
	446063	AI720140	Hs.151079	ESTs	3.2
25	423609	AA328348	Hs.218289	ESTs	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.2
	435808	AA702866	Hs.113150	ESTs	3.2
	424001	W67883	Hs.137476	paternally expressed 10	3.2
30	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	3.2
	418946	AI798841	Hs.164526	ESTs	3.2
	431750	AA514986	Hs.283705	ESTs	3.2
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	3.2
	428268	AA424957	Hs.294132	ESTs	3.2
35	418878	W20090	Hs.6616	ESTs	3.2
	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	3.2
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap	3.2
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.2
	404588				3.2
40	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	444910	AI201849		gb:qs76g04.x1 NCI_CGAP_Pr28 Homo sapiens	3.2
	407339	AA777542	Hs.132670	ESTs	3.2
	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	3.2
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	3.2
45	419340	AA236590	Hs.87530	ESTs	3.2
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone CO	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	421187	NM_014721	Hs.102471	KIAA0680 gene product	3.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	3.2
50	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.2
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.2
	438839	AW297945	Hs.128490	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
	427961	AW293165	Hs.143134	ESTs	3.2
55	429228	AI553633	Hs.337139	ESTs	3.2
	431548	AI834273	Hs.9711	novel protein	3.1
	441839	AW975512	Hs.29160	ESTs	3.1
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.1
	441274	AW593781	Hs.131357	ESTs	3.1
60	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	436154	AA764950	Hs.119898	ESTs	3.1
	406752	AI285598		gb:qu49f06.x1 NCI_CGAP_Lym6 Homo sapiens	3.1
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	3.1
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.1
65	436739	BE208022	Hs.127685	KIAA1627 protein	3.1
	451674	AA019104	Hs.175483	Homo sapiens cDNA: FLJ22016 fis, clone H	3.1
	421166	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	3.1
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
70	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	3.1
	424780	U39576	Hs.153058	butyrophilin, subfamily 1, member A1	3.1
	456551	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.1
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.1
75	431814	BE256242	Hs.270847	delta-tubulin	3.1
	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	436401	AI087958	Hs.29088	ESTs	3.1
	437439	H29796	Hs.269622	ESTs	3.1
	403277				3.1
80	408547	AA574291	Hs.57837	ESTs	3.1
	424131	AA335714	Hs.199665	ESTs	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	3.1
	434636	AA083764	Hs.6101	hypothetical protein MGC3178	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.1
	407905	AW103655	Hs.252905	ESTs	3.1
	452311	AW304029	Hs.252744	ESTs	3.1

	434849	AW292765	Hs.8053	ESTs	3.1
	446770	AV660309	Hs.154986	ESTs, Weakly similar to PLLP_HUMAN PLASM	3.1
	424238	AA337401	Hs.137635	ESTs	3.1
5	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.1
	447829	AI433029	Hs.164104	ESTs	3.1
	406506				3.1
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.1
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.1
10	451229	AW967707	Hs.48473	ESTs	3.1
	401103				3.1
	433589	AA886530	Hs.188912	ESTs	3.1
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypotheti	3.1
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	3.1
	404288				3.1
15	406195				3.1
	438202	AW169287	Hs.22588	ESTs	3.1
	425516	BE000707	Hs.29567	ESTs	3.1
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.1
20	422692	AA332376	Hs.24135	transmembrane protein vezatin; hypotheti	3.1
	435414	AW270550	Hs.116957	ESTs	3.1
	418950	T78517	Hs.13941	ESTs	3.1
	426890	AA393167	Hs.41294	ESTs	3.1
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	3.1
25	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.1
	459371	R20991		gb:yg06h01.r1 Soares infant brain 1NIB H	3.1
	421823	N40850	Hs.28625	ESTs	3.1
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.1
	452896	AA831508	Hs.32553	ESTs	3.1
30	425895	AI269484	Hs.161427	zinc finger protein 215	3.1
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	3.1
	407340	AA810168	Hs.284289	vitellogenesis-associated protein VIT-1	3.1
	401862				3.1
	444325	AW152618	Hs.16757	ESTs	3.1
35	408171	AA301228	Hs.43299	hypothetical protein FLJ12890	3.1
	423949	AI014546	Hs.130912	ESTs	3.1
	419519	AI198719	Hs.176376	ESTs	3.0
	434683	AW298724	Hs.202639	ESTs	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
40	415086	AI597963	Hs.118726	ESTs	3.0
	419220	AA811938	Hs.291759	ESTs	3.0
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	3.0
45	405090				3.0
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
	443253	AI041212	Hs.132117	ESTs	3.0
	444974	AI203500	Hs.151612	ESTs	3.0
	445717	AW664658	Hs.149332	ESTs	3.0
50	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
	414888	AI039185	Hs.77558	thyroid hormone receptor interactor 7	3.0
	424406	D54120	Hs.146409	cell division cycle 42 (GTP-binding prot	3.0
	410371	AA084482	Hs.115850	ESTs	3.0
55	426384	AI472078	Hs.303662	ESTs	3.0
	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	3.0
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo	3.0
60	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	3.0
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	3.0
	447482	AB033059	Hs.18705	KIAA1233 protein	3.0
	439416	W58294	Hs.56254	ESTs	3.0
	436635	AW104325	Hs.272093	ESTs, Weakly similar to I78885 serine/th	3.0
65	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.0
	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	3.0
	415452	F09134	Hs.12839	ESTs	3.0
	427874	AA732367	Hs.98198	ESTs	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
70	454193	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	3.0
	454678	AW813089		gb:RC3-ST0186-240400-111-b05 ST0186 Homo	3.0
	415122	D60708	Hs.22245	ESTs	3.0
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.0
	400227				3.0
75	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	3.0
	419503	AA243642	Hs.137422	ESTs	3.0
	446563	BE326588	Hs.141454	ESTs	3.0
	457285	AI038858	Hs.130522	Kv channel-interacting protein 1	3.0
	434998	AW975157	Hs.26037	ESTs	3.0
80	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.0
	424539	L02911	Hs.150402	activin A receptor, type I	3.0
	449856	AA203155	Hs.18200	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN A	3.0

	442994	AI026718	Hs.16954	ESTs	3.0
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	3.0
	421072	AI215069	Hs.89113	ESTs	3.0
	456273	AF154846	Hs.1148	zinc finger protein	3.0
5	404548				3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	441519	AA972740	Hs.127092	ESTs	3.0
	445413	AA151342	Hs.12677	CGI-147 protein	3.0
	418717	AI334430	Hs.86984	ESTs	3.0
10	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.0
	407758	D50915	Hs.38365	KIAA0125 gene product	3.0
	431906	AW328038	Hs.37486	ESTs	3.0
	424968	AA349086	Hs.259746	ESTs, Weakly similar to A46010 X-linked	3.0
	431023	AI283133	Hs.297420	ESTs	3.0
15	432596	AJ224741	Hs.278461	matriin 3	3.0
	452412	AA029608	Hs.61373	ESTs	3.0
	421309	AI222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to T2D4_HUMAN TRANS	2.9
	408321	AW405882	Hs.44205	cortistatin	2.9
20	439236	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	2.9
	400880				2.9
	417014	AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN !!!!	2.9
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.9
25	406603				2.9
	425573	AB006423	Hs.158308	serine (or cysteine) proteinase inhibito	2.9
	427878	C05766	Hs.181022	CGI-07 protein	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.9
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.9
30	422634	NM_016010	Hs.118821	CGI-62 protein	2.9
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.9
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	2.9
	408525	AW206972	Hs.253595	ESTs	2.9
	412248	BE176480		gb:RC3-HT0585-160300-022-c02 HT0585 Homo	2.9
35	432507	BE391093	Hs.324667	ESTs	2.9
	447290	AI476732	Hs.263912	ESTs	2.9
	424188	AW954552	Hs.142634	zinc finger protein	2.9
	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
40	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119	AA322201	Hs.131976	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	2.9
45	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	2.9
	444339	T96555	Hs.31562	ESTs	2.9
	446745	AW118189	Hs.156400	ESTs	2.9
	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
50	430573	AA744550	Hs.136345	ESTs	2.9
	451073	AI758905	Hs.206063	ESTs	2.9
	440575	AA889870	Hs.126006	ESTs	2.9
	402046				2.9
	426882	AA393108	Hs.97365	ESTs	2.9
55	435738	AA699633	Hs.269543	ESTs, Weakly similar to A56194 thromboxa	2.9
	420656	AA279098	Hs.187636	ESTs	2.9
	438323	AI985394	Hs.123369	ESTs	2.9
	453123	AI953718	Hs.221849	ESTs	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
60	431595	AA508196		gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens	2.9
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.9
	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Brn52 Homo sapien	2.9
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	2.9
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	2.9
	456034	AW450979		gb:UI-H-BI3-ala-a-12-O-UI.s1 NCI_CGAP_Su	2.9
65	442118	AA976718	Hs.202242	ESTs	2.9
	420727	H75701	Hs.99886	complement component 4-binding protein,	2.9
	433849	BE465884	Hs.280728	ESTs	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
70	429826	N93266	Hs.40747	ESTs	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
	441330	AI692984	Hs.129354	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	2.9
75	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.9
	444631	AW995395	Hs.84520	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.9
	458186	AA904244	Hs.153205	ESTs	2.9
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	2.9
	415757	AA830854	Hs.187810	ESTs	2.9
80	449299	AA299919	Hs.84561	ESTs	2.9
	457003	S78234	Hs.172405	cell division cycle 27	2.9
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.9
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.9
	426174	AA547959	Hs.115838	ESTs	2.9

	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	2.9
	429950	AW081608	Hs.105053	ESTs	2.9
	412733	AA984472	Hs.74554	KIAA0080 protein	2.9
5	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	442655	AW027457	Hs.30323	ESTs, Weakly similar to B34087 hypotheti	2.9
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	2.9
	430447	W17064	Hs.332848	SWI/SNF related, matrix associated, acti	2.9
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	2.9
10	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.9
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	2.9
	401094				2.9
	401526				2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
15	417320	AA195667	Hs.86022	ESTs	2.9
	418282	AA215535	Hs.98133	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	450006	AI241555	Hs.60171	ESTs	2.9
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	2.8
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	2.8
20	403329				2.8
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.8
	419038	AW134924	Hs.190325	ESTs	2.8
	440106	AA864968	Hs.127699	KIAA1603 protein	2.8
25	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.8
	431745	AW972448	Hs.163425	ESTs	2.8
	421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA,	2.8
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.8
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	2.8
30	441790	AW294909	Hs.132208	ESTs	2.8
	404443				2.8
	428129	AI244311	Hs.26912	ESTs	2.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.8
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	2.8
35	449327	AI638743	Hs.224672	ESTs	2.8
	400983				2.8
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	2.8
	411213	AA676939	Hs.69285	neuropilin 1	2.8
	420896	AW149342	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	2.8
40	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	2.8
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.8
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	440192	AA872282	Hs.190596	ESTs	2.8
45	448466	AI522109	Hs.171066	ESTs	2.8
	414869	AA157291	Hs.21479	ubiquitin 1	2.8
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
50	439235	N45513	Hs.46608	ESTs	2.8
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	2.8
	434812	AA649860	Hs.189496	ESTs	2.8
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	2.8
	455512	AW983608		gb:RC3-HN0001-240400-012-c01 HN0001 Homo	2.8
55	408380	AF123050	Hs.44532	diubiquitin	2.8
	435990	AI015862	Hs.131793	ESTs	2.8
	410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
	432798	AA565309	Hs.194015	ESTs	2.8
	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	2.8
60	438886	AA827728	Hs.128705	ESTs, Weakly similar to AF149422 2 unkno	2.8
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.8
	416940	N75620	Hs.43157	ESTs	2.8
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	2.8
	438398	AA806526	Hs.130277	ESTs	2.8
65	435313	AI789400	Hs.189729	ESTs	2.8
	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	2.8
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	2.8
	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	2.8
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.8
70	401323				2.8
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.8
	428532	AF157326	Hs.184786	TBP-interacting protein	2.8
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	2.8
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse l	2.8
75	406970	M29994		gb:Human alpha-I spectrin gene, exon 12.	2.8
	426172	AA371307	Hs.125056	ESTs	2.8
	452114	N22687	Hs.8236	ESTs	2.8
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430660	R11884	Hs.100826	ESTs	2.8
80	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.8
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.8
	429881	T80112	Hs.192245	ESTs	2.8
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.8

	409435	AI810721	Hs.95424	ESTs	2.8
	442191	W95186	Hs.8136	endothelial PAS domain protein 1	2.8
	407305	AA715284		gb:mv35f03.r1 NCI_CGAP_Br5 Homo sapiens	2.8
5	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheli	2.8
	412189	R60982	Hs.22581	ESTs	2.8
	420976	AI924940	Hs.108082	ESTs, Weakly similar to T31636 hypotheli	2.8
	448330	AL036449	Hs.207163	ESTs	2.8
	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
10	422505	AL120862	Hs.124165	ESTs	2.8
	427752	AA470687	Hs.104772	ESTs	2.8
	433513	AI566356	Hs.171437	ESTs	2.8
	433703	AA210863	Hs.3532	nemo-like kinase	2.8
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
	405621				2.8
15	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to	2.8
	450400	AI694722	Hs.279744	ESTs	2.8
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.8
	418342	BE002723	Hs.226627	leptin receptor	2.8
20	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	440320	AA879294		gb:nw86e09.s1 NCI_CGAP_Pr12 Homo sapiens	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	439831	AW136488	Hs.25545	ESTs	2.8
25	425661	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	2.8
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	2.8
	418658	AW874263	Hs.32468	ESTs	2.8
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
	421340	F07783	Hs.1369	decay accelerating factor for complement	2.8
30	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.8
	409241	AF070602	Hs.51649	Homo sapiens clone 24504 mRNA sequence	2.8
	448219	AA228092	Hs.42656	KIAA1681 protein	2.8
	408936	AL138043	Hs.293549	ESTs	2.8
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	2.8
35	426471	M22440	Hs.170009	transforming growth factor, alpha	2.8
	454455	AW752710		gb:IL3-CT0219-281099-024-A03 CT0219 Homo	2.8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	401335				2.7
	436577	W84774	Hs.17643	ESTs	2.7
40	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.7
	436007	AI247716	Hs.232168	ESTs	2.7
45	408874	AW818091	Hs.252730	ESTs	2.7
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	2.7
	435625	H50654	Hs.113999	ESTs	2.7
	435766	R11673	Hs.186498	ESTs	2.7
	410327	T33130	Hs.301746	RAP2A, member of RAS oncogene family	2.7
50	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
	427134	AA398409	Hs.173561	EST	2.7
	428137	AA421792	Hs.170999	ESTs	2.7
55	429710	AI337113	Hs.146025	hypothetical protein FLJ23594	2.7
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.7
	441928	AI370188	Hs.211454	ESTs	2.7
	409721	AW887732	Hs.257861	ESTs	2.7
60	427112	Z32887	Hs.290951	ESTs	2.7
	403776				2.7
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
	427839	AA608823	Hs.98244	ESTs	2.7
	432837	AA310693	Hs.87329	HSPC072 protein	2.7
65	438782	AA828380	Hs.126733	ESTs	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	458043	AW979009	Hs.326108	ESTs	2.7
	438171	AW976507	Hs.293515	ESTs	2.7
	452959	AI933416	Hs.189674	ESTs	2.7
70	439556	AI623752	Hs.163603	ESTs	2.7
	446152	AI292036	Hs.150028	ESTs	2.7
	434803	AW974640	Hs.303413	ESTs	2.7
	407771	AL138272	Hs.62713	ESTs	2.7
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.7
75	417543	AA203620	Hs.110153	ESTs	2.7
	401517				2.7
	403677				2.7
	416337	H48713		gb:yq78d02.r1 Soares fetal liver spleen	2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
80	446800	AI341635	Hs.156486	ESTs	2.7
	457906	AW975939	Hs.153290	Homo sapiens cDNA FLJ14318 fis, clone PL	2.7
	452277	AL049013	Hs.28783	KIAA1223 protein	2.7
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheli	2.7

	408715	AA768873	Hs.112250	hypothetical protein FLJ23518	2.7
	410743	AA089474	Hs.272153	ESTs	2.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.7
5	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.7
	427565	AI287280	Hs.97933	ESTs, Weakly similar to T46370 hypotheti	2.7
	406092				2.7
	410008	AA079552		gb:zm20h12.s1 Stratogene pancreas (93720	2.7
	438504	AW665281	Hs.224625	ESTs	2.7
10	414783	AW069569	Hs.278270	inactive progesterone receptor, 23 kD	2.7
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	2.7
	418686	Z36830	Hs.87268	annexin A8	2.7
	413795	AL040178	Hs.142003	ESTs	2.7
	457528	AW973791	Hs.292784	ESTs	2.7
15	444230	H95537	Hs.146067	ESTs	2.7
	403760				2.7
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.7
	428904	AI312526	Hs.46640	ESTs	2.7
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	2.7
20	458638	N78553	Hs.282204	nucleosomal binding protein 1	2.7
	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA	2.7
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.7
	433906	AI167816	Hs.43355	ESTs	2.7
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	2.7
25	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.7
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	2.7
	421585	U95626	Hs.302043	chemokine (C-C motif) receptor-like 2	2.7
	445158	AI992108	Hs.127206	ESTs	2.7
	421175	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.7
30	401793				2.7
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.7
	451343	AW975057	Hs.293353	ESTs	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
35	438475	W03856	Hs.13188	ESTs, Highly similar to Gene product wit	2.7
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	2.7
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	2.7
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	2.7
40	451487	AA018072		gb:ze51g02.r1 Soares retina N2b4HR Homo	2.7
	418269	AA806113	Hs.189025	ESTs	2.7
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	441963	AI733307	Hs.128002	ESTs	2.7
45	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.7
	426902	AI125334	Hs.97408	ESTs	2.7
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	2.7
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	2.7
	445265	AI218295	Hs.144942	ESTs	2.7
50	422988	AW673847	Hs.97321	ESTs	2.7
	428613	AB037749	Hs.186928	KIAA1328 protein	2.7
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	2.7
	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	2.7
	402800				2.7
55	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.7
	414729	BE466928	Hs.281901	ESTs	2.7
	453716	AA037675	Hs.152675	ESTs	2.7
	452693	T79153	Hs.48589	zinc finger protein 228	2.7
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	2.7
60	443305	AI050693	Hs.133318	ESTs	2.7
	416709	R99369	Hs.283108	hemoglobin, gamma G	2.7
	419077	AA233885	Hs.164526	ESTs	2.7
	453878	AW964440	Hs.19025	DC32	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
65	446817	AI700684	Hs.134166	ESTs	2.7
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	2.6
	410406	AI969703	Hs.1466	glycerol kinase	2.6
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.6
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	2.6
70	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.6
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	2.6
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
75	418217	AI910647	Hs.13442	ESTs	2.6
	428667	AI375550	Hs.74407	nucleolar protein p40; homolog of yeast	2.6
	414573	AI821846	Hs.71999	ESTs	2.6
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
80	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	2.6
	428483	AI908539	Hs.321444	KIAA0344 gene product	2.6
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
	405059				2.6
	425178	H16097	Hs.161027	ESTs	2.6

	442952	AI743261	Hs.131860	ESTs	2.6
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	2.6
	456179	H75490	Hs.271930	ESTs	2.6
5	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
	459456	AA486036	Hs.190124	ESTs	2.6
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	2.6
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
10	420621	AA278808		gb:zs79c09.r1 NCL_CGAP_GCB1 Homo sapiens	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	438295	AI394151	Hs.37932	ESTs	2.6
	445550	AI242754	Hs.137306	ESTs	2.6
	450469	AI955049	Hs.281326	ESTs	2.6
15	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen	2.6
	429250	H56585	Hs.198308	tryptophan rich basic protein	2.6
	437906	AA771704	Hs.194626	ESTs	2.6
	426775	AA384564	Hs.108829	ESTs	2.6
20	443372	AI792557	Hs.133107	ESTs	2.6
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	425465	L18964	Hs.1904	protein kinase C, iota	2.6
	422746	NM_004484	Hs.119651	glypican 3	2.6
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	2.6
25	424527	AW138558	Hs.267158	ESTs, Weakly similar to I54374 gene NF2	2.6
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	2.6
	411402	BE297855	Hs.69855	NRAS-related gene	2.6
	445264	AI218263	Hs.323472	EST	2.6
	458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Ce	2.6
30	415227	AW821113	Hs.72402	ESTs	2.6
	435429	AW592035	Hs.254414	ESTs, Weakly similar to 1805195B RNA-bin	2.6
	434445	AI349306	Hs.11782	ESTs	2.6
	448570	AI923944	Hs.30913	ESTs	2.6
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
35	422879	AI241409	Hs.188092	ESTs	2.6
	409026	AL137554	Hs.49927	protein kinase NYD-SP15	2.6
	425717	X07282	Hs.171495	retinoic acid receptor, beta	2.6
	429127	AA749382	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	2.6
40	438298	H23542	Hs.181788	ESTs	2.6
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.6
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.6
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.6
45	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
	437939	AW298600	Hs.141840	ESTs, Weakly similar to S59501 interfero	2.6
	430719	AA488988	Hs.293796	ESTs	2.6
	452864	AA033714	Hs.287629	hypothetical protein FLJ14260	2.6
	432095	AW022273	Hs.105769	ESTs	2.6
50	431086	AI829692	Hs.211561	ESTs	2.6
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	2.6
	423952	AW877787	Hs.136102	KIAA0853 protein	2.6
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	2.6
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.6
55	430933	AW863635		gb:MR3-SN0010-270300-103-h02 SN0010 Homo	2.6
	420691	AA829433	Hs.275343	ESTs	2.6
	429761	AI276780	Hs.135173	ESTs	2.6
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
60	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.6
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	2.6
	438647	AA813118	Hs.163230	ESTs	2.6
	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.6
65	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.6
	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.6
	428170	H05530	Hs.12565	ESTs	2.6
	457343	NM_013936	Hs.247862	olfactory receptor, family 12, subfamily	2.6
70	424020	R76946	Hs.39738	ESTs	2.6
	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.6
	411965	BE467339	Hs.280115	ESTs	2.6
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.6
	455488	AA102322		gb:z190f03.r1 Stratagene colon (937204)	2.6
75	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.6
	404285				2.6
	418744	AI887288	Hs.196379	ESTs, Weakly similar to putative p150 [H	2.6
	454714	AW815098		gb:QV4-ST0212-091199-023-f10 ST0212 Homo	2.6
80	429828	AB019494	Hs.225767	IDN3 protein	2.6
	436387	AA714760	Hs.240075	Homo sapiens cDNA FLJ13234 fis, clone OV	2.6
	448587	AI539652	Hs.28338	KIAA1546 protein	2.6
	432865	AI7653709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.6
	440479	AA886461	Hs.208161	ESTs	2.6
	443160	AI467915	Hs.36053	ESTs	2.6

	428978	AA442784	Hs.125445	ESTs	2.5
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.5
	453459	BE047032	Hs.257789	ESTs	2.5
5	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.5
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.5
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.5
	458760	AI498631	Hs.111334	ferritin, light polypeptide	2.5
	434131	AI858275	Hs.143659	ESTs	2.5
10	441805	AA285136	Hs.301914	neuronal specific transcription factor D	2.5
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	2.5
	417351	T90278	Hs.15049	ESTs	2.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sa	2.5
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	2.5
15	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	2.5
	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	453919	AW959912	Hs.7076	KIAA1705 protein	2.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.5
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	2.5
20	427491	R43279	Hs.22574	ESTs, Weakly similar to I38022 hypotheti	2.5
	435102	AW899053	Hs.76917	F-box only protein 8	2.5
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.5
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.5
	432887	AI926047	Hs.162859	ESTs	2.5
25	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5
	401078				2.5
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.5
	425201	AA352111		gb:EST60061 Activated T-cells XX Homo sa	2.5
	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
30	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
	444542	AI161293	Hs.280380	aminopeptidase	2.5
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	2.5
	428497	BE010877	Hs.98584	ESTs	2.5
	457336	AW969657	Hs.291029	ESTs	2.5
35	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	2.5
	423782	AI472209	Hs.323117	ESTs	2.5
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	2.5
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	2.5
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.5
40	417137	U46265	Hs.81281	mitochondrial ribosomal protein S21	2.5
	436787	AA908554	Hs.192756	ESTs	2.5
	440331	AL046412	Hs.202151	ESTs	2.5
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.5
	417169	R13550	Hs.246773	ESTs	2.5
45	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	2.5
	455286	BE144384		gb:MR0-HT0166-191199-004-c11 HT0166 Homo	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	2.5
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	2.5
50	446346	AI290205	Hs.309940	ESTs	2.5
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	2.5
	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	2.5
	425523	AB007948	Hs.158244	KIAA0479 protein	2.5
	433124	U51712	Hs.13775	hypothetical protein SMAP31	2.5
55	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.5
	425657	T89839	Hs.119471	ESTs	2.5
	401254				2.5
	426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	2.5
	449535	W15267	Hs.23672	low density lipoprotein receptor-related	2.5
60	433138	AB029496	Hs.59729	semaphorin sem2	2.5
	425804	BE501698	Hs.258189	ESTs	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	437267	AW511443	Hs.258110	ESTs	2.5
	454305	BE062633	Hs.28338	KIAA1546 protein	2.5
65	455631	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	2.5
	401878				2.5
	450350	T97817	Hs.174880	ESTs	2.5
	436532	AA721522		gb:nv54h12.r1 NCLCGAP_Ew1 Homo sapiens	2.5
	457460	AI143312	Hs.129206	casein kinase 1, gamma 3	2.5
70	427304	AA761526	Hs.163853	ESTs	2.5
	419721	NM_001650	Hs.288650	aquaporin 4	2.5
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	2.5
	446252	AI283125	Hs.150009	ESTs	2.5
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	2.5
75	434273	AA913143	Hs.26303	ESTs	2.5
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	2.5
	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN I	2.5
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.5
	452232	AW020603	Hs.158423	radial spoke protein 3	2.5
80	433764	AW753676	Hs.39982	ESTs	2.5
	412050	H96503	Hs.109087	Homo sapiens cDNA: FLJ22845 fis, clone K	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	2.5
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.5

	408813	AI580090	Hs.48295	RNA helicase family	2.5
	414109	BE250744		gb:600943376F1 NIH_MGC_17 Homo sapiens c	2.5
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.5
5	419985	H66373	Hs.15973	ESTs, Highly similar to bA393J16.3 [H.sa	2.5
	417859	T26453		gb:AB214F6R Infant brain, LLNL array of	2.5
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.5
	448015	AI458065	Hs.23196	ESTs	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
10	445865	AI262584	Hs.145575	ESTs	2.5
	451800	AW977435	Hs.323867	ESTs	2.5
	456987	AI557290	Hs.173536	ESTs	2.5
	403568				2.5
	435209	AW027809	Hs.187698	Homo sapiens cytomegalovirus partial fus	2.5
15	430371	D87466	Hs.240112	KIAA0276 protein	2.5
	418033	W68180	Hs.259855	elongation factor-2 kinase	2.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.5
	453619	H87648	Hs.33922	Homo sapiens, clone MGC:9084, mRNA, comp	2.5
	431071	AA491379		gb:aa65f05.r1 NCL_CGAP_GCB1 Homo sapiens	2.5
20	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.5
	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	2.4
	417318	AW953937	Hs.12891	ESTs	2.4
25	413382	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.4
	406748	AW339106	Hs.217493	annexin A2	2.4
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.4
	441817	AW969706	Hs.293332	ESTs	2.4
	450551	AJ010046	Hs.25155	neuroepithelial cell transforming gene 1	2.4
30	457940	AL360159	Hs.306517	Homo sapiens TRIPartite motif protein ps	2.4
	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	2.4
	436907	AA737171	Hs.131809	ESTs	2.4
	429399	AA452244	Hs.16727	ESTs	2.4
	448782	AL050295	Hs.22039	KIAA0758 protein	2.4
35	434404	AW445034	Hs.256578	ESTs	2.4
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	2.4
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	2.4
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	2.4
	450705	U90304	Hs.25351	iroquois homeobox protein 5	2.4
40	425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1 (J	2.4
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	2.4
	458986	AI802772	Hs.208655	ESTs	2.4
	443861	AW449462	Hs.134743	ESTs	2.4
	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo	2.4
45	415250	F02614	Hs.27319	ESTs	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
	443919	AI091284	Hs.135224	ESTs, Weakly similar to A47582 B-cell gr	2.4
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.4
	400385	NM_020389	Hs.283104	putative capacitative calcium channel	2.4
50	411322	AW887330	Hs.172405	cell division cycle 27	2.4
	434638	H50758		gb:yp86e06.r1 Soares fetal liver spleen	2.4
	435559	AF209198	Hs.42636	zinc finger protein 277	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
	448005	AW207437	Hs.170378	ESTs	2.4
55	454201	AB023191	Hs.44131	KIAA0974 protein	2.4
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.4
	449486	AI652715	Hs.270811	ESTs	2.4
	421516	AI362418	Hs.105379	FT005 protein	2.4
	412167	AW897230		gb:CM0-NN0057-150400-335-a11 NN0057 Homo	2.4
60	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	2.4
	400641				2.4
	430576	AA767125	Hs.293574	ESTs	2.4
	434423	NM_006769	Hs.3844	LIM domain only 4	2.4
65	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.4
	441499	AW298235	Hs.101689	ESTs	2.4
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.4
	417819	AI253112	Hs.133540	ESTs	2.4
	431728	NM_007351	Hs.268107	multimerin	2.4
70	425025	AW953168	Hs.12407	ESTs	2.4
	421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	2.4
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.4
	408867	AA437199	Hs.656	cell division cycle 25C	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
75	445038	AI635444	Hs.143917	dJ467N11.1 protein	2.4
	450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.4
80	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.4
	453864	AW021407	Hs.21068	hypothetical protein	2.4
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.4
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.4
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	2.4

	447357	AI375922	Hs.159367	ESTs	2.4
	452631	AI188658	Hs.87496	ESTs	2.4
	405041				2.4
	405472				2.4
5	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	2.4
	433868	AA612960	Hs.337300	ESTs	2.4
	437119	AI379921	Hs.177043	ESTs	2.4
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.4
10	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.4
	434936	AI285970	Hs.183817	ESTs	2.4
	408918	BE218603	Hs.279708	ESTs	2.4
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.4
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.4
15	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	2.4
	446659	AI335361	Hs.226376	ESTs	2.4
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	2.4
	434995	AW974995		gb:EST387100 MAGE resequences, MAGN Homo	2.4
	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.4
20	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	2.4
	427131	AA448460	Hs.112017	GE36 gene	2.4
	442039	AW276240	Hs.128352	ESTs	2.4
	448595	AB014544	Hs.21572	KIAA0644 gene product	2.4
	432949	AA570749	Hs.298866	ESTs	2.4
25	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.4
	417420	T85150	Hs.268814	ESTs	2.4
	427551	T96203		gb:ye48b07.r1 Soares fetal liver spleen	2.4
	420057	AA806899	Hs.184387	ESTs	2.4
	434950	AW974892		gb:EST386997 MAGE resequences, MAGN Homo	2.4
30	425497	AA524596		gb:nh34b02.s1 NCI_CGAP_Pr3 Homo sapiens	2.4
	438214	H06076	Hs.26320	TRABID protein	2.4
	416100	H18700	Hs.268799	ESTs	2.4
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
35	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	2.4
	419179	AW275291	Hs.113009	hypothetical protein FLJ22527	2.4
	436391	AJ227892	Hs.146274	ESTs	2.4
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	2.4
	447499	AW262580	Hs.147674	protocadherin beta 16	2.4
40	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.4
	412877	BE011168		gb:PM3-BN0218-100500-003-d08 BN0218 Homo	2.4
	435985	AA703154	Hs.191934	ESTs	2.4
	440674	BE561546		gb:601347208F1 NIH_MGC_8 Homo sapiens cD	2.4
	446476	AW294072	Hs.141376	ESTs	2.4
45	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.4
	435731	AA699581	Hs.186811	ESTs	2.4
	437105	AA744554	Hs.222127	ESTs	2.4
	406091				2.4
	457024	AA397546	Hs.119151	ESTs	2.4
50	404249				2.4
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	2.4
	424943	AJ077260	Hs.153924	death-associated protein kinase 1	2.4
	444229	AV648613	Hs.282397	ESTs	2.4
	404860				2.4
55	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	2.4
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.4
	420843	H96982	Hs.42321	ESTs	2.4
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.4
	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
60	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	2.4
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG	2.3
65	418782	AI792648	Hs.14665	ESTs	2.3
	447870	BE139479	Hs.161492	ESTs	2.3
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.3
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	2.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	2.3
70	424049	AB014524	Hs.138380	KIAA0624 protein	2.3
	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.3
	430702	U56979	Hs.250651	H factor 1 (complement)	2.3
	409620	AA076278	Hs.13277	hypothetical protein FLJ22054	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.3
75	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	2.3
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	2.3
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	2.3
	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
80	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	2.3
	404513				2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	448506	AI524673	Hs.38170	ESTs	2.3
	434811	AW971205	Hs.114280	ESTs	2.3

5	457065	AI476318	Hs.192480	ESTs	2.3
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	2.3
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	2.3
	423596	AA328195	Hs.234101	ESTs, Weakly similar to CTL1 protein [H.	2.3
	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.3
10	435867	AA954229	Hs.114052	ESTs	2.3
	440196	N72847	Hs.125221	ESTs	2.3
	401213				2.3
	407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo	2.3
	442490	AW965078	Hs.30212	thyroid receptor interacting protein 15	2.3
15	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.3
	438138	R98299	Hs.177502	ESTs	2.3
	440283	AI732892	Hs.190489	ESTs	2.3
	447039	AV661798	Hs.282915	ESTs	2.3
	412777	AI335773	Hs.270123	ESTs	2.3
20	421424	AW452690	Hs.258775	ESTs	2.3
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.3
	440555	D31292	Hs.6853	hypothetical protein FLJ22167	2.3
	451516	AI800515	Hs.12024	ESTs	2.3
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	2.3
25	421046	AA810854	Hs.89081	ESTs	2.3
	423604	AA486585	Hs.258901	ESTs	2.3
	409029	BE087807		gb:QV1-BT0681-290400-181-g02 BT0681 Homo	2.3
	444206	AW301017	Hs.146492	ESTs	2.3
	451836	T63673	Hs.173220	ESTs	2.3
30	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.3
	436671	AW137159	Hs.146151	ESTs	2.3
	434988	AI418055	Hs.161160	ESTs	2.3
	452862	AW378065	Hs.8687	ESTs	2.3
35	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	2.3
	410606	AW418779	Hs.114889	ESTs	2.3
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.3
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	2.3
	430217	N47863	Hs.336901	ribosomal protein S24	2.3
40	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	2.3
	421253	AI188102	Hs.31028	ESTs	2.3
	438180	AA808189	Hs.272151	ESTs	2.3
	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3
45	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	2.3
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	2.3
	448831	AL080123	Hs.22182	zinc finger protein 23 (K0X 16)	2.3
	412953	Z45794	Hs.238809	ESTs	2.3
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	2.3
50	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	423003	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	2.3
	428595	AB037795	Hs.186547	KIAA1374 protein	2.3
	437887	AA811524	Hs.29263	hypothetical protein FLJ11896	2.3
	447720	AL038765	Hs.161304	ESTs	2.3
55	452355	N54926	Hs.29202	G protein-coupled receptor 34	2.3
	408374	AW025430	Hs.155591	forkhead box F1	2.3
	440381	AA917808	Hs.190495	ESTs	2.3
	425478	AB007953	Hs.268840	ESTs	2.3
	432231	AA339977	Hs.274127	CLST 11240 protein	2.3
60	431757	AA196930	Hs.268526	Homo sapiens chromosome 21q22.1 anonymou	2.3
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.3
	452837	AL121053	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	2.3
	417426	NM_002291	Hs.82124	laminin, beta 1	2.3
	423739	AA398155	Hs.97600	ESTs	2.3
65	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	2.3
	425876	AW005887	Hs.234058	ESTs	2.3
	457411	AW085961	Hs.130093	ESTs	2.3
	413136	BE066941		gb:PM0-BT0340-091299-002-a11 BT0340 Homo	2.3
	420313	AB023230	Hs.96427	KIAA1013 protein	2.3
70	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
	436331	AI239495	Hs.120189	ESTs	2.3
	439275	AF086093	Hs.141566	ESTs	2.3
	449272	AW137656	Hs.197645	ESTs	2.3
75	454352	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo	2.3
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	2.3
	407242	M18728		gb:Human nonspecific crossreacting antig	2.3
	445326	AI220072	Hs.165893	ESTs	2.3
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.3
80	452607	AI160029	Hs.61438	ESTs	2.3
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N116 (f	2.3
	418851	AI417828	Hs.192435	ESTs	2.3
	458332	AI000341	Hs.220491	ESTs	2.3
	432565	AA553477	Hs.152428	ESTs	2.3
	437511	AI807500	Hs.125247	ESTs	2.3
	430957	AI937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.3
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	2.3

	448225	AI476429	Hs.19238	ESTs	2.3
	408955	BE315170	Hs.8087	NAG-5 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
5	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypotheti	2.3
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	440348	AW015802	Hs.47023	ESTs	2.3
	436340	R42246	Hs.21606	ESTs	2.3
10	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	2.3
	438462	AI624122	Hs.89578	general transcription factor IIH, polype	2.3
	411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.3
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	2.3
	412505	AA974491	Hs.21734	ESTs	2.3
	418236	AW994005	Hs.337534	ESTs	2.3
15	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	2.3
	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.3
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.3
	433404	T32982	Hs.102720	ESTs	2.3
20	409517	X90780	Hs.120036	troponin I, cardiac	2.3
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
	445641	AI245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	2.3
25	437770	AA767881	Hs.122897	ESTs	2.3
	409064	AA062954	Hs.141883	ESTs	2.3
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.3
	449869	W57990	Hs.60059	Homo sapiens cDNA FLJ11478 fis, clone HE	2.3
	422108	AA297914	Hs.111749	postmeiotic segregation increased (S. ce	2.3
	418251	AA832123	Hs.177723	ESTs	2.3
30	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA P	2.3
	413638	H71252		gb:ys12h12.s1 Soares fetal liver spleen	2.3
	415980	R52414		gb:yg80b05.r1 Soares infant brain 1NIB H	2.3
	449232	AW192780	Hs.196080	ESTs	2.3
35	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.3
	454389	AW752571		gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.3
	438089	W05391	Hs.83623	nuclear receptor subfamily 1, group I, m	2.3
	400238				2.3
	404488				2.3
40	407809	AW082279	Hs.244106	ESTs	2.3
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586I1518 (f	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	2.3
45	426567	AA381579	Hs.182962	ESTs	2.3
	435708	AI362949	Hs.75169	ESTs	2.3
	441417	AI733297	Hs.144474	ESTs	2.3
	445117	AI208754	Hs.147369	ESTs	2.3
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.2
50	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	2.2
	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	2.2
	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	2.2
	420653	AI224532	Hs.88550	ESTs	2.2
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.2
55	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	2.2
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.2
	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
60	437637	AJ003029	Hs.65792	syntrophin, gamma 2	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	446164	AW273539	Hs.288750	hypothetical protein FLJ23577	2.2
	450232	BE300815	Hs.201326	ESTs	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	402745				2.2
65	434008	AA740878	Hs.112982	ESTs	2.2
	439492	AF086310	Hs.103159	ESTs	2.2
	436853	BE328074	Hs.148661	ESTs	2.2
	417648	R06552		gb:yf09e12.r1 Soares fetal liver spleen	2.2
70	427690	AI253134	Hs.283410	ESTs	2.2
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.2
	450229	R18717	Hs.8929	hypothetical protein FLJ11362	2.2
	400756				2.2
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	2.2
75	403388				2.2
	433643	AI821787	Hs.179586	ESTs	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
80	439920	H05430	Hs.288433	neurotrophin	2.2
	432436	AW300248	Hs.181693	ESTs	2.2
	429493	AL134708	Hs.145998	ESTs	2.2
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.2
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	2.2

	442757	AI739528	Hs.28345	ESTs	2.2
	430212	AA469153		gb:nc67f04.s1 NCL_CGAP_Pr1 Homo sapiens	2.2
	437146	AA730977		gb:nw55f05.s1 NCL_CGAP_Ew1 Homo sapiens	2.2
5	432101	AI918950	Hs.123642	EphA3	2.2
	459644				2.2
	453887	BE564037	Hs.36237	hypothetical protein	2.2
	431170	AW971246	Hs.291022	ESTs	2.2
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.2
10	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	2.2
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	2.2
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.2
	425810	AI923627	Hs.31903	ESTs	2.2
	433037	NM_014158	Hs.279938	HSPC067 protein	2.2
15	407162	N63855	Hs.142634	zinc finger protein	2.2
	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	AI347274		gb:tc05d02.x1 NCL_CGAP_Co16 Homo sapiens	2.2
	454766	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414221	AW450979		gb:UL-H-BI3-ala-a-12-0-UL.s1 NCL_CGAP_Su	2.2
20	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: hamy2)	2.2
	400639				2.2
	406149				2.2
	424027	AW337575	Hs.201591	ESTs	2.2
	427531	AA405097	Hs.97957	ESTs	2.2
25	448353	BE407125	Hs.231510	ESTs	2.2
	417669	T99898		gb:ye68g01.r1 Soares fetal liver spleen	2.2
	449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	2.2
	452335	AW188944	Hs.61272	ESTs	2.2
	419216	AJ076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
30	447748	AI422023	Hs.161338	ESTs	2.2
	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	438550	AW976002	Hs.258402	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
35	444540	AI693927	Hs.265165	ESTs	2.2
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.2
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.2
	439443	AF086261	Hs.127892	ESTs	2.2
	418824	AW751661	Hs.53542	choreoacanthocytosis gene; KIAA0986 prot	2.2
40	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.2
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.2
	432702	AW973953	Hs.293744	ESTs	2.2
	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p	2.2
	425570	AA359558		gb:EST68590 Fetal lung II Homo sapiens c	2.2
45	414935	C15671		gb:C15671 Clontech human aorta polyA+mR	2.2
	453153	N53893	Hs.24360	ESTs	2.2
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	2.2
	439867	AA847510	Hs.161292	ESTs	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
50	433420	AI674093	Hs.293961	ESTs, Moderately similar to putative DNA	2.2
	434690	AI867679	Hs.148410	ESTs	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	431688	AA513906		gb:ng67c08.s1 NCL_CGAP_Lip2 Homo sapiens	2.2
55	403133				2.2
	414885	AA157531	Hs.269276	ESTs, Moderately similar to S65657 alpha	2.2
	432111	AW972777		gb:EST384871 MAGE resequences, MAGL Homo	2.2
	410073	AW408163	Hs.58488	catenin (cadherin-associated protein), a	2.2
	448869	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
60	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.2
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	2.2
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.2
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	2.2
	403378				2.2
65	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (2.2
	438580	AA811262	Hs.299202	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Claspin	2.2
	412282	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	2.2
	411966	AA099113	Hs.118609	ESTs	2.2
70	443915	Z40763	Hs.135292	ESTs	2.2
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.2
	446094	AK001760	Hs.13801	KIAA1685 protein	2.2
	436486	AA742221	Hs.120633	ESTs	2.2
	411139	AW819461		gb:RCS-ST0293-061299-031-C03 ST0293 Homo	2.2
75	409070	AA063003	Hs.224560	ESTs	2.2
	432713	AL118623	Hs.29494	PRO1912 protein	2.2
	419384	AA490866	Hs.39429	ESTs	2.2
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.2
	408444	AW661839	Hs.253204	ESTs	2.2
80	432128	AA127221	Hs.117037	ESTs	2.2
	418027	AB037807	Hs.83293	hypothetical protein	2.2
	446060	Z42061	Hs.27004	ESTs	2.2
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.2
	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU8_HUMAN A	2.2

	443401	AI394067	Hs.160159	ESTs	2.2
	424665	AW368576	Hs.139851	caveolin 2	2.2
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	2.2
5	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.2
	414564	AA164803	Hs.71994	ESTs, Weakly similar to I38022 hypotheti	2.2
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	2.2
	419160	AA911342	Hs.35524	KIAA1559 protein	2.2
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	2.2
10	442879	AF032922	Hs.8813	syntaxin binding protein 3	2.2
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.2
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	2.2
	432074	AA525248	Hs.149723	ESTs	2.2
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	2.2
15	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	2.2
	409723	AW885757	Hs.257862	ESTs	2.2
	425627	AF019612	Hs.297007	membrane-bound transcription factor prot	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	449369	AA001256	Hs.27260	ESTs	2.2
20	425514	AF112345	Hs.158237	integrin, alpha 10	2.2
	455821	BE143341		gb:MRO-HT0162-191099-002-d04 HT0162 Homo	2.2
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.2
	432284	AA532807	Hs.105822	ESTs	2.2
	403467				2.2
25	436032	AA150797	Hs.109276	latexin protein	2.2
	404356				2.2
	434205	AF119861	Hs.283032	hypothetical protein PRO2015	2.2
	405257				2.2
	402103				2.2
30	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.2
	432985	T92363	Hs.178703	ESTs	2.2
	417649	AW239285	Hs.82359	tumor necrosis factor receptor superfam	2.2
	431277	AA501806	Hs.249965	ESTs	2.2
	454056	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	2.2
35	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	448390	AL035414	Hs.21068	hypothetical protein	2.2
40	449939	T86420	Hs.272139	ESTs	2.2
	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.2
	404555				2.2
	418186	BE541042	Hs.23240	Homo sapiens cDNA: FLJ21848 fis, clone H	2.2
	419981	AA897581	Hs.128773	ESTs	2.2
45	449581	AI989517	Hs.181605	ESTs	2.2
	419229	AI827237	Hs.282884	ESTs	2.2
	403691				2.2
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.2
	443479	AF027219	Hs.9443	zinc finger protein 202	2.2
50	425329	AI961644	Hs.145444	Homo sapiens cDNA FLJ11494 fis, clone HE	2.2
	453345	AA302862	Hs.90063	neurocalcin delta	2.2
	424335	AW021508	Hs.28170	ESTs	2.2
	451072	AA013451	Hs.117929	ESTs	2.2
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	2.2
55	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.2
	438035	AA938198	Hs.146123	poly(A) polymerase gamma	2.2
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.2
	400241				2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
60	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	2.2
	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	446009	AI989885	Hs.231926	ESTs	2.2
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	2.1
	416441	BE407197		gb:601301552F1 NIH_MGC_21 Homo sapiens c	2.1
65	414891	R27124	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE	2.1
	430172	AA468591	Hs.161889	ESTs	2.1
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.1
	422985	AU076411	Hs.1602	dihydropyrimidine dehydrogenase	2.1
70	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	2.1
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	2.1
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	2.1
	438379	N23018	Hs.171391	C-terminal binding protein 2	2.1
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
75	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.1
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	2.1
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.1
	437132	AL049353	Hs.297268	ESTs	2.1
	415304	T66079	Hs.12799	ESTs	2.1
80	450152	AI138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	2.1
	421147	AW592167	Hs.293299	ESTs	2.1
	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.1
	451750	AA280851	Hs.226930	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.1

	406945	K01383	Hs.173451	metallothionein 1A (functional)	2.1
	452449	AW068658	Hs.20943	ESTs	2.1
	436009	H57130	Hs.120925	ESTs	2.1
5	418637	T86737	Hs.193536	ESTs	2.1
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	2.1
	449203	AI634578	Hs.282121	ESTs	2.1
	437751	AA767373	Hs.35669	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	428412	AA428240	Hs.126083	ESTs	2.1
10	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.1
	441967	AA972742	Hs.209786	ESTs	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.1
15	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
	431229	AA496479	Hs.259929	ESTs	2.1
	435148	AI918049	Hs.124961	ESTs	2.1
	436349	AI445255	Hs.115315	ESTs	2.1
	446895	AA166655	Hs.282803	ESTs	2.1
20	448582	AI538880	Hs.94812	ESTs	2.1
	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.1
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	2.1
	451874	AW963137	Hs.194233	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	448076	AJ133123	Hs.20196	adenylate cyclase 9	2.1
25	443484	AI091458	Hs.134559	ESTs	2.1
	430686	NM_001942	Hs.2633	desmoglein 1	2.1
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	2.1
	407624	AW157431	Hs.248941	ESTs	2.1
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.1
30	428923	BE047698	Hs.188785	ESTs	2.1
	422496	AA311301	Hs.278827	ESTs	2.1
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.1
	408418	AW963897	Hs.44743	KIAA1435 protein	2.1
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.1
35	427434	BE538374	Hs.301732	hypothetical protein MGC5306	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	459325	AW088369	Hs.282184	ESTs	2.1
	416996	W91892	Hs.59609	ESTs	2.1
40	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.1
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kd)	2.1
	418894	W73921	Hs.50743	ESTs	2.1
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.1
	437378	AI198823	Hs.160473	ESTs	2.1
	454100	AI693231	Hs.126043	chromosome 21 open reading frame 51	2.1
45	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	2.1
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	2.1
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.1
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	2.1
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	2.1
50	424103	NM_001918	Hs.139410	dihydrolipoamide branched chain transacy	2.1
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	2.1
	449911	AI262106	Hs.12653	ESTs	2.1
	449509	AA001615	Hs.84561	ESTs	2.1
	452762	AW501435	Hs.278582	v-aki murine thymoma viral oncogene homo	2.1
55	422839	AI674784	Hs.298908	ESTs	2.1
	435040	AI932350	Hs.152825	ESTs	2.1
	401200				2.1
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.1
	442262	BE170651	Hs.8700	deleted in liver cancer 1	2.1
60	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypotheti	2.1
	453908	AW613920	Hs.282178	ESTs	2.1
	446965	BE242873	Hs.16677	WD repeat domain 15	2.1
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
65	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
	455995	BE179408		gb:IL3-HT0618-060500-125-B07 HT0618 Homo	2.1
	422411	AW749443	Hs.22511	ESTs	2.1
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	2.1
	446893	AI610818	Hs.7110	ESTs	2.1
70	442992	AI914699	Hs.13297	ESTs	2.1
	407021	U52077		gb:Human mariner1 transposase gene, comp	2.1
	436938	AW139680	Hs.161393	ESTs	2.1
	433194	AB040883	Hs.83243	KIAA1450 protein	2.1
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	2.1
75	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	2.1
	434739	AA804487	Hs.144130	ESTs	2.1
	406468				2.1
	457023	AA001732	Hs.173233	hypothetical protein FLJ10970	2.1
	416226	N55342	Hs.34372	ESTs	2.1
80	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.1
	432810	AA863400	Hs.23054	ESTs	2.1
	412894	R09778	Hs.186510	ESTs	2.1
	430802	D13752	Hs.184927	cytochrome P450, subfamily XIB (steroid	2.1
	436981	AA740891	Hs.293316	ESTs	2.1

	452501	AB037791	Hs.29716	hypothetical protein FLJ10980	2.1
	449838	AB020653	Hs.24024	KIAA0846 protein	2.1
	447160	AA330310	Hs.24181	ESTs	2.1
5	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	2.1
	440137	AA866199	Hs.171397	ESTs	2.1
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	2.1
	436471	AA719813	Hs.117662	ESTs	2.1
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	2.1
10	426782	R14614	Hs.191254	ESTs	2.1
	430027	AB023197	Hs.227743	KIAA0980 protein	2.1
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.1
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	2.1
	427115	AW972853	Hs.112237	ESTs	2.1
15	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.1
	400451				2.1
	435255	W87434	Hs.106015	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	418375	NM_003081	Hs.84389	synaptoosomal-associated protein, 25kD	2.1
20	442835	AI021989	Hs.131903	ESTs	2.1
	400196				2.1
	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.1
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	2.1
	438940	AF075045	Hs.271609	ESTs	2.1
25	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.1
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	2.1
	410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	2.1
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.1
30	419088	AI538323	Hs.52620	integrin, beta 8	2.1
	447373	AI381922	Hs.158781	ESTs	2.1
	457465	AW301344	Hs.122908	DNA replication factor	2.1
	413918	AW015898	Hs.71245	ESTs	2.1
	402820				2.1
35	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
	428552	AW274560	Hs.129520	ESTs	2.1
	435464	BE548300	Hs.192999	ESTs, Moderately similar to KIAA0961 pro	2.1
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	2.1
40	420838	AW118210	Hs.5244	ESTs	2.1
	428231	U17989	Hs.183105	nuclear autoantigen	2.1
	434933	R91095	Hs.4276	KIAA1701 protein	2.1
	444870	AI200621	Hs.148504	ESTs	2.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.1
45	429183	AB014604	Hs.197955	KIAA0704 protein	2.1
	439155	H81076	Hs.269001	ESTs	2.1
	442787	W93048	Hs.250723	hypothetical protein MGC2747	2.1
	429864	AA460039	Hs.286	ribosomal protein L4	2.1
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.1
	437140	AA312799	Hs.283689	activator of CREM in testis	2.1
50	421991	NM_014918	Hs.110488	KIAA0990 protein	2.1
	446534	AI307356	Hs.175225	ESTs	2.1
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.1
	444838	AV651680	Hs.208558	ESTs	2.1
	402318				2.1
55	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	421306	AA806207	Hs.125889	ESTs	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	429088	D61542	Hs.227716	KIAA0934 protein	2.1
60	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	2.1
	428060	AA420616	Hs.249483	ESTs	2.1
	419953	BE267154	Hs.125752	ESTs	2.1
	443718	AI083580	Hs.221373	ESTs	2.1
	444187	AW138466	Hs.151274	ESTs	2.1
65	428048	AA705745		gb:zf41b11.s1 Soares_fetal_heart_NbHH19W	2.1
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.1
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.1
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.1
	430335	D80007	Hs.239499	KIAA0185 protein	2.1
70	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.1
	434029	AA621763	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.1
	410945	AW811552		gb:QV2-ST0145-071299-017-h10 ST0145 Homo	2.1
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.1
	433374	AI821409	Hs.332789	EST	2.1
75	445644	R77766	Hs.271593	ESTs, Moderately similar to A47582 B-cel	2.1
	450271	AI693900	Hs.200920	ESTs	2.1
	448084	AI467800	Hs.271000	ESTs, Weakly similar to I38022 hypotheti	2.1
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	2.1
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	2.1
80	435542	AA687376	Hs.269533	ESTs	2.1
	443544	AI076315	Hs.16359	ESTs	2.1
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	2.1
	405759				2.1
	446242	N66336	Hs.7360	ESTs	2.1

	457938	AI373638	Hs.133900	ESTs	2.1
	433017	Y15067	Hs.279914	zinc finger protein 232	2.1
	436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	2.1
5	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.1
	439224	AW471088	Hs.145950	ESTs, Highly similar to T08692 hypotheti	2.1
	410976	R36207	Hs.25092	hypothetical protein MGC10744	2.1
	454574	AW809109		gb:MR4-ST0117-070100-027-a04 ST0117 Homo	2.1
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	2.1
10	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	2.1
	446891	AL036877	Hs.282878	ESTs	2.1
	434294	AJ271379	Hs.76194	ribosomal protein S5	2.1
	449057	AB037784	Hs.22941	KIAA1363 protein	2.1
	432769	AA620814	Hs.144959	ESTs	2.1
15	441224	AU076964	Hs.7753	calumenin	2.1
	407891	AA486620	Hs.41135	endomucin-2	2.1
	429017	AA463605	Hs.66295	multi-PDZ-domain-containing protein	2.1
	406817	AI936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
	430566	AA481282	Hs.190149	ESTs	2.1
20	449208	AW263635	Hs.48643	ESTs	2.1
	451397	AA017432	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	2.1
	452042	H38857	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	2.1
	444779	AI192105	Hs.147170	ESTs	2.0
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	2.0
25	415954	AA171850	Hs.42251	ESTs	2.0
	420273	AI652864	Hs.197257	ESTs	2.0
	411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.0
	422389	AF240635	Hs.115897	protocadherin 12	2.0
	446994	AV650435	Hs.16755	MBIP protein	2.0
30	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	2.0
	422654	AA314316	Hs.163725	ESTs	2.0
	425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	2.0
	405634				2.0
	451562	H04150	Hs.107708	ESTs	2.0
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.0
	422095	AI688872	Hs.282804	hypothetical protein FLJ22704	2.0
	442010	AI032680	Hs.132213	ESTs	2.0
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	2.0
	425312	AA354940	Hs.145958	ESTs	2.0
40	415191	AA190381	Hs.120810	ESTs	2.0
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	2.0
	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1	2.0
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.0
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	2.0
45	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	2.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	2.0
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
50	429418	AI381028	Hs.118769	ESTs	2.0
	445829	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.0
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	2.0
55	400462				2.0
	422003	AA361760	Hs.296326	ESTs	2.0
	444585	AW170015	Hs.6594	ESTs	2.0
	444898	AI201548	Hs.308338	ESTs	2.0
	403525				2.0
60	443031	AW134696	Hs.49418	ESTs	2.0
	430818	AI311928		gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	2.0
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PNO099 son3 prot	2.0
	440941	BE268362	Hs.7535	COBW-like protein	2.0
	409627	AW997628	Hs.313637	ESTs	2.0
65	433258	AI806626	Hs.207300	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.0
	412863	AA121673	Hs.59757	zinc finger protein 281	2.0
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.0
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	2.0
	417280	AW173116	Hs.262206	ESTs	2.0
70	423528	AB011137	Hs.300938	KIAA0565 gene product	2.0
	424800	AL035588	Hs.153203	MyoD family inhibitor	2.0
	446019	AI362520	Hs.279789	histone deacetylase 3	2.0
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.0
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	2.0
75	430473	AW130690	Hs.59962	ESTs	2.0
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	2.0
	438118	AW753311	Hs.259415	ESTs	2.0
	400859				2.0
	405829				2.0
80	415258	AW752247	Hs.293853	ESTs	2.0
	420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypotheti	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	2.0
	453118	AW195849	Hs.252757	ESTs	2.0

5	430706	NM_003540	Hs.247816	H4 histone family, member C	2.0
	420568	F09247	Hs.247735	protocadherin alpha 10	2.0
	452759	AW590773	Hs.258996	ESTs	2.0
	408496	AI683802	Hs.136182	ESTs	2.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	2.0
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	2.0
	450086	AW016343	Hs.233301	ESTs	2.0
	410853	H04588	Hs.30469	ESTs	2.0
10	438607	AW080237	Hs.252884	ESTs	2.0
	422232	D43945	Hs.113274	transcription factor EC	2.0
	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
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	446551	AI308176	Hs.65636	ESTs	2.0
	438315	R56795	Hs.82419	ESTs	2.0
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	401986				2.0
	420335	AA258771	Hs.43616	Homo sapiens mRNA for FLJ00029 protein,	2.0
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
20	435413	AI267476	Hs.46669	ESTs	2.0
	458175	AW296024	Hs.150434	ESTs	2.0
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.0
	417494	AI369494	Hs.222137	ESTs	2.0
	416045	H15990	Hs.31403	ESTs	2.0
25	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	2.0
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	2.0
	411578	AW238524		gb:xp27c05.x1 NCL_CGAP_HN10 Homo sapiens	2.0
	453116	AI276680	Hs.146086	ESTs	2.0
	426692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.0
30	435608	AW183971	Hs.250896	ESTs	2.0
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	458308	AI828155	Hs.211055	ESTs	2.0
	438177	BE327015	Hs.281391	ESTs	2.0
	415205	H71616	Hs.135233	ESTs	2.0
	427244	AA402400	Hs.178045	ESTs	2.0
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	405966				2.0
40	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	427739	AW196755	Hs.98105	NYD-SP14 protein	2.0
	433584	AW295399		gb:U1-H-BI2-ahv-h-03-0-UI.s1 NCL_CGAP_Su	2.0
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	439474	AI824060	Hs.211501	ESTs	2.0
45	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.0
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	453108	AI311457	Hs.99472	ESTs	2.0
	447101	N72185	Hs.44189	ESTs	2.0
50	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	2.0
	426226	AA769045		gb:oa80h07.s1 NCL_CGAP_GCB1 Homo sapiens	2.0
	401157				2.0
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.0
	425646	AW157044	Hs.158512	cyclin-dependent kinase-like 2 (CDC2-rel	2.0
55	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	2.0
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	2.0
	402855				2.0
	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	2.0
	445672	AI907438	Hs.282862	ESTs	2.0
60	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.0
	411941	AW876909	Hs.25201	ESTs, Weakly similar to FAT DROME CADHER	2.0
	430664	AW969834	Hs.303303	ESTs	2.0
	402812				2.0
	457434	AW628192	Hs.18851	hypothetical protein FLJ10875	2.0
65	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
	402048				2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	2.0
	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
70	437373	H67505	Hs.191979	KIAA1733 protein	2.0
	439217	AF086041	Hs.42975	ESTs	2.0
	446609	BE395090	Hs.15535	Homo sapiens clone 24582 mRNA sequence	2.0

75 TABLE 3B: List of accession numbers for primekeys lacking unigenelD's for Table 3A. For each such probeset is listed a gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

80 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT number Accession

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	409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
	410008	116812_1	AA079552 BE142525 BE142527
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	412248	1285000_1	BE176480 AW903298 AW903313
	412282	1287679_1	BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
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	416871	1626761_1	H98716 N90792 N24283
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	417859	1703724_1	T26453 Z44226 R20425
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	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	420621	195113_1	AA278808 BE082076 BE081812 BE081581
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	422156	212379_1	N34524 AA305071 AW954803 AA502335 A1433430 A1203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512
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	422977	223410_1	AA631498 A1017191 AA491211 AA761823 AA714555 AA768099 AA808286 A1934069 AA570223 AA574389 AA582438 A1745346 AW964510
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	426603	269825_1	AA382291 AA994657
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	431322	331543_1	AW970622 AA503009 AA502998 AA502805 T92188
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	432189	342819_1	AA527941 AI810608 AI620190 AA635266
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528755
	432779	354024_1	AW979241 AA565006 AA847102
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	432869	355475_1	AW974094 AA569074 AA602574
	433347	36388_1	AF023130 AF181250 AA984703 AA694303 AA351792
	433492	367934_1	AW605849 AW262898 N41060 AA594852
	433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
	433644	371919_1	AW342028 AA641080 AA603282
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45	435634	409239_1	T82384 R05307 AA693714
	436532	421802_1	AA721522 AW975443 T93070
	437146	43371_1	AA730977 AI261584 AA334473 Z43283 AW875861 AW938044 BE150701 AW936262 AA306862 BE565575 BE567380 AA728920 AA167612
	438005	447553_1	AI239729 AI251752 AA485791 BE568425 AW962958
	438458	457837_1	BE151746 BE336853 D63271 T94955 AA774994
50	438909	46684_1	AW975186 AA807807 D29548
	438993	467651_1	AF085839 R69137 AW188788 R69254
	440320	491930_1	AA828995 AA834879 AI926361
	440674	49997_1	AA879294 N67538 AI474541
	443613	575391_1	BE561546 Z25124 AI307139 Z28800
55	443657	576685_1	AI079356 W23287
	444314	600667_1	R14973 R14967 AI081006
	444610	612257_1	AI140497 AW749625 AW749626 AW749644
	444910	624951_1	AI174783 R83569 R12271
	446096	661959_1	AI201849 BE069007 AW946544
60	446901	697809_1	AI276454 AI633717 AI275116
	447197	711623_1	AI347274 AW844024
	448404	761515_1	R36075 AI366546 R36167
	449540	80945_2	BE089973 AI498612 AW805032
65	450024	82296_1	AA001713 H63836
	450458	83586_1	AA005129 AA679084 AA694399
	450522	837264_1	AA009926 BE149301
	451024	85565_1	AI698839 AI909260 AI909259
	451487	87131_1	AA442176 AA259181
	452453	918300_1	AA018072 N46370 R84847
70	452542	921410_1	AI902519 AI902518 AI902516
	453823	982526_1	AW812256 AW812257 AI906423 AI906422
	453901	986414_1	AL137967 BE064160 BE064186
	454190	1049996_1	BE065902 AW749032 AW003637
75	454193	1050256_1	AW177821 AW177896 AW177867
			BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091
			AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220
			AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129
			AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108
			AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156
			AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598 BE140957
80	454352	1129667_1	AW389668 AW389657 AW609198 AW389649
	454359	1130674_1	N71277 AW390764
	454389	115682_1	AW752571 AW847602 AA077979
	454403	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093

5	454455	1206965_1	AW752710 BE180336 BE180186
	454566	1224432_1	AW807605 AW807690 AW807839 AW807752 AW807673 AW807667 AW807955 AW807760 AW807615 AW807898 AW807849 AW807821
			AW807832 AW807842 AW807827 AW807822 AW807829 AW807830 AW807825 AW807603 AW807612 AW807908 AW807595 AW807617
			AW807678 AW807687 AW807918 AW807921 AW807596 AW807602 AW807688 AW807609 AW807684 AW807770 AW807593 AW807754
			AW807679 AW807957 AW807683 AW807763 AW807902 AW807840 AW807769 AW807685 AW807847 AW807674
			AW807686 AW807670 AW807917 AW807677 AW807680 AW807900 AW807669 AW807952 AW807907 AW807846 AW807756
			AW807835 AW807608 AW807753 AW807601 AW807956
	454574	1225636_1	AW809109 AW809112 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132
10	454600	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786
			AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960
	454678	1228915_1	AW813089 W28102
	454693	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
	454714	1230493_1	AW815098 BE154843 BE154831
15	454766	1234022_1	AW866497 AW819775 AW819868 AW866602 AW866561
	454784	1234630_1	AW820626 AW820621 AW820608
	454790	1234752_1	AW820852 AW820773 AW821088
	454836	1236509_1	AW833711 AW833620 AW833699
	454962	1246760_1	AW847645 AW847791 AW854083 AW853945
20	455047	1250536_1	AW852530 AW852527 AW852526
	455092	1252971_1	BE152428 AW855572 AW855607
	455100	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	455107	1253874_1	BE154113 AW856797 AW856847 AW861128 AW856817
	455114	1254106_1	AW857121 AW857123 AW861238
25	455170	1256906_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
	455201	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
	455226	1262534_1	AW902103 AW869012 AW869139
	455252	1266222_1	AW876627 AW876630 AW876631 AW876625
	455286	1273576_1	BE144384 AW887474 AW887403 BE144386
30	455310	1278158_1	AW893961 AW893998 AW894034 AW894019
	455431	1289854_1	AW938484 BE001245 BE001190
	455488	129372_1	AA102322
	455511	1321229_1	BE144762 AW979091
35	455512	1321443_1	AW983608 AW983628 AW983610 AW983688 AW983601 AW983645 AW983607 AW983640 AW983625 AW983612 AW983642 AW983687
			AW983602 AW983624 AW983634 AW983637 AW983632 AW983617 AW983635 AW983630 AW983636 AW983639 AW983616 AW983689
			AW983641 AW983621 AW983603 AW983609 AW983623 AW983644 AW983618 AW983615 AW983611 AW983604 AW983686 AW983622
			AW983619 AW983633 AW983589 AW983605 AW983626 AW983643 AW983631 AW983627 AW983613 AW983614 AW983685 AW983593
			AW983590 AW983594 AW983620 AW983638 AW983592 AW983588
	455571	1331885_1	BE003714 BE003721 BE003720 BE003716
40	455631	1347545_1	BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072
	455678	1349716_1	BE066007 BE066017 BE066074
	455685	1350393_1	BE066976 BE066928 BE066927
	455807	1370914_1	BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
	455821	1372714_1	BE143341 BE143344 BE143378 BE143358
45	455866	1377119_1	BE149024 BE149056 BE152826 BE149025 BE149057 BE152819 BE149030 BE149062 BE149023 BE149055
	455992	1398552_1	BE179015 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997
	455995	1398903_1	BE179408 BE179798 BE179980
	456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368
			BE011362 BE011215 BE011365 BE011363
50	458804	75803_1	AL157625 N72696 BE622492
	458861	798085_1	AI630223 AI630470
	459160	920051_1	AI904723 AI904725 AI904729 AI904722 AI904758 AI904736
	459201	925883_1	AW391177 W45021
	459267	966605_1	AJ003631 AJ003650 AJ003651

TABLE 29C

60	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
65	Pkey	Ref	Strand	Nt_position
	400451	8113550	Minus	82189-82320
	400462	9929659	Minus	197610-197785
70	400608	9887666	Minus	96756-97558
	400639	9887597	Plus	23150-23590
	400641	8117693	Plus	4786-4992
	400756	8119084	Minus	38734-38857
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
	400880	9931121	Plus	29235-29336,36363-36580
75	400889	9958234	Minus	169782-170036
	400983	8081198	Plus	107903-108832
	401045	8117619	Plus	90044-90184,91111-91345
	401049	7232177	Plus	149157-150692
	401078	3687273	Plus	105052-105171
80	401094	9965511	Plus	137130-137302,139283-139506
	401103	8568122	Minus	98330-98449
	401157	9438289	Minus	114133-114247,114567-114645
	401189	9690246	Minus	90815-90929

	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
	401213	9858408	Plus	98243-98380,98489-98619
	401254	9796309	Plus	152209-152383
5	401323	9212516	Plus	213509-214450
	401335	9884881	Plus	15736-16352
	401497	7381770	Plus	92607-92813
	401517	7677912	Plus	29278-29770
	401526	7770561	Plus	91570-93177
10	401575	7229804	Minus	76253-76364
	401694	3540172	Minus	64056-64168
	401793	7263888	Minus	102945-103083
	401862	7770606	Minus	55839-55993,59145-59293
	401878	8099802	Minus	162268-162474,163089-163195
	401986	4406829	Minus	31137-31293
15	402046	8072415	Plus	166394-166556,168167-168395
	402048	8072512	Plus	43936-44078
	402102	8117771	Minus	174566-174740
	402103	7249203	Plus	14453-15414
20	402230	9966312	Minus	29782-29932
	402318	7582559	Minus	12843-13403
	402490	9797648	Plus	149982-150929
	402745	9212200	Minus	76516-76690
	402800	6010175	Plus	43921-44049,46181-46273
25	402812	6010110	Plus	25026-25091,25844-25920
	402820	6456853	Minus	82274-82443
	402855	9662953	Minus	59763-59909
	403133	7331427	Plus	38314-38634
	403271	7230852	Plus	134283-134485
30	403277	8072597	Minus	27494-27642
	403310	8139936	Minus	183883-184026
	403329	8516120	Plus	96450-96598
	403356	8569930	Plus	92839-93036
	403378	9438244	Minus	44264-44443
35	403388	9438331	Plus	112733-113001,114599-114735
	403467	9929556	Minus	73431-73602
	403515	7656757	Minus	173358-179553
	403525	7960440	Plus	152431-153243
	403534	8076917	Minus	46652-47332
40	403568	8101145	Minus	85509-85658
	403574	8101156	Plus	5542-6176
	403637	8671936	Minus	142647-142771,145531-145762
	403677	7331517	Minus	55008-55083,62860-63051
	403691	7387384	Minus	88280-88463
45	403760	7712202	Minus	45910-46260,47563-47824
	403776	7770611	Minus	1414-1513,1624-1756
	403895	7381715	Minus	3502-4002,4070-4308
	403937	7711761	Minus	12609-12773
	404043	9558573	Plus	29042-29135,46597-46699
50	404097	7770701	Plus	55512-55781
	404200	6010176	Minus	7066-7210
	404249	8655533	Plus	64270-64633
	404274	9885189	Plus	104127-104318
	404285	2326514	Plus	32282-32416
55	404288	2769644	Plus	3512-3691
	404356	7630858	Minus	126433-126623
	404443	7579073	Minus	87198-87441
	404476	8080699	Plus	101841-102043
	404488	8113286	Minus	64835-64994
60	404513	8151941	Minus	112837-113339
	404548	8570305	Minus	83896-84162
	404555	7243881	Minus	63963-64157
	404561	9795980	Minus	69039-70100
	404588	6456726	Minus	40059-40210
65	404593	9944086	Minus	74922-75788
	404599	8705107	Plus	110443-110733
	404860	8979555	Plus	65852-66081
	404916	7341826	Plus	91057-91188
	404957	7407927	Plus	147512-148011
70	405041	7547195	Plus	121230-121714
	405059	7656683	Plus	349-822
	405090	8072525	Minus	38552-39202
	405257	7329310	Plus	73121-73273
	405336	6094635	Plus	33267-33563
75	405472	8439781	Plus	106297-106447,108462-108596
	405494	8050952	Minus	70284-70518
	405547	1054740	Plus	124361-124520,124914-125050
	405621	5523811	Plus	59362-59607
	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
80	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405759	3288022	Minus	18283-18399
	405829	7109593	Minus	15628-16127
	405848	7651809	Minus	28135-28244

405966	8247788	Minus	51762-51978
405970	8247789	Minus	45795-46295
406018	6758904	Minus	37795-38168
406091	9123919	Minus	197370-197935
406092	9123919	Plus	251370-251797,252168-252882
406149	7144791	Minus	44464-45164
406195	7289992	Minus	36293-36827
406333	9213235	Plus	64689-64798
406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
406506	7711374	Minus	6843-8077
406554	7711566	Plus	106956-107121
406603	8272659	Minus	39506-39694

TABLE 30A: ABOUT 1840 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO HYPERSENSITIVITY PNEUMONITIS (HP)

Table 30A lists about 1840 genes that are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with hypersensitivity pneumonitis (HP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 Gene Chip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" hypersensitivity pneumonitis sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" hypersensitivity pneumonitis level was set to the 90th percentile amongst hypersensitivity pneumonitis samples.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of IPF (idiopathic pulmonary fibrosis) to HP (hypersensitivity pneumonitis)

Pkey	ExAccn	Unigene ID	Unigene Title	R1
450478	AW451709	Hs.271200	ESTs	20.2
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
405654				11.8
440209	H05049	Hs.22269	neurexin 3	10.8
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	10.4
439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	10.2
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	9.5
416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.3
420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	9.2
403574				9.1
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
419519	AI198719	Hs.176376	ESTs	8.2
435256	AF193766	Hs.13872	cytokine-like protein C17	8.1
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	8.1
429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	8.0
405443				7.8
428766	AA477989	Hs.98800	ESTs	7.7
441802	AA968636	Hs.127877	ESTs	7.6
453649	Y07494	Hs.34114	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 (+)	7.5
447410	AI470235	Hs.172698	EST	7.2
442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
405494				6.9
442377	AA993807	Hs.167367	ESTs	6.9
409928	AL137163	Hs.57549	hypothetical protein dJ473B4	6.8
420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	6.8
415236	R41400		gb:yf94b12.s1 Soares infant brain 1N1B H	6.8
451562	H04150	Hs.107708	ESTs	6.8
403310				6.7
445189	AI936450	Hs.147482	ESTs	6.7
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.7
439780	AL109688		gb:Homo sapiens mRNA full length insert	6.6
402076				6.6
415025	AW207091	Hs.72307	ESTs	6.5
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	6.5
438557	AW364104	Hs.143509	hypothetical protein FLJ21924	6.5
428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	6.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	6.4
409545	BE296182	Hs.19002	hypothetical protein MGC4675	6.4
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.4
411966	AA099113	Hs.118609	ESTs	6.4
440274	R24595	Hs.7122	scrapie responsive protein 1	6.3
442879	AF032922	Hs.8813	synixin binding protein 3	6.3
419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
420185	AL044056	Hs.158047	ESTs	6.3
415672	N53097	Hs.193579	ESTs	6.2
455488	AA102322		gb:z190f03.r1 Stratagene colon (937204)	6.2
420026	AI831190	Hs.166676	ESTs	6.1
446868	AV660737	Hs.135100	ESTs	6.1
431622	AW979271	Hs.293184	ESTs	6.1
407266	AJ235664		gb:Homo sapiens mRNA for Immunglobulin	6.1
421300	AW297398	Hs.96617	ESTs	6.0
416045	H15990	Hs.31403	ESTs	6.0

	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	6.0
	424693	BE169810	Hs.47557	ESTs	6.0
	436397	AA715013	Hs.169835	ESTs	6.0
5	440504	AI948966	Hs.130017	ESTs, Weakly similar to JN0908 H+-transp	6.0
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	6.0
	403625				6.0
	418986	AI123555	Hs.81796	ESTs	5.9
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.9
10	400292	AA250737	Hs.72472	ESTs	5.9
	442849	R10099	Hs.269805	ESTs	5.9
	440887	AI799488	Hs.135905	ESTs	5.8
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	431374	BE258532	Hs.251871	CTP synthase	5.7
15	444963	AI916973	Hs.213603	ESTs	5.7
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	5.6
	444992	R37658	Hs.21375	ESTs	5.6
	416575	W02414	Hs.38383	ESTs	5.5
20	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
	451830	H18433	Hs.21542	KIAA1035 protein	5.5
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	5.5
	404043				5.5
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	5.5
25	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	5.5
	434683	AW298724	Hs.202639	ESTs	5.5
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	5.5
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	5.5
	428895	AA437124	Hs.187247	ESTs	5.4
30	450018	AA421642	Hs.24309	hypothetical protein FLJ11106	5.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.4
	454039	AW079064	Hs.245540	ESTs	5.3
	403637				5.3
35	414725	AA769791	Hs.125300	ring finger protein 21, interferon-respo	5.3
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG	5.3
	403329				5.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	5.3
	459664				5.3
40	401497				5.3
	410797	AW857191		gb:RC2-CT0304-080100-011-b12 CT0304 Homo	5.2
	411402	BE297855	Hs.69855	NRAS-related gene	5.2
	448844	AI581519	Hs.177164	ESTs	5.2
	435202	AI971313	Hs.170204	KIAA0551 protein	5.1
45	439418	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	5.1
	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	5.1
	434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	5.1
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	5.1
50	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.0
	437636	AA764781	Hs.291844	ESTs	5.0
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
	455464	AW983901		gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.0
	418771	AA807881	Hs.25329	ESTs	5.0
55	434820	AI821863		gb:ns90f05.x5 NCL_CGAP_Pr3 Homo sapiens	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
	454482	BE147919		gb:RC3-HT0230-160200-016-a08 HT0230 Homo	4.9
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	4.9
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	4.9
60	423607	AA328329	Hs.6591	ESTs	4.9
	407415	AF073328		gb:Homo sapiens tetracycline transporter-	4.9
	401878				4.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	4.9
	451325	AA021283	Hs.59788	ESTs	4.9
65	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	4.9
	406333				4.9
	409105	AW467539	Hs.255877	ESTs	4.8
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	4.8
	421482	AL135462	Hs.104715	inversin	4.8
70	442757	AI739528	Hs.28345	ESTs	4.8
	459717				4.8
	436637	AI783629	Hs.26766	ESTs	4.8
	412222	AA528283	Hs.292737	ESTs	4.8
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	4.8
75	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
	441640	AI733345	Hs.144104	ESTs	4.8
	422977	AA631498		gb:np83h04.s1 NCL_CGAP_Thy1 Homo sapiens	4.8
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	4.8
80	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.8
	411965	BE467339	Hs.280115	ESTs	4.7
	403341				4.7
	411726	AW858612		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	4.7
	443271	BE568568	Hs.195704	ESTs	4.7

	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	426097	BE327369	Hs.112238	ESTs	4.7
	439199	R40373	Hs.26299	ESTs	4.7
5	440728	AW086077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	4.6
	434381	AA631834		gb:np77h05.s1 NCI_CGAP_Pr2 Homo sapiens	4.6
	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	431242	AA987742	Hs.251278	KIAA1201 protein	4.6
10	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	442360	AI374621	Hs.29055	ESTs	4.6
	452171	AI863302	Hs.211930	EST	4.6
	440801	AA906366	Hs.190535	ESTs	4.5
	411738	AW859353		gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
15	431447	AA505138	Hs.291341	ESTs	4.5
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
	401365				4.5
	408281	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	4.5
	411657	AW855583		gb:CM4-CT0278-221099-027-f07 CT0278 Homo	4.5
20	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	4.5
	428528	AI004034	Hs.98638	ESTs	4.5
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.5
	417252	AA195014	Hs.85971	ESTs	4.5
	417135	AA422067	Hs.50547	ESTs	4.5
	403089				4.4
25	420691	AA829433	Hs.275343	ESTs	4.4
	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	4.4
30	454438	AA224053	Hs.172405	cell division cycle 27	4.4
	435434	AA680387	Hs.187850	ESTs	4.4
	420828	AA280778	Hs.186878	ESTs	4.3
	435586	AI279137	Hs.151498	ESTs	4.3
	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
35	416170	H42454	Hs.220645	ESTs	4.3
	408691	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	4.3
	428912	AW103117	Hs.98949	ESTs, Weakly similar to MEA6 [H.sapiens]	4.3
	455511	BE144762		gb:CMO-HT0180-041099-065-b04 HT0180 Homo	4.3
	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	4.3
40	401189				4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	422654	AA314316	Hs.163725	ESTs	4.3
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
45	417919	AI928203	Hs.86379	ESTs	4.3
	405784				4.3
	431853	AA521034	Hs.70834	ESTs	4.3
	409629	AW449589	Hs.279724	ESTs	4.2
	403281				4.2
50	427173	BE255017	Hs.97540	ESTs	4.2
	433717	AF063536		gb:AF063536 Homo sapiens library (Yu Y)	4.2
	406777	T23625	Hs.150580	putative translation initiation factor	4.2
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	4.2
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.2
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	4.2
	449762	N93057	Hs.54888	ESTs	4.2
	421106	AA877124	Hs.172844	ESTs	4.2
	439382	BE247684	Hs.103070	ESTs	4.1
	404957				4.1
60	436332	AL049679	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	4.1
	446393	AW014174	Hs.301956	zinc finger protein	4.1
	452728	AI915676	Hs.239708	ESTs	4.1
	456386	W28481		gb:47e1 Human retina cDNA randomly prime	4.1
	406288	AW068311	Hs.311054	Homo sapiens mRNA full length insert cDN	4.1
65	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	403344				4.1
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.1
70	401596	AA172106	Hs.110950	Rag C protein	4.1
	418693	AI750878	Hs.87409	thrombospondin 1	4.1
	414299	AA142989	Hs.71730	ESTs	4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	458552	AW136139	Hs.245856	ESTs	4.0
75	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	441201	AW118822	Hs.128757	ESTs	4.0
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	4.0
	440472	AA886169	Hs.169071	ESTs	4.0
80	418379	AA218940	Hs.137516	fidgetin-like 1	4.0
	435878	R08330	Hs.20152	ESTs	4.0
	437263	AA747822		gb:nx97a04.s1 NCI_CGAP_GCB1 Homo sapiens	4.0
	444087	AV647899	Hs.282375	ESTs	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0

	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010566, mRNA,	4.0
	405521				4.0
	411597	AW852925		gb:PM0-CT0248-131099-001-f10 CT0248 Homo	4.0
5	415655	W05433	Hs.49890	ESTs	4.0
	404822				4.0
	441107	AA917075	Hs.190520	ESTs	4.0
	404834				4.0
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	4.0
10	428102	AA968441	Hs.126866	ESTs	4.0
	436511	AA721252	Hs.291502	ESTs	4.0
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	4.0
	453098	Z25935	Hs.86379	ESTs	3.9
	410811	AW805687	Hs.300648	ESTs	3.9
15	425048	H05468	Hs.164502	ESTs	3.9
	431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	452768	AW069459	Hs.61539	ESTs	3.9
20	455241	AW876249		gb:PM4-PT0019-131299-006-B05 PT0019 Homo	3.9
	409070	AA063003	Hs.224560	ESTs	3.9
	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.9
	419091	T85332	Hs.178294	ESTs	3.9
	422591	L07648	Hs.118630	MAX-interacting protein 1	3.9
25	403188				3.9
	418857	D10216	Hs.89394	POU domain, class 1, transcription factor	3.9
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	3.9
	436149	AI754308	Hs.159452	ESTs	3.9
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
30	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.9
	451221	AI949701	Hs.210589	ESTs	3.9
35	455475	AW948126		gb:RC0-MT0013-280300-031-a12 MT0013 Homo	3.9
	433197	AB040889	Hs.281022	KIAA1456 protein	3.9
	429881	T80112	Hs.192245	ESTs	3.9
	415598	AI433165	Hs.9856	ESTs	3.9
	431220	N52937	Hs.102679	ESTs	3.9
40	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
	404443				3.9
	407340	AA810168	Hs.284289	vitellogenesis-associated protein VIT-1	3.9
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retrovirus	3.9
	412400	AW948066		gb:RC0-MT0012-290300-031-h10 MT0012 Homo	3.9
45	427167	AI239607	Hs.99196	hypothetical protein MGC11324	3.9
	438090	AA777534	Hs.191992	ESTs	3.8
	407938	AA905097	Hs.85050	phospholamban	3.8
	440454	AI733037	Hs.129990	ESTs	3.8
	417706	T90797	Hs.268623	ESTs	3.8
50	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	407762	AW235638	Hs.29475	ESTs	3.8
	420727	H75701	Hs.99886	complement component 4-binding protein,	3.8
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	3.8
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	3.8
55	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens	3.8
	459429	AA278779	Hs.335696	EST	3.8
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	437458	AL390131	Hs.128751	Homo sapiens cDNA FLJ12235 fis, clone MA	3.8
	451073	AI758905	Hs.206063	ESTs	3.8
60	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	3.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosyl	3.8
	444414	AW293214	Hs.8752	transmembrane protein 4	3.8
	402615				3.7
	410585	AW770523	Hs.337501	ESTs	3.7
65	425168	R96366		gb:yq37d04.s1 Soares fetal liver spleen	3.7
	449729	R72032	Hs.29235	ESTs	3.7
	459359	N99545		gb:za40a05.r1 Soares fetal liver spleen	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	439001	AF075068		gb:Homo sapiens full length insert cDNA	3.7
70	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen	3.7
	404193				3.7
	416379	N38857	Hs.203933	ESTs	3.7
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	3.7
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	3.7
75	412589	R28660	Hs.24305	ESTs	3.7
	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	3.7
	453375	AI990114	Hs.240091	ESTs	3.7
80	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-hergulin	3.7
	451882	AI821324	Hs.100445	ESTs	3.7
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp588E1624 (f	3.7
	405001	U58196	Hs.296281	interleukin enhancer binding factor 1	3.7
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	3.7

	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.7
	432781	NM_014133	Hs.278940	PRO0618 protein	3.7
	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.7
5	406964	M21305		gb:Human alpha satellite and satellite 3	3.7
	430682	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.7
	449804	AI535663	Hs.39379	ESTs	3.7
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.7
	430503	AA533574	Hs.152274	ESTs	3.7
10	443305	AI050693	Hs.133318	ESTs	3.7
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.7
	452280	AI911410	Hs.167224	ESTs	3.6
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	406992	S62472		gb:beta-pol=DNA polymerase beta (exon a	3.6
15	441416	AI990139	Hs.148609	ESTs	3.6
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
	413998	AW103807	Hs.243933	ESTs	3.6
	440385	AA884283	Hs.192136	ESTs	3.6
	431673	AW971302	Hs.293233	ESTs	3.6
20	401887				3.6
	404793				3.6
	422054	AA322506		gb:EST25146 Cerebellum II Homo sapiens c	3.6
	432030	AI908400	Hs.143789	ESTs	3.6
	449645	AI961092	Hs.196155	ESTs	3.6
25	404476				3.6
	449336	AL119995	Hs.15260	ESTs, Highly similar to AC007228 2 BC372	3.6
	401200				3.6
	403937				3.6
30	437918	AI761449	Hs.121629	ESTs	3.6
	443394	AI055865	Hs.133485	ESTs	3.6
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	3.6
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	436269	AA707472	Hs.190760	ESTs	3.6
35	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	3.6
	416394	H64111		gb:yr57f03.r1 Soares fetal liver spleen	3.6
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	439326	W07140	Hs.54721	ESTs	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
40	435766	R11673	Hs.186498	ESTs	3.6
	448067	R68568	Hs.183373	src homology 3 domain-containing protein	3.6
	441605	AA984647	Hs.128801	ESTs	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
45	418405	AI868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.5
	450350	T97817	Hs.174880	ESTs	3.5
	451704	AI755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	459037	AW439497	Hs.290656	EST	3.5
	419247	S65791	Hs.89764	fragile X mental retardation 1	3.5
50	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	426724	AA383623	Hs.293616	ESTs	3.5
	434273	AA913143	Hs.26303	ESTs	3.5
	438042	AW296971	Hs.255593	ESTs	3.5
	410500	R09442		gb:ylf26c09.r1 Soares fetal liver spleen	3.5
55	416154	Z46122		gb:HSC0VB031 normalized infant brain cDN	3.5
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.5
	454447	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	3.5
	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
	444338	AI937026	Hs.146642	ESTs	3.5
60	427687	AW003867	Hs.1570	histamine receptor H1	3.5
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	3.5
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.5
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	3.5
	403515				3.5
65	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	439953	AA918129	Hs.124638	ESTs	3.5
	457620	AA602711	Hs.336753	EST	3.5
	442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypothei	3.5
	453931	AL121278	Hs.25144	ESTs	3.5
70	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	3.5
	413468	BE504766		gb:h240g01.x1 NCL_CGAP_GC6 Homo sapiens	3.5
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.5
	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypot	3.5
75	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.5
	410908	AA121686	Hs.10592	ESTs	3.5
	440364	AA910460	Hs.128626	ESTs	3.5
	406190				3.5
80	430762	AI343652	Hs.105667	ESTs	3.5
	451182	D52562	Hs.296317	KIAA1789 protein	3.4
	432437	W07088	Hs.293685	ESTs	3.4
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
	405970				3.4
	407676	AW064111	Hs.279823	ESTs	3.4

	413141	BE166323		gb:QV4-HT0492-270100-086-e12 HT0492 Homo	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
5	459371	R20991		gb:yg06h01.r1 Soares infant brain 1NIB H	3.4
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	3.4
	423841	AW753957		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.4
	420430	AI703192		gb:wd92h04.x1 NCI_CGAP_Lu24 Homo sapiens	3.4
10	443921	AI091310	Hs.134848	ESTs	3.4
	444453	AW379394	Hs.145126	ESTs	3.4
	443475	AI066470	Hs.134482	ESTs	3.4
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.4
	453263	R91778	Hs.99369	ESTs	3.4
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	3.4
15	456303	AA224872	Hs.115088	ESTs	3.4
	431474	AL133990	Hs.190642	ESTs	3.4
	439702	AW085525	Hs.134182	ESTs	3.4
	458797	AW001835	Hs.13323	hypothetical protein FLJ22059	3.4
	430140	AW296771	Hs.221999	ESTs	3.4
20	423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	3.4
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.4
	446672	T05514		gb:EST03403 Fetal brain, Stralagene (cat	3.4
	431548	AI834273	Hs.9711	novel protein	3.4
	416182	NM_004354	Hs.79069	cyclin G2	3.4
25	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
	417663	R07483	Hs.180461	ESTs	3.3
	405455				3.3
	426235	AI631964	Hs.34447	ESTs	3.3
	439567	AI056618	Hs.134314	ESTs	3.3
30	444848	AW451176	Hs.195954	ESTs	3.3
	451426	AW205003	Hs.208063	ESTs	3.3
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	3.3
	401626				3.3
	405780				3.3
35	417991	AA731452	Hs.190008	ESTs	3.3
	443212	AW269515	Hs.102500	hypothetical protein FLJ20481	3.3
	403356				3.3
	404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	3.3
40	413581	BE150618		gb:RC3-HT0272-110100-013-c06 HT0272 Homo	3.3
	426701	AI968103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.3
	445510	AA946676	Hs.282824	ESTs	3.3
	418663	AK001100	Hs.41690	desmocollin 3	3.3
	447617	AI400762	Hs.176675	ESTs	3.3
	448150	AI472167	Hs.302739	ESTs	3.3
45	410140	AL134435	Hs.22269	neurexin 3	3.3
	443283	BE568610		gb:601342622F1 NIH_MGC_53 Homo sapiens c	3.3
	454777	AW820027		gb:QV0-ST0294-240300-173-g04 ST0294 Homo	3.3
	410767	AJ001873	Hs.66185	Homo Sapiens mRNA, partial cDNA sequence	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
50	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	438456	AA913381	Hs.190513	ESTs	3.3
	411186	AW821257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.3
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	3.3
	433567	AF073299	Hs.103132	solute carrier family 9 (sodium/hydrogen	3.3
55	433805	AA706910	Hs.112742	ESTs	3.3
	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.3
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	456555	AW592167	Hs.293299	ESTs	3.3
	419189	T95862	Hs.112318	6.2 kd protein	3.3
60	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	3.3
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	3.3
	413200	AA127395	Hs.222414	ESTs	3.3
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.3
	416737	AF154335	Hs.79691	LIM domain protein	3.3
65	428356	AL046991	Hs.10338	ESTs	3.3
	429216	AI369472	Hs.65407	ESTs	3.3
	432488	AA551010	Hs.216640	ESTs	3.3
	433386	AW360833		gb:PM1-CT0243-201099-004-d08 CT0243 Homo	3.3
	400889				3.3
70	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	446190	AI279299	Hs.256564	ESTs	3.3
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	3.3
	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	3.3
75	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
	434294	AJ271379	Hs.76194	ribosomal protein S5	3.3
	452372	AI885742	Hs.228474	ESTs	3.3
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	3.2
80	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	3.2
	430548	AW450575	Hs.163203	ESTs, Weakly similar to B34087 hypothe	3.2
	427119	AW880562	Hs.114574	ESTs	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
	437845	AA769578	Hs.90488	ESTs	3.2

5	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	414394	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.2
	417175	R44558	Hs.94002	ESTs	3.2
	456536	AW135986	Hs.257859	ESTs	3.2
	401132				3.2
10	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	450947	AI745400	Hs.204662	ESTs	3.2
	456605	AI827786	Hs.259044	ESTs	3.2
	452879	AW905328	Hs.180842	ribosomal protein L13	3.2
15	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	3.2
	429479	AA453488	Hs.99333	ESTs	3.2
	448090	AI608821	Hs.270289	ESTs	3.2
	401324				3.2
	404731				3.2
20	419936	AI792788		gb:ol91d05.y5 NCL_CGAP_Kid5 Homo sapiens	3.2
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	3.2
	433990	AA889328	Hs.112950	ESTs	3.2
	415239	R42608	Hs.139270	ESTs	3.2
	418878	W20090	Hs.6616	ESTs	3.2
25	438079	R09664	Hs.191223	ESTs	3.2
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	457460	AI143312	Hs.129206	casein kinase 1, gamma 3	3.2
	454145	AA046872	Hs.62798		3.2
	446577	AB040933	Hs.15420	KIAA1500 protein	3.2
30	430664	AW969834	Hs.303303	ESTs	3.2
	404588				3.2
	407834	AW084991	Hs.26100	ESTs	3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	440790	AW593050	Hs.128580	ESTs	3.2
35	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	3.2
	421916	R34441	Hs.101007	Homo sapiens cDNA: FLJ23546 fis, clone L	3.2
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
	444771	AB023201	Hs.11912	KIAA0984 protein	3.2
40	445233	AV653034	Hs.297559	ESTs	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.2
45	403623				3.2
	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3.2
	444050	AW138295	Hs.135024	ESTs	3.2
	421036	AA810560	Hs.303577	ESTs	3.2
	401459				3.1
50	404404				3.1
	450438	AI696071	Hs.253800	ESTs	3.1
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	3.1
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypothe	3.1
	441274	AW593781	Hs.131357	ESTs	3.1
55	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	400816				3.1
	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
	431906	AW328038	Hs.37486	ESTs	3.1
60	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	450271	AI693900	Hs.200920	ESTs	3.1
	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	3.1
	415273	Z39840	Hs.22229	ESTs	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
65	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.1
	446364	AB006624	Hs.14912	KIAA0286 protein	3.1
	436638	AI271945	Hs.134984	ESTs	3.1
	418079	R40058	Hs.6911	ESTs	3.1
	448466	AI522109	Hs.171066	ESTs	3.1
70	448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
	415046	R40018	Hs.56400	ESTs	3.1
	448134	AI470790	Hs.34494	ESTs	3.1
	456027	BE327387	Hs.13913	KIAA1577 protein	3.1
	458023	AW978161	Hs.268555	5'-3' exoribonuclease 2	3.1
75	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.1
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.1
	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	449138	AW294215	Hs.195631	ESTs	3.1
	455756	BE079307		gb:RC1-BT0623-120200-011-g09 BT0623 Homo	3.1
80	428170	H05530	Hs.12565	ESTs	3.1
	429878	AA460188	Hs.127263	ESTs	3.1
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	3.1
	438369	T77886	Hs.83428	nuclear factor of kappa light polypeptid	3.1
	415840	R15955	Hs.21758	ESTs	3.1
	444955	AW002844	Hs.148641	ESTs	3.1
	436020	AA778177	Hs.121724	ESTs	3.1
	453051	AW196690	Hs.224269	ESTs	3.1

	425178	H16097	Hs.161027	ESTs	3.1
	402145				3.1
	410685	AA497117	Hs.129600	ESTs, Moderately similar to ALU1_HUMAN A	3.1
5	449238	AA428229	Hs.331561	muscle-specific RING-finger protein 3	3.1
	456737	BE247203	Hs.124831	CGI-67 protein	3.1
	438214	H06076	Hs.26320	TRABID protein	3.1
	436250	AY004867	Hs.85844	neurotrophic tyrosine kinase, receptor,	3.1
	411622	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.0
10	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
	449357	AI076363	Hs.288806	Homo sapiens cDNA FLJ11778 fis, clone HE	3.0
	418950	T78517	Hs.13941	ESTs	3.0
	431508	NM_012481	Hs.182979	ribosomal protein L12	3.0
	405090				3.0
15	445409	AI949081	Hs.147862	ESTs	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.0
	408235	AA053381	Hs.75969	proline-rich protein with nuclear target	3.0
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	3.0
20	452073	AA625150	Hs.82098	ESTs	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	427244	AA402400	Hs.178045	ESTs	3.0
	448405	AW207634	Hs.170849	ESTs	3.0
	433767	AA609245		gb:af13a11.s1 Soares_testis_NHT Homo sap	3.0
25	421376	AA287948	Hs.134110	ESTs	3.0
	441519	AA972740	Hs.127092	ESTs	3.0
	404367				3.0
	453502	AL039786	Hs.21273	transcription factor NYD-sp10	3.0
	421948	L42583	Hs.334309	keratin 6A	3.0
30	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
	400608				3.0
	404042				3.0
	405229				3.0
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0
35	415452	F09134	Hs.12839	ESTs	3.0
	430371	D87466	Hs.240112	KIAA0276 protein	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	429014	AI800518	Hs.118158	ESTs	3.0
40	405605				3.0
	400227				3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439693	AI741816	Hs.125897	ESTs	3.0
	427533	R36022	Hs.179566	hypothetical protein FLJ22624	3.0
45	418355	L42563	Hs.1165	ATPase, H+/K+ transporting, nongastric,	3.0
	433536	AI732163	Hs.188909	ESTs, Weakly similar to alternatively sp	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	449623	C00719	Hs.120440	EST	3.0
	445568	H00918	Hs.268744	KIAA1796 protein	3.0
50	440448	AA885428	Hs.125646	ESTs	3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	444148	AW003204	Hs.151167	ESTs	3.0
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	3.0
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	3.0
55	440925	AW511090	Hs.130419	ESTs	3.0
	428398	AI249368	Hs.98558	ESTs	3.0
	415913	H70302		gb:yr95f07.r1 Soares fetal liver spleen	3.0
	418145	AF121260	Hs.83577	cysteine and glycine-rich protein 3 (car	3.0
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	3.0
60	400335	Y13187	Hs.248067	Homo sapiens dmd gene, intron 11	3.0
	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	3.0
	436938	AW139680	Hs.161393	ESTs	3.0
	437980	R50393	Hs.278436	KIAA1474 protein	3.0
	455955	BE162394		gb:PM2-HT0451-170100-004-a08 HT0451 Homo	3.0
65	414899	AW975433	Hs.36288	ESTs	2.9
	403786				2.9
	430187	AI799909	Hs.158989	ESTs	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.9
70	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.9
	457041	AA399018	Hs.250835	ESTs	2.9
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.9
	422336	AI761322	Hs.115285	dihydrolipoamide S-acetyltransferase (E2	2.9
	451664	AA889081	Hs.153952	5' nucleotidase (CD73)	2.9
75	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.9
	455249	AW876538		gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.9
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.9
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (fr	2.9
	405302				2.9
80	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119	AA322201	Hs.131976	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	2.9

	425793	AA363946	Hs.20969	ESTs	2.9
	401462				2.9
	458817	AI522129	Hs.173119	ESTs	2.9
5	422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.9
	419875	AA853410	Hs.93557	proenkephalin	2.9
	423047	NM_005323	Hs.123064	H1 histone family, member T (testis-spec	2.9
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.9
	401368				2.9
10	418531	R96760	Hs.183758	ESTs	2.9
	447290	AI476732	Hs.263912	ESTs	2.9
	441143	AI027604	Hs.159650	ESTs	2.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	2.9
	405783				2.9
15	444459	AI680624	Hs.148676	ESTs	2.9
	402112	R58624	Hs.2186	eukaryotic translation elongation factor	2.9
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.9
	444827	R09764	Hs.20416	ESTs	2.9
	451195	U10492	Hs.438	mesenchyme homeo box 1	2.9
20	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
	431595	AA508196		gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens	2.9
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.9
	456699	BE068121		gb:CM1-BT0368-061299-060-a02 BT0368 Homo	2.9
25	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Brn52 Homo sapien	2.9
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
	423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
30	443185	NM_006134	Hs.284142	chromosome 21 open reading frame 4	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	2.9
	437183	AI928184	Hs.122011	ESTs	2.9
	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
35	442726	AW136066	Hs.19145	ESTs	2.9
	456189	H91010	Hs.44940	ESTs	2.9
	441115	R69910	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	2.9
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.9
	415628	F13080		gb:HSC3ID041 normalized infant brain cDN	2.9
40	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	443246	T75157	Hs.337603	ESTs, Weakly similar to T08680 hypotheli	2.9
	450877	AI799608	Hs.29178	ESTs	2.9
	439063	AF085922	Hs.113968	ESTs	2.9
	401526				2.9
45	408751	N91553	Hs.258343	ESTs	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	444125	AI124882	Hs.118121	ESTs	2.9
	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.9
50	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.9
	452589	BE159915	Hs.61406	ESTs, Weakly similar to 2004399A chromos	2.8
	403011				2.8
	436154	AA764950	Hs.119898	ESTs	2.8
	408221	AA912183	Hs.47447	ESTs	2.8
55	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.8
	415399	T26994	Hs.177198	ESTs	2.8
	441817	AW969706	Hs.293332	ESTs	2.8
	443556	AA256769	Hs.94949	methylmalonyl-CoA epimerase	2.8
	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo	2.8
60	439703	AF086538	Hs.196245	ESTs	2.8
	411024	BE062590		gb:QV1-BT0260-281099-023-f05 BT0260 Homo	2.8
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.8
	434715	BE005346	Hs.116410	ESTs	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
65	439235	N45513	Hs.46608	ESTs	2.8
	453736	AL118674	Hs.34871	zinc finger homeobox 1B	2.8
	404967				2.8
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	412887	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.8
70	426942	AA393551	Hs.97450	ESTs	2.8
	403513				2.8
	419077	AA233885	Hs.164526	ESTs	2.8
	421823	N40850	Hs.28625	ESTs	2.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	2.8
75	451007	H38108	Hs.32759	ESTs	2.8
	407803	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	2.8
	409642	AW450809	Hs.257347	ESTs	2.8
	439492	AF086310	Hs.103159	ESTs	2.8
	420814	AA721156	Hs.190440	ESTs	2.8
80	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	2.8
	428350	AW873520	Hs.112017	GE36 gene	2.8
	405456				2.8
	442459	AI264628	Hs.125428	ESTs	2.8
	415763	Z42285	Hs.5181	proliferation-associated 2G4, 38kD	2.8

5	428532	AF157326	Hs.184786	TBP-interacting protein	2.8
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	449539	W80363	Hs.58446	ESTs	2.8
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.8
	408749	H65489	Hs.250659	ESTs	2.8
10	404652				2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	424960	BE245380	Hs.153952	5' nucleotidase (CD73)	2.8
	402131				2.8
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
15	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	444217	AV648751	Hs.282395	ESTs	2.8
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	2.8
	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	2.8
	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
20	433513	AI566356	Hs.171437	ESTs	2.8
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
	451496	AW503407		gb:UI-HF-BNO-akw-d-11-0-UI.r1 NIH_MGC_50	2.8
	420273	AI652864	Hs.197257	ESTs	2.8
	451949	U03884	Hs.463	potassium inwardly-rectifying channel, s	2.8
25	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	425012	T77666	Hs.92414	Homo sapiens cDNA: FLJ22030 fis, clone H	2.8
	441609	AA946764	Hs.133460	ESTs	2.8
	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
30	451206	H86228	Hs.271780	ESTs, Weakly similar to I38022 hypotheti	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
	418888	AJ076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	2.8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
35	459450	AA426429	Hs.98463	EST	2.8
	424188	AW954552	Hs.142634	zinc finger protein	2.7
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	2.7
	427443	AA402713	Hs.97872	ESTs	2.7
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.7
40	413091	BE065063		gb:RC1-BT0313-110500-017-e02 BT0313 Homo	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	445611	AW418497	Hs.145583	ESTs	2.7
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.7
45	408243	Y00787	Hs.624	interleukin 8	2.7
	407308	H67394	Hs.331325	ESTs, Weakly similar to I38022 hypotheti	2.7
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.7
	404587	M99587	Hs.104134	homeo box (H6 family) 1	2.7
	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.7
50	416431	AW384459	Hs.172004	titin	2.7
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
	427134	AA398409	Hs.173561	EST	2.7
	428137	AA421792	Hs.170999	ESTs	2.7
55	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	441218	BE327561	Hs.202345	ESTs	2.7
	440911	AA909536	Hs.143562	ESTs	2.7
	411131	AW819212		gb:CM1-ST0283-071299-061-c07 ST0283 Homo	2.7
	438602	AI167149	Hs.123374	ESTs, Weakly similar to mariner transpos	2.7
60	441191	AI693930	Hs.148816	ESTs	2.7
	403776				2.7
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
	427839	AA608823	Hs.98244	ESTs	2.7
	429905	AL080128	Hs.225998	DKFZP434C153 protein	2.7
65	449396	BE169100	Hs.195029	ESTs	2.7
	450777	AA255646	Hs.60478	ESTs, Moderately similar to S47073 finge	2.7
	458043	AW979009	Hs.326108	ESTs	2.7
	405523				2.7
	434849	AW292765	Hs.8053	ESTs	2.7
70	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti	2.7
	438055	AA776655	Hs.270942	ESTs	2.7
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	2.7
	405738				2.7
	417806	AI867277	Hs.183733	ESTs	2.7
75	430698	AA492071		gb:ne97b04.s1 NCL_CGAP_Kid1 Homo sapiens	2.7
	441969	AI733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	446092	N33522	Hs.145894	ESTs	2.7
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.7
80	444931	AV652066	Hs.75113	general transcription factor IIIA	2.7
	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.7
	453264	AA034137	Hs.271955	ESTs	2.7
	438370	AA843242	Hs.48523	ESTs	2.7
	406092				2.7
	454874	AW836407	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.7
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7

	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU8_HUMAN A	2.7
	441884	AW172630	Hs.144884	ESTs	2.7
	416211	R14625		gb:yg45c03.r1 Soares infant brain 1N1B H	2.7
5	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	2.7
	453696	AI989482	Hs.146286	kinesin family member 13A	2.7
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.7
	425876	AW005887	Hs.234058	ESTs	2.7
10	450458	AA009926		gb:zi07e05.r1 Soares_fetal_liver_spleen_	2.7
	406603				2.7
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	410871	D78367	Hs.66739	keratin 12 (Meesmann corneal dystrophy)	2.7
	412706	R97106	Hs.167546	ESTs	2.7
15	422897	AA679784	Hs.4290	ESTs	2.7
	436329	AI798750	Hs.163960	Homo sapiens heat shock transcription fa	2.7
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0512 Homo	2.7
	452594	AJ076405	Hs.29981	solute carrier family 26 (sulfate transp	2.7
20	419296	AA236115	Hs.120785	ESTs	2.7
	454747	AW818535		gb:RC1-ST0278-140300-016-f05 ST0278 Homo	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	411409	AW844803		gb:RC3-CN0056-170300-015-f08 CN0056 Homo	2.7
	426662	AA879474	Hs.122710	ESTs	2.7
	400268				2.7
25	438782	AA828380	Hs.126733	ESTs	2.7
	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	2.7
	412486	AF210650	Hs.150858	NAG19 protein	2.7
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	2.7
30	457900	AW976692	Hs.291665	ESTs	2.7
	417376	AA253314	Hs.154103	LIM protein (similar to rat protein kina	2.7
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
	435608	AW183971	Hs.250896	ESTs	2.7
	413627	BE182082	Hs.246973	ESTs	2.7
35	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
	441396	AW293677	Hs.186890	ESTs	2.6
	452046	AB018345	Hs.27657	KIAA0802 protein	2.6
	454936	AW846082		gb:MR3-CT0176-081099-002-d01 CT0176 Homo	2.6
40	454434	AA083558	Hs.261286	ESTs	2.6
	436888	AI942357	Hs.187870	ESTs	2.6
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	416690	H84078	Hs.108551	ESTs	2.6
45	436471	AA719813	Hs.117662	ESTs	2.6
	426559	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.6
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hig	2.6
	455544	AW993880		gb:RC3-BN0034-240400-017-d09 BN0034 Homo	2.6
50	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	2.6
	429864	AA460039	Hs.286	ribosomal protein L4	2.6
	456273	AF154846	Hs.1148	zinc finger protein	2.6
	402603				2.6
55	411162	AW819944		gb:QV0-ST0294-240300-172-e03 ST0294 Homo	2.6
	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
60	438295	AI394151	Hs.37932	ESTs	2.6
	450181	H05254	Hs.201198	ESTs	2.6
	433764	AW753676	Hs.39982	ESTs	2.6
	433229	AB040925	Hs.91625	KIAA1492 protein	2.6
	443718	AI083580	Hs.221373	ESTs	2.6
65	418246	AI472179	Hs.121276	ESTs, Weakly similar to R5HU7A ribosomal	2.6
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	2.6
	400365	Y10259	Hs.274501	H.sapiens ACTH receptor mRNA 3'UTR	2.6
	419318	AW969742	Hs.291005	ESTs	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	404414				2.6
70	446444	AI743737	Hs.24370	ESTs	2.6
	411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.6
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	2.6
	418310	AA814100	Hs.86693	ESTs	2.6
75	454481	AW794878	Hs.314230	ESTs, Highly similar to clock [H.sapiens	2.6
	441216	BE299830	Hs.192908	ESTs	2.6
	438257	AW474419	Hs.224794	ESTs	2.6
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	419505	AA243660	Hs.143061	ESTs	2.6
80	417596	R07343	Hs.226823	ESTs, Moderately similar to I54374 gene	2.6
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	454867	AW835924		gb:PM1-LT0018-250200-002-e09 LT0018 Homo	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6

	457630	AI680803	Hs.112627	ESTs	2.6
	424210	T71397	Hs.222707	KIAA1718 protein	2.6
	447748	AI422023	Hs.161338	ESTs	2.6
5	411970	AA099142	Hs.13804	hypothetical protein dJ462023.2	2.6
	441233	AA972965	Hs.135568	ESTs	2.6
	400706				2.6
	436033	H75391	Hs.255748	ESTs	2.6
	440836	AW370882	Hs.222080	ESTs	2.6
10	431086	AI829692	Hs.211561	ESTs	2.6
	455110	BE154505		gb:PM0-HT0343-281299-003-e06 HT0343 Homo	2.6
	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.6
	413088	BE064962		gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.6
15	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	2.6
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.6
	442690	AI014727	Hs.160047	ESTs, Weakly similar to B28096 line-1 pr	2.6
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	2.6
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.6
	403271				2.6
20	429761	AI276780	Hs.135173	ESTs	2.6
	437085	AA743935	Hs.202329	ESTs	2.6
	450822	AW771860	Hs.205130	ESTs	2.6
	457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	2.6
25	416585	X54162	Hs.79386	leiomodlin 1 (smooth muscle)	2.6
	430357	AW976789	Hs.165607	ESTs	2.6
	417249	N58198	Hs.182898	ESTs	2.6
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	2.6
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.6
30	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	446302	AI285848	Hs.149757	ESTs	2.6
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.6
	428944	AA780181	Hs.41182	Homo sapiens DC47 mRNA, complete cds	2.6
	419647	AA348947	Hs.91816	hypothetical protein	2.6
35	455500	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	2.6
	419435	AI200540	Hs.14877	ESTs, Weakly similar to (define not ava	2.6
	452450	AW854891	Hs.194720	ATP-binding cassette, sub-family G (WHIT	2.6
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	2.6
	436421	AI678031	Hs.122813	ESTs, Weakly similar to ZN22_HUMAN ZINC	2.6
40	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.6
	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	2.6
	426698	AA394104	Hs.97489	ESTs	2.6
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.6
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.5
45	447624	AI640326	Hs.62713	ESTs	2.5
	411736	AW859089		gb:MR1-CT0350-150200-002-d02 CT0350 Homo	2.5
	416334	H53139	Hs.36271	ESTs	2.5
	446818	AI342668	Hs.279765	ESTs	2.5
50	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	442278	AI733477	Hs.166313	ESTs	2.5
	453393	AW956392	Hs.110376	ESTs	2.5
	420854	AW296927		gb:U1-H-BW0-ajc-c-07-0-UIs1 NCI_CGAP_Su	2.5
	408729	AA195764	Hs.72639	ESTs	2.5
55	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	2.5
	411660	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
	409156	N76186	Hs.173518	M-phase phosphoprotein homolog	2.5
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.5
	430291	AV660345	Hs.238126	CGI-49 protein	2.5
60	401785				2.5
	402369				2.5
	439079	AF085937	Hs.38348	ESTs	2.5
	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	2.5
	411463	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	2.5
65	413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo	2.5
	404988				2.5
	409446	AI561173	Hs.67688	ESTs	2.5
	412613	AA653507	Hs.285711	hypothetical protein FLJ13089	2.5
	417909	R35614		gb:yg66e08.r1 Soares infant brain 1NIB H	2.5
70	454743	AW818456	Hs.79347	KIAA0211 gene product	2.5
	406364				2.5
	404108				2.5
	411934	AW876538		gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.5
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	2.5
75	443526	AW792804	Hs.134002	ESTs	2.5
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.5
	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	2.5
	458771	AW295151	Hs.163612	ESTs	2.5
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	2.5
80	426589	AW954460		gb:EST366530 MAGE resequences, MAGC Homo	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	2.5
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	2.5
	434784	AA649051	Hs.164007	ESTs	2.5

	429322	D86984	Hs.199243	KIAA0231 protein	2.5
	446252	AI283125	Hs.150009	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
5	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
	449410	AA001356	Hs.18159	ESTs	2.5
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	2.5
	458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Ce	2.5
10	416944	N22809		gb:yw41e07.s1 Weizmann Olfactory Epithel	2.5
	423010	W25436	Hs.90725	ESTs, Moderately similar to I38022 hypot	2.5
	412505	AA974491	Hs.21734	ESTs	2.5
	446399	AI298405	Hs.150080	ESTs	2.5
	412139	BE044976		gb:hn25b10.x1 NCI_CGAP_Thy7 Homo sapiens	2.5
	403691				2.5
15	424025	AI701852	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	2.5
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.5
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.5
	457770	BE065030	Hs.124179	ESTs	2.5
20	427731	AA411750	Hs.20943	ESTs	2.5
	426920	AA393351	Hs.132121	ESTs	2.5
	427794	AA709186	Hs.282963	ESTs	2.5
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
25	414550	BE379808		gb:601159567T1 NIH_MGC_53 Homo sapiens c	2.5
	436391	AJ227892	Hs.146274	ESTs	2.5
	401989				2.5
	423346	AI267677	Hs.127416	synaptojanin 1	2.5
	444905	AW135863	Hs.209228	ESTs	2.5
30	424539	L02911	Hs.150402	activin A receptor, type I	2.5
	400861				2.5
	458426	AI084514	Hs.249587	ESTs	2.5
	429520	AA160142	Hs.205058	hypothetical protein FLJ20075	2.5
	403568				2.5
35	430692	X80240		gb:H.sapiens endogenous retrovirus HERV-	2.5
	451078	AI927694	Hs.204470	ESTs	2.5
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.5
	427888	AA417088	Hs.137598	ESTs	2.5
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens c	2.5
40	422840	U44059	Hs.121481	thyrotrophic embryonic factor	2.5
	404708				2.5
	405008				2.5
	453772	BE281431	Hs.16323	Homo sapiens, Similar to G antigen 8, cl	2.5
45	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	449311	AI657014		gb:tt49a12.x1 NCI_CGAP_GC6 Homo sapiens	2.5
	454277	AW295069	Hs.31743	ESTs, Weakly similar to Z157_HUMAN ZINC	2.5
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
50	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	2.4
	407851	NM_014496	Hs.40434	ribosomal protein S6 kinase, 90kD, polyp	2.4
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.4
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-lin	2.4
	406468				2.4
55	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.4
	408617	R61736	Hs.124128	ESTs	2.4
	409627	AW997628	Hs.313637	ESTs	2.4
	416665	H72974		gb:yu28a10.s1 Soares fetal liver spleen	2.4
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.4
60	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	2.4
	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	2.4
	429654	AI435046	Hs.164318	ESTs	2.4
	432253	AW090822	Hs.274174	transcription elongation factor (SIII) e	2.4
	439786	AV652707	Hs.33756	Homo sapiens mRNA full length insert cDN	2.4
65	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
	453052	R63050	Hs.223813	ESTs	2.4
	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypotheti	2.4
	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: hamy2)	2.4
	452843	AI796769	Hs.208320	ESTs	2.4
70	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	2.4
	449695	AA164569	Hs.34550	ESTs	2.4
	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.4
	400641				2.4
75	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.4
	432808	NM_015985	Hs.278973	angiopoietin-3	2.4
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411561	H81164	Hs.285017	hypothetical protein FLJ21799	2.4
	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypotheti	2.4
80	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
	435663	AI023707	Hs.134273	ESTs	2.4
	455879	BE153275		gb:PM0-HT0335-180400-008-e11 HT0335 Homo	2.4
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.4

	409041	AB033025	Hs.50081	KIAA1199 protein	2.4
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.4
5	448889	BE140902		gb:IL1-HT0028-240699-001-C11 HT0028 Homo	2.4
	439481	AF086294	Hs.125844	ESTs	2.4
	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	2.4
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	2.4
	409298	AA070211		gb:zm68c04.s1 Stratagene neuroepithelium	2.4
10	411322	AW887330	Hs.172405	cell division cycle 27	2.4
	447640	AI417187		gb:lg75g11.x1 Soares_NhHMPu_S1 Homo sapi	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
	458763	AI693417	Hs.293309	ESTs	2.4
	404638				2.4
15	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.4
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	2.4
	408238	W95901		gb:ze43d11.r1 Soares retina N2b4HR Homo	2.4
	436747	AW977192	Hs.291343	ESTs	2.4
20	437048	AA743240	Hs.91582	ESTs	2.4
	413143	BE067232		gb:PM3-BT0347-170200-001-b05 BT0347 Homo	2.4
	404561				2.4
	444009	AI380792	Hs.135104	ESTs	2.4
	400250				2.4
25	403891				2.4
	417002	T79613	Hs.14613	ESTs	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	441227	AW295407	Hs.128893	ESTs	2.4
	445038	AI635444	Hs.143917	dJ467N11.1 protein	2.4
30	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	459344	AW499533	Hs.257976	ESTs	2.4
	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	2.4
	457652	AF116656	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.4
35	450068	AW207212	Hs.280925	ESTs	2.4
	444750	AW242684	Hs.243623	ESTs	2.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	407264	L34727		gb:Homo sapiens T-cell receptor beta (TC	2.4
	443169	AI038687	Hs.133338	ESTs	2.4
40	426536	AI949749	Hs.44441	ESTs	2.4
	449752	AI668626	Hs.61773	Homo sapiens cDNA FLJ11648 fis, clone HE	2.4
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF I [2.4
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
45	430484	D82880	Hs.241548	RAS p21 protein activator 2	2.4
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.4
	447375	AI376660	Hs.257822	ESTs	2.4
	444230	H95537	Hs.146067	ESTs	2.4
	439911	AA854024	Hs.189110	ESTs	2.4
50	421296	NM_002666	Hs.103253	perilipin	2.4
	449385	AI650471	Hs.270370	ESTs	2.4
	430044	AA464510	Hs.152812	ESTs	2.4
	427131	AA448460	Hs.112017	GE36 gene	2.4
	409103	AF251237	Hs.112208	XAGE-1 protein	2.4
55	421354	AA766485	Hs.269664	ESTs	2.4
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	2.4
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein	2.4
	441358	AW173212	Hs.129041	ESTs	2.4
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	2.4
60	414290	AI568801	Hs.71721	ESTs	2.4
	427342	AL110150	Hs.176680	Homo sapiens mRNA; cDNA DKFZp586D0724 (f	2.4
	459459	AA460445		gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_	2.4
	434638	H50758		gb:yp86e06.r1 Soares fetal liver spleen	2.4
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.4
65	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
	431169	AW971240		gb:EST383329 MAGe resequences, MAGL Homo	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	458734	AI554946	Hs.158794	ESTs	2.4
	449529	AI990559	Hs.232033	ESTs	2.4
70	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	2.4
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.4
	418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	2.4
	430957	AI937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.4
	418188	AW139413	Hs.151880	ESTs	2.4
75	424103	NM_001918	Hs.139410	dihydrolipoamide branched chain transacy	2.4
	454324	AW608930	Hs.52184	hypothetical protein FLJ20618	2.4
	437369	AA765230	Hs.121742	ESTs	2.4
	453211	W84829		gb:zh53f04.r1 Soares_fetal_liver_spleen_	2.4
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.4
80	400462				2.4
	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
	424195	U50536	Hs.142907	Human BRCA2 region, mRNA sequence CG011	2.4
	434163	AW974720	Hs.25206	group XII secreted phospholipase A2	2.4

	435985	AA703154	Hs.191934	ESTs	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	2.4
	458661	AI299789	Hs.166999	ESTs, Moderately similar to I38344 titin	2.4
	459023	AW968226	Hs.60798	ESTs	2.4
5	406005				2.4
	456561	AI868634	Hs.246358	ESTs, Weakly similar to T32250 hypotheti	2.4
	452161	R43077	Hs.221747	ESTs	2.4
	436590	AI393115	Hs.127655	ESTs	2.4
10	430151	AW968203		gb:EST380398 MAGE resequenes, MAGJ Homo	2.4
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	433479	AW511459	Hs.249972	ESTs	2.4
	441676	BE564206	Hs.49889	ESTs	2.4
	407965	W21483	Hs.41707	heat shock 27kD protein 3	2.4
15	450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
	452958	AA883929	Hs.40527	ESTs	2.4
	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	2.4
	405347				2.4
	440577	AA889945	Hs.326381	EST	2.4
20	455780	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo	2.4
	457024	AA397546	Hs.119151	ESTs	2.4
	404249				2.4
	437511	AI807500	Hs.125247	ESTs	2.4
	421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	2.4
25	425146	AW954627		gb:EST366697 MAGE resequenes, MAGC Homo	2.4
	428277	AA425220	Hs.179203	ESTs	2.4
	444870	AI200621	Hs.148504	ESTs	2.4
	402090				2.4
	458507	AI185703	Hs.206957	ESTs	2.4
30	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	2.4
	446534	AI307356	Hs.175225	ESTs	2.4
	453111	AB014598	Hs.31720	hephaestin	2.4
	405230				2.4
	405935				2.4
35	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
	420724	AA279694	Hs.191540	ESTs	2.4
	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.3
40	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRNA	2.3
	440621	AW296024	Hs.150434	ESTs	2.3
	423417	AP000365	Hs.128342	potassium large conductance calcium-acti	2.3
	424131	AA335714	Hs.199665	ESTs	2.3
	450737	AW007152	Hs.203330	ESTs	2.3
45	453687	T55674	Hs.283108	hemoglobin, gamma G	2.3
	442704	AI015463	Hs.130987	ESTs	2.3
	457756	AA126136	Hs.38125	interferon-induced protein 75, 52kD	2.3
	412732	AW993300		gb:RC2-BN0033-180200-015-g06 BN0033 Homo	2.3
	418998	F13215	Hs.287849	ESTs, Weakly similar to T22074 hypotheti	2.3
50	419751	AW195581	Hs.93121	KIAA0761 protein	2.3
	429485	AW197086	Hs.99338	ESTs	2.3
	433377	AI752713	Hs.43845	ESTs	2.3
	434896	AW022054	Hs.136591	ESTs	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
55	444711	AI188739	Hs.148488	ESTs	2.3
	445621	AI733818	Hs.145549	ESTs	2.3
	449182	AW292381	Hs.224150	ESTs	2.3
	430987	Y08564	Hs.248190	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.3
	404068				2.3
60	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.3
	438315	R56795	Hs.82419	ESTs	2.3
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	2.3
	447998	AI768289	Hs.304389	ESTs	2.3
	410150	AW382942	Hs.6774	ESTs	2.3
65	432792	AA448114	Hs.278950	protocadherin beta 1 .	2.3
	443363	AI792629	Hs.133293	ESTs	2.3
	440729	AA904739	Hs.128204	ESTs	2.3
	411045	AW854691	Hs.115325	RAB7, member RAS oncogene family-like 1	2.3
	459207	AW138410	Hs.45051	ESTs	2.3
70	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.3
	458684	BE281115	Hs.98855	hypothetical protein FLJ20909	2.3
	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.3
	401899				2.3
	432116	AA902953	Hs.308538	ESTs	2.3
	404196				2.3
75	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	413308	W28131		gb:42f7 Human retina cDNA randomly prime	2.3
	430264	AA470519		gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens	2.3
	443482	AW188093	Hs.250385	ESTs	2.3
80	453305	R39224	Hs.267997	EHM2 gene	2.3
	451963	AI825440	Hs.224952	ESTs	2.3
	453043	AW136440	Hs.224277	ESTs	2.3
	435559	AF209198	Hs.42636	zinc finger protein 277	2.3
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	2.3

	434120	AI436050	Hs.143937	ESTs	2.3
	429768	AA805719	Hs.192154	ESTs	2.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.3
5	455841	BE145836		gb:MR0-HT0208-101299-202-b08 HT0208 Homo	2.3
	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	2.3
	430706	NM_003540	Hs.247816	H4 histone family, member C	2.3
	428268	AA424957	Hs.294132	ESTs	2.3
	458833	AW236702	Hs.171431	ESTs, Weakly similar to A46010 X-linked	2.3
10	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	2.3
	444109	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.3
	428411	AW291464	Hs.10338	ESTs	2.3
	433098	AW190593	Hs.151143	ESTs	2.3
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	2.3
15	453178	AA496086	Hs.61648	ESTs	2.3
	404569				2.3
	413841	M34276	Hs.75576	plasminogen	2.3
	424068	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	2.3
	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	2.3
20	442710	AI015631	Hs.23210	ESTs	2.3
	444206	AW301017	Hs.146492	ESTs	2.3
	451264	AI768235		gb:wg82g08.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.3
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3
	429080	AA446228	Hs.99057	ESTs	2.3
25	404166				2.3
	416327	R99822	Hs.36172	ESTs	2.3
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.3
	438504	AW665281	Hs.224625	ESTs	2.3
	435325	AI038388	Hs.119309	ESTs	2.3
30	421253	AI188102	Hs.31028	ESTs	2.3
	427046	BE246180	Hs.121385	ESTs	2.3
	432711	AA563785	Hs.152465	ESTs, Weakly similar to I38022 hypotheti	2.3
	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3
35	448458	AW614367	Hs.171054	ESTs	2.3
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	2.3
	417768	R24732	Hs.175139	ESTs	2.3
	427374	AI150033	Hs.143686	ESTs	2.3
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.3
40	423600	AI633559	Hs.310359	ESTs	2.3
	413006	W03857	Hs.34298	ESTs	2.3
	434698	BE044674		gb:hm46f02.x1 NCI_CGAP_RDF1 Homo sapiens	2.3
	407639	AW205369	Hs.312830	ESTs	2.3
	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo	2.3
45	448117	H49129	Hs.172982	ESTs	2.3
	443931	H23213	Hs.22657	ESTs	2.3
	450795	AW173371	Hs.60435	ESTs	2.3
	418632	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.3
	419441	AW023731	Hs.274368	MSTP032 protein	2.3
50	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	2.3
	418291	BE300369	Hs.289038	hypothetical protein MGC4126	2.3
	455964	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.3
	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
55	449272	AW137656	Hs.197645	ESTs	2.3
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	2.3
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.3
	444715	AV650947	Hs.282464	ESTs	2.3
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	2.3
60	444140	AV648089	Hs.282383	ESTs	2.3
	423949	AI014546	Hs.130912	ESTs	2.3
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	445711	T79611	Hs.193691	ESTs	2.3
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	2.3
65	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.3
	429180	AA806287	Hs.58893	ESTs	2.3
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	2.3
	425523	AB007948	Hs.158244	KIAA0479 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
70	419337	AW291112	Hs.209978	ESTs	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypotheti	2.3
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
	436294	AA708310		gb:zg07b07.s1 Soares_pineal_gland_N3HPG	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
75	433939	AL133887	Hs.254122	hypothetical protein	2.3
	450048	AI693269	Hs.202273	ESTs	2.3
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	2.3
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	2.3
	405920				2.3
80	405747				2.3
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.3
	420457	AA482280	Hs.191656	ESTs	2.3
	407726	AA435679	Hs.88594	ESTs	2.3
	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.3

	409517	X90780	Hs.120036	troponin I, cardiac	2.3
	435352	AI056599	Hs.120893	ESTs	2.3
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
5	444098	AV647969	Hs.109694	KIAA1451 protein	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.3
	449015	AL038958	Hs.22868	protein tyrosine phosphatase, non-recept	2.3
	411377	AW841462		gb:RC6-CN0014-080300-012-B09 CN0014 Homo	2.3
10	429276	AF056085	Hs.198612	G protein-coupled receptor 51	2.3
	411816	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.3
	455280	AW886156		gb:RC5-OT0078-150300-021-E08 OT0078 Homo	2.3
	407809	AW082279	Hs.244106	ESTs	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kd (con	2.3
15	445117	AI208754	Hs.147369	ESTs	2.3
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.2
	420230	AL034344	Hs.284186	forkhead box C1	2.2
	411517	AW850267		gb:IL3-CT0219-161199-031-A09 CT0219 Homo	2.2
	403678				2.2
20	457003	S78234	Hs.172405	cell division cycle 27	2.2
	404531	Z25884	Hs.121483	chloride channel 1, skeletal muscle (Th	2.2
	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	2.2
	409427	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo	2.2
25	434745	AW974445	Hs.185155	ESTs, Weakly similar to T12482 hypotheti	2.2
	400696				2.2
	407259	L02256		gb:Human Fab fragment binding syncytial	2.2
	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
30	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	458303	AI264628	Hs.125428	ESTs	2.2
	405692				2.2
	403572				2.2
35	415380	F07953	Hs.16085	putative G-protein coupled receptor	2.2
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.2
	417859	T26453		gb:AB214F6R Infant brain, LLNL array of	2.2
	456472	AK001714	Hs.95744	hypothetical protein similar to ankyrin	2.2
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.2
40	428231	U17989	Hs.183105	nuclear autoantigen	2.2
	454086	AW885909	Hs.6975	PRO1073 protein	2.2
	425071	NM_013989	Hs.154424	deiodinase, lodothyronine, type II	2.2
	416348	H65887	Hs.272163	ESTs	2.2
	403780				2.2
45	414262	AW975616	Hs.291469	ESTs	2.2
	419423	D26488	Hs.90315	KIAA0007 protein	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
50	416588	H66558		gb:yu16e04.r1 Soares fetal liver spleen	2.2
	425368	AB014595	Hs.155976	cullin 4B	2.2
	425886	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.2
	441638	AW293202	Hs.133451	ESTs	2.2
	446845	AI343645	Hs.156108	ESTs	2.2
55	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	2.2
	436574	AW293527	Hs.126465	ESTs	2.2
	424584	H10692	Hs.13310	ESTs	2.2
	456347	U00803	Hs.89426	fyn-related kinase	2.2
	446901	AI347274		gb:tc05d02.x1 NCL_CGAP_Co16 Homo sapiens	2.2
60	459364	W69284		gb:zd46c03.r1 Soares_fetal_heart_NbHH19W	2.2
	430686	NM_001942	Hs.2633	desmoglein 1	2.2
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	2.2
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.2
	403525				2.2
65	453343	AA905353	Hs.121622	ESTs	2.2
	421574	AJ000152	Hs.105924	defensin, beta 2	2.2
	449327	AI638743	Hs.224672	ESTs	2.2
	454769	AW819848		gb:QV0-ST0294-070300-151-b04 ST0294 Homo	2.2
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	2.2
70	401614				2.2
	404767				2.2
	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	436193	AA706059	Hs.255286	ESTs	2.2
75	439626	N22415	Hs.189080	ESTs	2.2
	456481	AA258033	Hs.108110	DKFZP547E2110 protein	2.2
	441453	AW176106	Hs.285459	ESTs	2.2
	424946	M64572	Hs.153932	protein tyrosine phosphatase, non-recept	2.2
	437332	AA814943		gb:oc07d06.s1 NCL_CGAP_GCB1 Homo sapiens	2.2
80	454419	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	2.2
	416225	AA577730	Hs.188684	ESTs, Weakly similar to P4259 ferritin	2.2
	450579	AW136774	Hs.48614	ESTs	2.2
	400664				2.2
	447613	AL041057	Hs.33363	DKFZP434N093 protein	2.2

	402689	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	2.2
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.2
	432797	AA565264	Hs.136443	ESTs	2.2
	405608				2.2
5	426365	AA376667	Hs.10283	RNA binding motif protein 8B	2.2
	405634				2.2
	423646	H02364		gb:yj35d06.r1 Soares placenta Nb2HP Homo	2.2
	434690	AI867679	Hs.148410	ESTs	2.2
10	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
15	433781	AA609379	Hs.192083	ESTs	2.2
	450587	AI828854	Hs.258538	striatin, calmodulin-binding protein	2.2
	434077	AF116659	Hs.321151	Homo sapiens PRO1412 mRNA, complete cds	2.2
	448756	AI739241	Hs.171480	ESTs	2.2
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.2
20	454471	AW902125		gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.2
	419107	AW085152	Hs.292987	ESTs	2.2
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.2
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	2.2
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	2.2
25	456056	AA463550	Hs.337532	ESTs, Weakly similar to A47582 B-cell gr	2.2
	409998	M78345	Hs.98265	KIAA1877 protein	2.2
	422352	AA766296	Hs.99200	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Claspin	2.2
	433919	AA746311		gb:oa56d12.r1 NCL_CGAP_GCB1 Homo sapiens	2.2
30	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	2.2
	431632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fis, clone HE	2.2
	454716	AW850684		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.2
	413752	BE161807		gb:MR3-HT0446-300300-203-h01 HT0446 Homo	2.2
	458037	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	2.2
	434239	AF119910	Hs.283047	hypothetical protein PRO2964	2.2
35	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	2.2
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.2
	400697				2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
40	447039	AV661798	Hs.282915	ESTs	2.2
	404593				2.2
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.2
	421976	AL138443	Hs.23450	mitochondrial ribosomal protein S25	2.2
	401673				2.2
45	425001	U55184	Hs.154145	hypothetical protein FLJ11585	2.2
	447816	NM_007233	Hs.274329	TP53 target gene 1	2.2
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	2.2
	419118	AA234223	Hs.139204	ESTs	2.2
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.2
50	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
	454749	AW818649		gb:RC1-ST0278-040400-018-e02 ST0278 Homo	2.2
	456933	AA363946	Hs.20969	ESTs	2.2
	402942				2.2
	437064	AI023264		gb:ov64h08.s1 Soares_testis_NHT Homo sap	2.2
55	458623	AI305223	Hs.148056	ESTs	2.2
	415257	F03016	Hs.27513	ESTs	2.2
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	2.2
	442783	AI017586	Hs.131181	ESTs	2.2
	444313	AI140494	Hs.197955	KIAA0704 protein	2.2
60	453444	AL036531		gb:DKFZp564l1162_r1 564 (synonym: hfr2)	2.2
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
	430013	AA463833	Hs.151275	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.2
	437138	AI935622	Hs.271245	ESTs	2.2
	406298				2.2
65	409723	AW885757	Hs.257862	ESTs	2.2
	414481	AW451956	Hs.8383	bromodomain adjacent to zinc finger doma	2.2
	433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
70	445061	AI253094	Hs.145227	ESTs	2.2
	442617	AW340093	Hs.130538	ESTs	2.2
	438298	H23542	Hs.181788	ESTs	2.2
	454916	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	2.2
	428017	AA424983	Hs.98312	ESTs	2.2
75	451149	AL047586	Hs.10283	RNA binding motif protein 8B	2.2
	418076	R61388	Hs.6724	ESTs	2.2
	403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	2.2
	441811	AI073548	Hs.164597	ESTs	2.2
	434763	AA648618		gb:ns07a11.r1 NCL_CGAP_Ew1 Homo sapiens	2.2
80	447453	AW608645	Hs.18800	hypothetical protein FLJ20281	2.2
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.2
	415424	Z44766		gb:HSC28G081 normalized infant brain cDN	2.2
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	2.2
	421216	AV649282	Hs.102664	vesicle-associated membrane protein 4	2.2

	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.2
	448700	BE614182	Hs.123075	ESTs	2.2
	457741	BE044740		gb:hm55g10.x1 NCL_CGAP_RDF1 Homo sapiens	2.2
5	437927	AI039789	Hs.25982	hypothetical protein FLJ21031	2.2
	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
	436640	AA724411	Hs.156065	ESTs	2.2
10	438290	AA843719	Hs.122341	ESTs	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	455735	BE161124		gb:PM0-HT0425-141299-001-A06 HT0425 Homo	2.2
	458455	AV648310	Hs.213488	ESTs	2.2
	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S	2.2
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	2.2
15	424063	NM_002019	Hs.138671	fms-related tyrosine kinase 1 (vascular	2.2
	441874	AA970389	Hs.128055	ESTs	2.2
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.2
	433629	R13140	Hs.13359	ESTs	2.2
	415266	AA164199	Hs.270152	ESTs	2.2
20	440633	AI140686	Hs.263320	ESTs	2.2
	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.2
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.2
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.2
	401240				2.2
25	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
	436992	AA741074	Hs.120750	ESTs	2.2
30	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.1
	400040				2.1
	458762	AW802754		gb:IL2-UM0076-030400-061-H01 UM0076 Homo	2.1
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	2.1
35	419953	BE267154	Hs.125752	ESTs	2.1
	410648	AW792909		gb:CM0-UM0001-010300-258-c05 UM0001 Homo	2.1
	423717	AA330036	Hs.152003	ESTs	2.1
	436683	AW991278	Hs.57787	ESTs	2.1
	445225	AI216555	Hs.202398	ESTs	2.1
40	410991	AW812790		gb:RC3-ST0186-141299-014-g08 ST0186 Homo	2.1
	412639	AW961284	Hs.296235	ESTs	2.1
	447777	AI424223		gb:te95a05.x1 NCL_CGAP_Pr28 Homo sapiens	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
	404526	AI912555	Hs.157195	peptide YY, 2 (seminalplasmin)	2.1
45	452492	BE063096		gb:CM4-BT0266-091199-039-a02 BT0266 Homo	2.1
	417154	AI674701	Hs.21388	ESTs	2.1
	428152	AA422030		gb:zv26h05.r1 Soares_NhHMPu_S1 Homo sapi	2.1
	442312	AI820617	Hs.129216	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	456513	AA279143	Hs.88561	ESTs	2.1
50	430712	AW044647	Hs.196284	ESTs	2.1
	441445	AI221959	Hs.187937	ESTs	2.1
	420288	AW071225	Hs.245556	ESTs	2.1
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo	2.1
	447033	AI357412	Hs.157601	ESTs	2.1
55	436853	BE328074	Hs.148661	ESTs	2.1
	455189	AW864176		gb:PM0-SN0014-260400-002-b08 SN0014 Homo	2.1
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	2.1
	458356	AI024855	Hs.131575	ESTs	2.1
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.1
60	424480	AA341442	Hs.205299	ESTs	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.1
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
65	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
	417725	R25257	Hs.21503	ESTs	2.1
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	2.1
	439474	AI824060	Hs.211501	ESTs	2.1
70	446895	AA166655	Hs.282803	ESTs	2.1
	448582	AI538880	Hs.94812	ESTs	2.1
	452783	AA028167	Hs.61486	ESTs	2.1
	442430	R89164	Hs.48320	double ring-finger protein, Dorfing	2.1
	428908	AW303529	Hs.144955	ESTs	2.1
75	427335	AA448542	Hs.251677	G antigen 7B	2.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.1
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	2.1
	416951	AA190926	Hs.190785	ESTs, Moderately similar to S65657 alpha	2.1
	439950	AW937417	Hs.293561	ESTs	2.1
80	458227	Z40670	Hs.181340	ESTs	2.1
	447179	AW015633	Hs.157299	ESTs	2.1
	454950	AW847460		gb:RC3-CT0208-270999-021-e04 CT0208 Homo	2.1
	404453				2.1
	420844	AA595522		gb:nh22c09.s1 NCL_CGAP_Pr1 Homo sapiens	2.1

	426456	AA580748	Hs.130658	ESTs	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	430879	BE149423	Hs.10554	hypothetical protein FLJ12761	2.1
5	444584	AI168422		gb:ck30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.1
	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.1
	453853	AL040600	Hs.188083	ESTs	2.1
	414083	AL121282	Hs.257786	ESTs	2.1
	401645				2.1
10	436577	W84774	Hs.17643	ESTs	2.1
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.1
	409168	N94037	Hs.312938	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	410276	AI554545	Hs.68301	ESTs	2.1
	443372	AI792557	Hs.133107	ESTs	2.1
	422093	AF151852	Hs.111449	CGI-94 protein	2.1
15	402333				2.1
	409374	R87083	Hs.19081	ESTs	2.1
	412011	NM_000406	Hs.73064	gonadotropin-releasing hormone receptor	2.1
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
20	416085	H18072	Hs.92576	ESTs	2.1
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.1
	452374	AL037405	Hs.339639	ESTs	2.1
	450061	AI797034	Hs.201115	ESTs	2.1
25	450180	AW449644	Hs.257182	ESTs	2.1
	405120				2.1
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.1
	458890	AW865523		gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.1
30	435600	AL047034	Hs.119747	ESTs	2.1
	440964	AI733106	Hs.130218	ESTs	2.1
	417455	AW007066	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	2.1
	436461	AW511956	Hs.293261	ESTs	2.1
	436777	AA731199	Hs.293130	ESTs	2.1
35	427521	AW973352	Hs.290585	ESTs	2.1
	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.1
	413231	D87461	Hs.75244	BCL2-like 2	2.1
	423969	AI830571	Hs.331633	hypothetical protein DKFZp566N034	2.1
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	2.1
40	443777	AV646510	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	2.1
	416148	H22453	Hs.169187	ESTs	2.1
	402528				2.1
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	446209	AI375025	Hs.153368	ESTs	2.1
45	453362	H14988	Hs.107375	ESTs	2.1
	417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.1
	401069				2.1
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.1
50	410966	AW812088		gb:RC4-ST0173-191099-032-a07 ST0173 Homo	2.1
	447124	AW976438	Hs.17428	RBP1-like protein	2.1
	449939	T86420	Hs.272139	ESTs	2.1
	411693	AW857271		gb:CM0-CT0307-210100-158-g09 CT0307 Homo	2.1
	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.1
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	2.1
55	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	2.1
	404694				2.1
	406668	T62745	Hs.184411	albumin	2.1
	441092	T99289	Hs.126556	EST	2.1
	454643	BE006345		gb:RC2-BN0127-240300-011-d05 BN0127 Homo	2.1
60	426646	AA382787	Hs.122713	ESTs	2.1
	431605	AW972407		gb:EST384498 MAGE resequences, MAGL Homo	2.1
	414452	AA454038	Hs.29032	ESTs	2.1
	401991				2.1
	457176	AA436837		gb:zv57g07.s1 Soares_testis_NHT Homo sap	2.1
65	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	428208	AA442327	Hs.104854	ESTs	2.1
	445049	AV652718		gb:AV652718 GLC Homo sapiens cDNA clone	2.1
	419116	AF292402	Hs.283093	neuromedin U receptor 2	2.1
	427894	AL135709	Hs.28921	zinc finger protein	2.1
70	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	2.1
	424323	AA338791	Hs.177788	ESTs	2.1
	404582				2.1
	418631	AA225921	Hs.115105	ESTs	2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
75	452539	AW105321	Hs.49367	ESTs	2.1
	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
	440310	AA878939	Hs.125406	ESTs	2.1
	433297	AV658581	Hs.282633	ESTs	2.1
	410900	AW810169		gb:MR4-ST0124-040500-007-h07 ST0124 Homo	2.1
80	419386	AA236867	Hs.143868	ESTs, Weakly similar to I38022 hypotheti	2.1
	402451				2.1
	447842	AW160804	Hs.247302	twisted gastrulation	2.1
	453880	AI803166	Hs.28462	ESTs, Weakly similar to I38022 hypotheti	2.1
	425189	H16622		gb:ym26c07.r1 Soares Infant brain 1NIB H	2.1

	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.1
	400612				2.1
	402318				2.1
5	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	2.1
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	412029	AW886238		gb:RC5-OT0078-280300-022-F01 OT0078 Homo	2.1
	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
10	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	444498	AI151413	Hs.26330	ESTs	2.1
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	2.1
	425324	M89470	Hs.155644	paired box gene 2	2.1
	430719	AA488988	Hs.293796	ESTs	2.1
	432577	BE208545	Hs.317590	hypothetical protein FLJ14640	2.1
15	407593	AW044083	Hs.237008	ESTs	2.1
	401098				2.1
	440299	AI871778	Hs.250112	ESTs	2.1
	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	2.1
	428627	BE002993	Hs.187660	putative Rab5 GDP/GTP exchange factor ho	2.1
20	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	2.1
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	2.1
	439831	AW136488	Hs.25545	ESTs	2.1
	451829	AW964081	Hs.247377	ESTs	2.1
	404595				2.1
25	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
	456083	U46922	Hs.77252	fragile histidine triad gene	2.1
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	2.1
	406413				2.1
	439483	T69980	Hs.58323	Homo sapiens cDNA FLJ11613 fis, clone HE	2.1
30	446242	N66336	Hs.7360	ESTs	2.1
	449625	NM_014253	Hs.23796	odz (odd Oz/ten-m, Drosophila) homolog 1	2.1
	457938	AI373638	Hs.133900	ESTs	2.1
	413101	BE065215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo	2.1
	408350	AW183350	Hs.250127	ESTs	2.1
35	419812	NM_000562	Hs.93210	complement component 8, alpha polypeptid	2.1
	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A recepto	2.1
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	2.1
	409955	U60665	Hs.57692	chromosome 6 open reading frame 10	2.1
	435579	AI332373	Hs.156924	ESTs	2.1
40	436088	AA704687	Hs.191294	ESTs	2.1
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.1
	416100	H18700	Hs.268799	ESTs	2.1
	403218	AL134878	Hs.119500	ribosomal protein, large P2	2.1
	409747	H60964	Hs.331250	ESTs	2.1
45	428764	W21550		gb:zb52f12.r1 Soares_fetal_Jung_NbHL19W	2.1
	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.1
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.1
	428299	AL038004	Hs.29419	ESTs	2.1
	406817	AI936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
50	411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
	412446	AI768015	Hs.92127	ESTs	2.1
	414012	AW452334	Hs.128148	ESTs	2.1
	421966	AA904519	Hs.130710	ESTs	2.1
	430566	AA481282	Hs.190149	ESTs	2.1
55	456606	AA292862	Hs.275369	ESTs	2.1
	451604	T65365	Hs.172851	arginase, type II	2.0
	440926	AW196772	Hs.131323	ESTs	2.0
	420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 fis, clone PL	2.0
	459082	BE551721	Hs.282149	ESTs	2.0
60	413241	BE073771	Hs.302414	Homo sapiens clone FLB8945 PRO2411 mRNA,	2.0
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	2.0
	447552	AI394125	Hs.160413	ESTs	2.0
	420905	AA521307	Hs.186651	ESTs	2.0
	428052	AA420477	Hs.26993	ESTs	2.0
65	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.0
	432527	AW975028	Hs.102754	ESTs	2.0
	430202	T85775		gb:yd60g02.r1 Soares fetal liver spleen	2.0
	446610	AV659433	Hs.282984	ESTs, Weakly similar to I38022 hypotheti	2.0
	427961	AW293165	Hs.143134	ESTs	2.0
70	455290	U75810		gb:HSU75810 Human Homo sapiens cDNA clon	2.0
	445564	AB028957	Hs.12896	KIAA1034 protein	2.0
	412811	H06382	Hs.21400	ESTs	2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
75	429418	AI381028	Hs.118769	ESTs	2.0
	431511	NM_012386	Hs.258581	Homo sapiens p95 paxillin-kinase linker	2.0
	445829	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	453123	AI953718	Hs.221849	ESTs	2.0
80	455401	AW936369		gb:QV4-DT0021-301299-071-d07 DT0021 Homo	2.0
	406666	V00495	Hs.184411	albumin	2.0
	445688	AI248205	Hs.153244	ESTs	2.0
	446131	NM_000929	Hs.290	phospholipase A2, group V	2.0
	440388	AI693520	Hs.223000	ESTs	2.0

	457128	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.0
	404416				2.0
	444187	AW138466	Hs.151274	ESTs	2.0
5	431552	AI815863	Hs.259873	axonal transport of synaptic vesicles	2.0
	455814	BE141689		gb:CM1-HT0092-220999-016-b09 HT0092 Homo	2.0
	454759	AW819455		gb:RC5-ST0293-021299-031-A04 ST0293 Homo	2.0
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.0
	404420				2.0
10	408112	AW451982	Hs.248613	ESTs	2.0
	432702	AW973953	Hs.293744	ESTs	2.0
	448587	AI539652	Hs.28338	KIAA1546 protein	2.0
	446854	BE268103	Hs.208914	hypothetical protein MGC10999	2.0
	410569	AA766825	Hs.205675	ESTs	2.0
15	432596	AJ224741	Hs.278461	matrilin 3	2.0
	402341				2.0
	452919	AW962167		gb:EST374240 MAGE resequences, MAGG Homo	2.0
	433632	AA649921	Hs.112553	ESTs	2.0
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.0
20	451927	AL355687	Hs.27261	Homo sapiens mRNA full length insert cDN	2.0
	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.0
	450895	N66727	Hs.10957	ESTs	2.0
	408459	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypothe	2.0
	400842				2.0
25	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.0
	400859				2.0
	405829				2.0
	411863	BE075244	Hs.12420	ESTs	2.0
	415258	AW752247	Hs.293853	ESTs	2.0
30	416093	R60685	Hs.268698	ESTs, Moderately similar to ALUC_HUMAN I	2.0
	420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypothe	2.0
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
35	457039	H29990	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.0
	454578	AW809178		gb:MR4-ST0118-261099-012-c07 ST0118 Homo	2.0
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0
	415173	AW501735	Hs.253015	ESTs	2.0
40	449011	AI655376	Hs.192693	ESTs	2.0
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.0
	416057	AI927382	Hs.29857	ESTs	2.0
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.0
45	408531	AW207553	Hs.253639	ESTs	2.0
	434663	AA641972	Hs.130058	ESTs	2.0
	428085	AA421081	Hs.12388	ESTs	2.0
	425006	R38685	Hs.332622	ESTs	2.0
	446139	H77395	Hs.39749	ESTs	2.0
	400049				2.0
50	428333	AW972668	Hs.293044	ESTs	2.0
	429458	BE161832	Hs.292689	ESTs	2.0
	425087	R62424	Hs.126059	ESTs	2.0
	457122	AI026157	Hs.33728	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	400310	X63966	Hs.135631	H.sapiens synthetic gene for platelet-de	2.0
55	451805	AI968300	Hs.208220	ESTs	2.0
	401986				2.0
	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0
	417756	Z43056		gb:HSC12B021 normalized infant brain cDN	2.0
	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.0
60	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
	429110	L29301	Hs.2353	opioid receptor, mu 1	2.0
	433755	AW085934	Hs.120868	ESTs	2.0
	434118	AF116715	Hs.256256	Homo sapiens PRO2829 mRNA, complete cds	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
65	443748	AW206447		gb:UI-H-BI1-afg-g-02-0-UI.s1 NCI_CGAP_Su	2.0
	445205	D83776	Hs.12413	KIAA0191 protein	2.0
	458175	AW296024	Hs.150434	ESTs	2.0
	446419	AW576760	Hs.160726	Homo sapiens cDNA FLJ11680 fis, clone HE	2.0
	441627	AA947552	Hs.58086	ESTs	2.0
70	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.0
	455614	AI693369	Hs.202274	ESTs	2.0
	449899	AI610700	Hs.103280	ESTs	2.0
	420111	AA255652		gb:zs21h11.1 NCI_CGAP_GCB1 Homo sapiens	2.0
	437354	AA749215	Hs.291886	ESTs	2.0
75	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.0
	419691	W03298	Hs.193521	ESTs	2.0
	439724	AF086565	Hs.60351	EST	2.0
	413362	BE088812		gb:CM2-BT0693-230300-129-d08 BT0693 Homo	2.0
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	2.0
80	434361	AF129755	Hs.117772	ESTs	2.0
	442479	AF069484		gb:AF069484 Homo sapiens astrocytoma lib	2.0
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	2.0
	459323	AW062490		gb:MR0-CT0065-100899-001-d01 CT0065 Homo	2.0
	449438	AA927317	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon	2.0

	400285				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
5	417383	W02642	Hs.136102	KIAA0853 protein	2.0
	447153	AA805202	Hs.315562	ESTs	2.0
	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	2.0
	455696	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo	2.0
	456510	AK001652	Hs.99423	ATP-dependent RNA helicase	2.0
10	449815	AI671000	Hs.199739	ESTs	2.0
	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.0
	400238				2.0
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.0
	445073	AW291389	Hs.13056	hypothetical protein FLJ13920	2.0
15	455221	AW867751		gb:MR0-SN0038-290300-001-a03 SN0038 Homo	2.0
	413174	AA723564	Hs.191343	ESTs	2.0
	435810	BE349853	Hs.2785	keratin 17	2.0
	418687	R61650	Hs.22581	ESTs	2.0
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.0
20	431750	AA514986	Hs.283705	ESTs	2.0
	453242	T98327	Hs.18343	ESTs	2.0
	437074	AI286235	Hs.128905	hypothetical protein FLJ13204	2.0
	459411	N52920		gb:yv34h09.s1 Soares fetal liver spleen	2.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.0
25	409929	R38772	Hs.172619	myelin transcription factor 1-like	2.0
	406378				2.0
	459208	BE261314	Hs.149039	ESTs, Weakly similar to I38022 hypothe	2.0
	445260	AI218133	Hs.147617	ESTs	2.0
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.0
30	445020	AI205655	Hs.147221	ESTs	2.0
	402048				2.0
	412695	AW984439		gb:PM3-HN0011-220300-002-c05 HN0011 Homo	2.0
	416408	R94725	Hs.35354	ESTs	2.0
	423347	AI660412	Hs.234557	ESTs	2.0
35	427836	AA416642	Hs.116176	ESTs	2.0
	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
	436902	AW247145	Hs.192729	ESTs	2.0
	440122	AI733011	Hs.127678	ESTs	2.0
	442901	AI023654	Hs.114191	ESTs	2.0
40	444097	AW517412	Hs.150757	ESTs	2.0
	447278	AI934935	Hs.158669	ESTs	2.0
	451361	AA053854		gb:zf52f02.r1 Soares retina N2b4HR Homo	2.0
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.0
	454423	AW603985		gb:RC4-CN0048-140100-011-a04 CN0048 Homo	2.0
45	458801	N98648	Hs.276860	ESTs, Weakly similar to C Chain C, Human	2.0

TABLE 30B

50	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
55	Pkey	CAT number	Accession
	407593	1003161_1	AW044083 AW044094 AW370634
	407594	1003220_1	AW057584 AW057585 AW044153 R34370
	407639	1006924_1	AW205369 AW058599 AW207608
	407676	1008294_1	AW064111 AW064450 AW064429
60	407721	10108_1	Y12735 NM_003582 AW238970 R38268 R41411 R41419 T16717 AA002193 H62028 AI359545 AW105201 AW087158 AA699728 AI095264 AA002065 H62029 AI289101 AA884804 AA904950 AA609672 AI139874 H77896
	407726	101126_1	AA435679 AA470655 H22526 AA044031 AA876426 W63767 AI421140 AI418990 H42329 H88910 AL041066 H88909 W94610 AW352277 W94648 W94167 AW952568 AI419653 AA335501 AA393641 AA044353 H41626 H22525 R58582 AW297645 C75230 AW368034 AW468904 AI272755
	407762	101439_1	AW235638 AA346882 AW866803 AA361281 AW963163 AA044373 AA136755
65	407764	1014849_1	BE008347 BE008320 BE083307 BE083311 AW075968
	407788	10163_1	BE514982 BE614814 AW393078 AW238480 AA055637 N27644 AA641158 M87068 AA161019 AA161003 AA587315 AA716746 AA593632 AI354870 AW183492 Y07755 NM_005978 AW872948 AI608987 H64656 AF086003 AA643149 AI819402 H64555 AA858398 AA594885 AI436747 BE122811 AA587026 AW857106 AI950679 AA596012 AA654004 AW238238 AI971395 AA459074 AA458884 AI608591 BE181995 BE181970 AW195797 C00271 BE182043
70	407803	1017498_1	AW081681 N36967 N36959
	407809	1017982_1	AW082279 AW082688
	407811	10180_1	AW190902 AI802788 AI041650 AI037867 AF110137 NM_013372 H99469 N35377 AW151676 AI678451 AW078795 AW087935 AI884505 AW044602 AB032372 AF045800 AI621183 AI750578 AA376403 AI910477 AA373348 AA373673 AI752124 AL359060 W48619 AA373298 AA373975 AW604409 AW604404 AW368603 AA545734 AW361415 AA373557 AW956164 AW853798 AI750595 AL359059 AA344024 N31127 AW580737 N27040 AA071138 AI753050 AA599801 W48852 AA669811 AA112124 AI940705 W52686 AA084001 C01826 AI940729 AA373544 AW957491 AW383224 AW383164 AW383192 AW383125 AW383194 AW842507 AI940795 H80042 AW631119 W47324 W42884 AI750594 AI754387 AI753734 AA372833 AW069006 AI750577 AW473621 AI888605 AA600082 AI041803 W51909 W25447 AI521673 AI087351 AA670070 W47325 AA071381 W42791 AI090390 AI085102 AI302125 AA788723 AW069430 AW069485 AI754608 AA373014 BE140150 BE140166 BE140102 BE140143 BE140157 BE140117 BE140098 AW005943 BE140108 BE140176 BE140171 BE140144 BE140175 BE140160 BE140152 BE140099 BE140177 BE140167 BE140145 BE140109 BE140163 BE140172 BE140161 BE140179 BE140147 BE140107 BE140146 BE140155 BE140173 BE140148 BE140174 BE140158 BE140149 BE140116 BE140156 BE140105 BE140103 BE140164 AW138508 BE140153 AW806557 BE140121 BE140162 C01953 AW806500 BE140124 AA329219 AW955642 AW069165 AI968107 N21113 AI754594 AW069264 AI754660 BE551937 AA543066 AA703927 AW130486 AI814434 AI924946 AA789056 AW173667 AW069841 AI022286 AI753523 AI753558 AI753482 AW068940 AI753002 AA669866
75			
80			

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	456083	14855_1	AW291315 AI589104 AI949122 AW025986 AW275328 N51358 AA131190 AA723731 N86864 AA091367 AI738620 AA345291 AA774160 R51372
			AI373904 R37681 W72195 AA476597 AI025596 AI242078 AA384072 BE349121 AI203442 AA885019 AI424214 AI964081 AI219465 AW103904
			AA017216 AW591839 AI890043 BE247650 AW793376 AA224322 AI784198 AW190649 BE247646 AA055073 D19892 AA428076 AA165625

			R34233 AA469355 AI302148 AI690055 AA946756 AI697829 BE218045 AA027985 AI734957 AA436215 AW362506 AA469277 AA436214 AW362508 R79964 AW362504 AW362505 AA027984 AI417795 BE066043 AW967592 AA165661 AA251567 C05877 R19957 R53161 R52318 Z44555 BE066030 AW769414 R35560 H08481 AA017309 H91010 N39092 N48447 W299698 BE270312 AI333779 R68946 AF154846 AA400924 AF075093 AA626790 AI0202783 H53869 H53499 AI001163 AA714166 L32164 AA768900 AW182419 AW977136 AI915355 AA994468 AI377886 AI654131 AI674302 AW074683 AA224872 AI791642 AA228308 AI821503 AA230172 AA224838 U00803 NM_002031 AW195632 C05922 W28481 AW967500 AW966876 AW976565 AI417020 AI057022 AA251316 AA744820 AI806037 AW966871 AA251713 AF080576 T49825 AA281037 T49826 AK001714 AW960785 AK001831 BE075311 AW273355 AA928445 AI698734 AW977909 AW268863 AI392846 AA811609 AI565035 AW007245 AI754385 AI092244 AA906509 AW438768 AW751668 AA459681 AA861761 AW118314 D63077 AI537049 AA782718 AW050550 AA430988 AA130556 AA383461 AA337522 AA130593 AA258033 AA459485 AK001652 AK001245 AJ010840 AA443492 AA361206 AA384559 AA205216 AI990275 BE075308 AA927343 AA372625 AI572799 BE466582 N30525 AA813191 AA456509 AA854999 N30537 AA463668 BE149580 AA301443 AI366930 AA010769 AA248189 AW043967 AA011050 AI193868 AA508116 N20812 AI190726 AW663652 AI161405 AA909896 H52712 AI081806 AI862934 AI167935 AA460738 AI345960 AA460140 AA346920 BE565501 AA456419 AA953554 AA806622 AI242924 AI619442 AI082684 AA947786 AA601594 BE044119 BE349995 AA091744 AW959301 H70392 AA279143 AA419462 AW135986 BE467356 BE221523 BE468135 AA282464 T70755 AW592167 AA284280 W47266 AW972765 AW069452 W47267 AI186593 AA526308 AA525432 AI858634 BE465909 AI057197 AI968927 AI969337 N21608 W25410 AI792468 AI734237 N28843 N58992 AI820802 N93619 AI668704 AI367790 AI204569 AI827786 AW303478 AI216657 AW592056 AA928804 AA890107 AA292862 AA398885 BE247203 BE244171 AW205198 AI245208 AI284388 BE048356 AW293524 NM_016014 AF151825 AI026799 BE048322 AI568420 AI041696 AI796313 AW003505 AI492609 AI564777 AW590366 AW236586 AI191469 AI571792 AA490835 AA843378 AA843160 AA932149 AA687136 AI829606 AA490836 BE005634 AW965621 F12793 R56751 R52429 T75124 R58675 AI205826 AA258787 BE467912 AI744557 AA554436 AI640749 AI077333 BE221602 AI538508 AA968618 AI671472 AI290360 AI863656 AI910555 AW104195 AI648463 H24708 AA280869 AA279428 AA987634 AA480878 AA836072 AW877911 AA521155 AA305609 AI110686 AF063561 AA480937 AA281170 H96495 BE005402 AW367567 AW367372 AW367351 AW367585 AW601230 AA847183 AA442049 AW896013 BE568756 T09279 T36094 AA287495 Z42413 AA328761 AW139131 AA252554 AA323777 AW950315 AA999676 AI815004 AI203869 AI016834 AW136782 AA999661 AA825909 AW071102 AA826127 AA838505 AA885039 AA287392 AI470496 C01794 AA249575 AL118643 BE538611 R56578 R56014 R17173 AW135076 R45909 AW370767 R77253 U13897 BE165997 AA363946 AA628263 AA628262 S78234 T87689 NM_001256 U00001 M78440 BE280314 BE568566 AI075160 W31156 AA256407 AA255817 R16014 AI203880 AW117283 AA504316 AW105046 AW370478 AI378553 AA732100 AA815109 AW297995 BE501979 AW293480 AA972091 BE082548 N98929 AA255818 AA256301 AI559887 R16115 AA384982 AW949878 AA085260 AL135314 AA211035 AI689616 BE004600 BE004767 BE004597 AW800545 AW197262 AA996213 AW452890 AI458977 AA188660 AA491202 BE327143 AA489098 AW172396 AI399903 AA5830687 AI916706 AW860246 AW006356 AI288368 AW193267 AA670452 AA445924 AI276764 AA428407 AA836037 AI886571 AA922445 AA557273 AA599272 AA937432 AW594254 AV650497 AI889557 BE221149 AA934793 AA373059 AA883898 AA491005 T87690 AA167622 AA167635 AA084655 AA207057 AA633879 AA706479 AA706213 AA706197 AA679805 AA683208 AA679343 AA613172 AA679833 AA085131 AA679793 AA601666 AA210946 AA583228 AA601229 AA084718 AA584501 AA224217 AA706452 AA489324 AA587310 AA082786 AA586892 N23070 AA211405 AA082906 AA489789 AA209324 AA206631 AA167636 AA188956 AA666070 AA199718 AA214195 AA113862 AA206791 AA633796 AA223986 AA083048 AA085009 AA085307 AA207042 AA214235 AA166892 AA188689 AA211101 AA706139 AA773961 AA773972 AA189090 AA668591 AA213387 AA206041 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T82077 BE105666 AA811950 AA397546 AA699372 AA699363 AA399064 AI301740 AL119574 AW504484 BE560671 BE269112 AW897591 T31233 U17279 AW504792 T32181 Z47338 T05711 AL121247 AW504876 AW161725 AI204992 D38743 D38661 AW895130 AA985067 AL120318 AA326654 AW955387 AA776607 D38742 AI267812 AL035910 BE008426 BE008367 AA423862 BE348785 AA249436 AA326809 AA325529 AW361428 N24212 AW302831 AI583363 AW470460 AL038861 AA234531 AI376141 AI194854 W35263 N39248 D52746 D55494 AA083749 D52828 T30063 T31624 D54617 AA112066 BE018814 AW882900 M78702 T31558 T31691 AW859799 AA310616 AW389747 AA317897 T31158 AI077640 AA386250 T10323 D53660 F05613 AL120458 H15866 AW895727 AW895802 AW899191 AA128798 N31267 H14732 BE208125 N64235 H97218 AA236449 BE087062 F11649 F11648 Z42310 T32845 U47717 H43263 Z44143 T05325 T16885 AL138108 H84437 AA197265 N46693 AW020269 AA070847 AW022743 AW885792 M78703 AA486340 T07147 N36340 T35393 AW841129 AI288455 BE005370 AI497892 C14978 AA487674 T30747 AW022976 AA860826 AA730653 AA857741 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AI127576 T82460 AI368362 AI435204 AI478453 AI093082 AI469352 AW338517 AI200250 AI031694 AI887286 AI033758 AW080370 AW029140 N32140 N52949 N50055 H47004 R76054 R61887 R73087 AI160363 H64018 W88748 AI081703 AA149098 R40542 N77209 H04380 AA234491 R08896 D57030 AI767209 AA600348 N70842 AA044422 AI888195 AA777676 AI538758 C16174 R38565 AI799219 H74312 F10055 W37697 F10343 AA610106 R52523 R22142 H88895 R77674 R44673 AA045199 R31568 AA505916 AI360773 F10337 AA733180 AI016479 AW183400 AW779199 D58102 H64348 D57909 R26653 AW051234 Z41044 AA876777 F03579 AI680446 AA745688 T24075 T35116 T35115 R02091 Z30229 AI872774 AW772549 AI540411 AI784282 R25646 AA541817 T77442 R26596 BE166424 T77229 R23696 AA399018 AW242359 AI868208 AW020951 AA412180 AI026157 AA838752 AI146272 AA910825 AI266100 N24580 H97503 BE327388 AI697814 W56675 AA423842 AA423880 H40134
5	456189 456208 456273	1620717_1 165094_1 1731_1	
10	456303 456347 456386 456443 456472	176684_1 18004_1 1842693_-1 188540_1 19126_1	
15	456481 456510	192210_1 19507_1	
20			
25	456513 456536 456555 456561	195409_1 198330_1 199748_1 200378_1	
30	456605 456606 456737	203819_1 203847_1 22551_1	
35			
40	456933 457003	256540_2 27203_1	
45			
50			
55	457024 457030	274501_1 27473_1	
60			
65			
70	457039 457040	275248_1 27530_2	
75			
80	457041 457122	275843_1 287827_1	

5	457128	28930_1	AI932995 BE064464 AW371902 AW371841 AI885885 BE064457 AA524113 AA721037 AA504343 AA778099 AI800598 AI693112 AI864633 AI690228 AI400990 AW969089 AW371927 AW371912 AW383562 BE151089 AW383568 BE218503 AW383570 AW371899 BE151097 AW371900 AW293095 AW292008 AA434179 AA714780 R45868 W01182 AW957767 AW119223 AI207864 W01578 AA354403 AA805177 AI613299 AW269636 AA481528 AW079101 AF131777 R60489 T81289 AA481594 BE181020 AA465433 AW808125 T84992 AA749191 AA436837 AA442594 AA443927 AA444106
	457176	296527_1	AW820035 T20260 T20259 AL049415 AA737756 W46965 W00799 AW340968 AW027417 AW263261 AI420674 AA814921 AA736509 N69991
	457187	298994_1	AW368643 W47065 AI090172 AI924139 BE468071 AA375842 AA375767 AW628849 AI422731 AA494558 AA969233 AI142954 AI161089 AI167233
	457225	30546_1	W94484 AI681576 AA249694 AI695943 AA832347 AA476621 AA937792 AI702870 AA455748 AW195100 AI638530 BE502479 AI383418 AA039630 C20777
	457314	318637_1	AA479597 Z45151 H28821
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	457506	34672_1	AF131757 T79901
	457620	371514_1	AA602711 BE078290
	457630	373784_1	AI680803 AI703329 AA609004 AI305245 AI457796 AW295787
	457652	37972_1	AF116656 AI114583 AW838134 AW838525 AW885447 H83251 AW838349 AW838378 AW838175 H83252
15	457653	37979_2	AI820719 AI273515 AW592687 AI263784 AI351926 R46866
	457653	37979_2	BE044740 AW827360 AW827623 BE161439 BE044718 BE046207 BE046551 AA653908 BE166581
	457741	395767_1	AA126136 H62964 BE245159 AF280094 AA431918 BE386201 AA707576 AI074267 AA969194 AA693596 H62844 AW134991 AA126014 AI077443
	457756	3_1	AA699881 AI037956 AA961277 AW204185 AI540791 AI273273 AW627957 AA926890 AI014851 AW081056 AA443705 AW137571 BE139390
			AI583851 AI583822 AI583814 AW268341 AI590502 AW302642 AI053871 AI254692 AI591255 AI590260 AI583359 AI583341 AI583752 AI224227
20			AW302089 AW466960 AA810124 AW302684 AI272921 AI141003 AW589738 AA074714 AA621482 AI796501 AW024557 AA621074 T62627
			AA639206 AI913538 AA075135 R54613 AA352975 AW206892 AI868280 AW449243 AA907317 AW134573 AI590492 AI610050 AI834309 AI375556
			AI284991 AW968038
	457770	402530_1	BE065030 AA670100 AA781546 AI022472 AA846803 AI497780 N68386 AI382890
	457802	410073_1	T78013 AA699327 W87785 W88613
25	457900	434061_1	AW976692 AA806542 AA745856
	457938	439837_1	AI373638 AI073389 AI087143 AA764776 AA913318
	458023	463717_1	AW978161 AW978165 AI016938 AI539270 AW294958 AW511089 AA814849
	458037	46627_1	AF074982 R27906 R31333 R31591 R27812
	458043	466952_1	AW979009 AA828038 AA828148
30	458067	46875_2	AA393603 Z19481 AA252342 AI807614 AI913804 AA040176 AA971879 H53388 AF085972 AI291424 H53349 AW015078 AA768307 AA127921
			AA723700 AA040841 AA993954 AA213655 AA127972 AA913063 BE327712 AI017585 AA988186 AA628183 AI205930 AA833558 AA974107
			AI004390 H48931 AA724004
	458175	498744_1	AW296024 AA897109 AI015000
	458227	517913_1	Z40670 BE504110 BE219908 AW468668 AI002334
35	458257	526854_1	U48351 AA969182 BE327312 AW138276 BE467567 AI680815 AI422668
	458303	543175_1	AI264628 AF017648 AI872732
	458356	555234_1	AI024855 AI024877
	458426	579269_1	AI084514 N46645 AW183984
	458455	59100_1	AV648310 AV661871 AI928475 AV647819 T55845
40	458507	614471_1	AI185703 AI805813 AW292764
	458552	633259_1	AW136139 AI216724
	458623	662297_1	AI305223 AI458577 AI275569
	458624	662652_1	AI362790 AI275996 N48887
	458661	677016_1	AI299789 BE551384
45	458684	68549_1	BE281115 T53860 AV659439 AV659421 BE539929
	458734	719515_1	AI554946 AW362008 AW362553 AI683342 AI376781
	458762	73076_1	AW802754 BE619228
	458763	731371_1	AI693417 AI418256 AW627792 F32979
	458771	737397_1	AW295151 AI425004 AW470228 AI693738 H50554 R99198 H50553 R99197
50	458797	75398_2	AW001835 AW612725 AW136670 AI798956 BE467368 AA280216 AI216754 BE622057 AL121193 AW853470 AW853450 AW369075 AW369108
			AW578479 AW369106 AW361242 AW361190 N79183
	458801	75669_1	N98648 AI458157 BE041652 BE218014 BE622355 AA369340 AA369515 AW962780 AW962704
	458817	764459_1	AI522129 T56009 R53849
	458833	777505_1	AW236702 AI566105 Z40396
55	458861	798085_1	AI630223 AI630470
	458890	812733_2	AW865523 AW865128 AW865467 AW865127 AW865466
	458925	82655_1	R15891 R61471 R61469 N69765 AI014624 AA007214 AW592075 H09780 AA709038 AI335898 H11055 AI559229 F09750 T72573 AA935558
			AA988654 AA826438 AI002431 AI299721
	459023	86727_1	AW968226 AI139249 AI701692 AA017303 AW469622 AA259148 AA811690 AA807996 AA744260 AA824494 AA731710 T25332 AA258101
60			AA970687
	459037	87417_1	AW439497 AI826059 AA018402 AA837392
	459082	889533_1	BE551721 H51878 AI823338 C01488 AW813562
	459124	916575_1	AW301478 AW301560 AI889207
	459207	926704_1	AW138410 AI912712 N40186
65	459208	92717_1	BE261314 AI243406 AA027322
	459275	97318_1	AI808913 AW028342 W81290 AI571379 AI382808 AA037071 W79688 R48751 N31808 AI870233 R48752 AW024895 AI333754
	459278	9751_1	AW294659 AI204928 AA351653 H51220 R86843 AA993182 U79298 R15294 F05089 Z42963 R17818 T77498 AA332319 W56049 AA331586
			AW881873 AW881865 AW881876 R52345 AI652070 AA400044 AA401512 T08151 W05486 N68378 T33846 AI190920 R43021 AI949980 Z39084
			T63413 W37269 F01343 R86669 AI621055 AW117593 AI193211 AW297932 AI500709 AA400056
70			
75			
80			

Table 30C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey Ref Strand Nt_position

	400462	9929659	Minus	197610-197785
	400608	9887666	Minus	96756-97558
5	400612	9929646	Minus	151513-151662
	400631	8247025	Minus	56203-56313,56424-56482,57073-57185,57513-57593,57747-57941
	400641	8117693	Plus	4786-4992
	400664	8118496	Plus	13558-13721,13942-14090,14554-14679
	400696	8118812	Minus	77737-77899
10	400697	8118812	Minus	79073-79198
	400706	7249204	Minus	78299-78686
	400816	8569993	Plus	161221-162078
	400842	1927148	Plus	90462-90673
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
15	400861	9757506	Plus	163855-164016
	400889	9958234	Minus	169782-170036
	401069	3927852	Minus	45682-45831
	401098	9965518	Minus	85632-86174
	401132	8705350	Minus	85679-85795
20	401189	9690246	Minus	90815-90929
	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
	401240	3355450	Plus	77433-77636
	401324	9863791	Plus	234057-234174
	401365	9796180	Minus	119572-119672
25	401368	8670914	Minus	65508-65662
	401459	9212270	Minus	182001-183323
	401462	6682291	Plus	112763-112909
	401497	7381770	Plus	92607-92813
	401526	7770561	Plus	91570-93177
	401596	3293210	Plus	63639-63890
30	401614	7839924	Plus	17350-17735
	401626	8575943	Minus	238100-238432
	401645	7657839	Minus	34986-35133
	401673	7689903	Minus	122587-122705,122765-123047
35	401694	3540172	Minus	64056-64168
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401878	8099802	Minus	162268-162474,163089-163195
	401887	7229981	Plus	93973-94120
	401899	7230209	Minus	155620-155815
40	401986	4406829	Minus	31137-31293
	401989	4309964	Minus	118611-118821
	401991	4156128	Plus	2398-2513
	402048	8072512	Plus	43936-44078
	402076	8117410	Plus	128316-128627
45	402090	7249154	Minus	104806-104939,106898-107052
	402112	8139750	Plus	10507-10713
	402131	7704961	Minus	33114-33209,33496-33678
	402145	8018280	Plus	113086-114800
	402318	7582559	Minus	12843-13403
50	402333	8844110	Minus	165693-165856
	402341	7656696	Plus	22583-23699
	402369	9558577	Minus	50417-50522
	402451	9796677	Minus	48137-48343
	402528	7630857	Minus	169609-169742
55	402603	9909396	Minus	141663-141852
	402615	9926801	Plus	131390-132157
	402689	8348025	Minus	5885-6209
	402942	9368398	Plus	102152-102386
	403011	6693597	Minus	3468-3623
60	403053	8748888	Plus	146568-146659,147539-147811
	403089	8954241	Plus	171964-172239
	403188	9838289	Minus	157618-157755
	403218	7630969	Plus	58039-58149
	403271	7230852	Plus	134283-134485
	403281	8072630	Minus	7521-7728
65	403306	8099945	Plus	127100-127251
	403310	8139936	Minus	183883-184026
	403317	8318526	Minus	50623-50834
	403329	8516120	Plus	96450-96598
70	403341	8569175	Plus	30699-30910
	403344	8569726	Plus	70823-70990
	403356	8569930	Plus	92839-93036
	403513	7656757	Minus	155310-155436,158402-158535
	403515	7656757	Minus	173358-179553
75	403525	7960440	Plus	152431-153243
	403534	8076917	Minus	46652-47332
	403568	8101145	Minus	85509-85658
	403572	8101156	Minus	1253-1675
	403574	8101156	Plus	5542-6176
80	403623	8569879	Minus	3519-5426
	403625	8569879	Plus	6551-7111
	403637	8671936	Minus	142647-142771,145531-145762
	403678	7331517	Minus	119573-120430
	403691	7387384	Minus	88280-88463

	403776	7770611	Minus	1414-1513,1624-1756
	403780	8076989	Plus	93160-93409
	403786	8083636	Minus	73028-73217
5	403891	7331467	Minus	191508-193220
	403937	7711761	Minus	12609-12773
	404042	9558573	Plus	5140-5208,8633-8763
	404043	9558573	Plus	29042-29135,46597-46699
	404068	3168621	Minus	18123-18766
10	404108	8247074	Minus	63603-64942
	404166	7596822	Plus	86147-86509
	404193	3881948	Minus	94185-94322
	404196	3805917	Minus	67928-68109
	404249	8655533	Plus	64270-64633
15	404367	9965011	Minus	114391-114628
	404404	7272262	Plus	82112-82244
	404414	7382165	Plus	143127-143398
	404416	7382420	Minus	143042-143216,144704-144853,145800-146048
	404420	7407952	Minus	129817-130586
	404443	7579073	Minus	87198-87441
20	404453	7657714	Plus	27768-29179
	404476	8080699	Plus	101841-102043
	404518	8151988	Plus	84494-84603
	404526	8152087	Plus	121918-122123,125198-125348
25	404531	8247909	Plus	20152-20362
	404561	9795980	Minus	69039-70100
	404569	7249169	Minus	104257-104348,104822-104970
	404582	9739220	Plus	53230-53424
	404587	8698840	Minus	69781-70096
30	404588	6456726	Minus	40059-40210
	404593	9944086	Minus	74922-75788
	404595	9958262	Minus	16764-16900
	404638	9796751	Minus	99433-99528,100035-100161
	404652	9796969	Minus	108172-108296
35	404694	9799957	Minus	128092-128227
	404708	9800828	Plus	77522-77658
	404731	7230299	Minus	168609-168781,182951-183081
	404767	7882827	Minus	23244-23759
	404793	7232206	Minus	61087-61590
40	404822	3810614	Plus	7541-8132
	404834	6911603	Minus	37948-38226
	404957	7407927	Plus	147512-148011
	404967	7523744	Minus	89944-90729
	404988	4662677	Minus	72406-72600,72779-72856
45	405001	6015406	Minus	104646-104819
	405008	6088019	Minus	64091-64267
	405090	8072525	Minus	38552-39202
	405120	8099940	Plus	140176-140340
	405229	7249019	Plus	51081-51701
50	405230	7249032	Minus	97493-97682
	405302	2078453	Minus	121688-121840
	405347	2979602	Minus	977-1116
	405443	7408143	Plus	90716-90887,101420-101577
	405455	7656675	Plus	134112-134671
55	405456	7656676	Plus	150052-150208
	405494	8050952	Minus	70284-70518
	405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
	405605	5836195	Minus	117070-117270
60	405608	5815499	Minus	66822-66925
	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405738	9943998	Plus	44370-45410
65	405747	8469069	Minus	153933-154060
	405780	7248203	Minus	48204-48371
	405783	5738434	Minus	27238-27885
	405784	7417368	Minus	77798-78000
	405829	7109593	Minus	15628-16127
70	405920	6758795	Plus	120621-120971
	405935	6758795	Minus	163112-163652
	405970	8247789	Minus	45795-46295
	406005	8247801	Minus	39912-40220
	406018	6758904	Minus	37795-38168
75	406076	9123123	Plus	89972-90319
	406092	9123919	Plus	251370-251797,252168-252882
	406190	7289992	Minus	22395-22901
	406288	7549620	Plus	111718-112008
	406298	5686278	Minus	30084-30770
80	406333	9213235	Plus	64689-64798
	406364	9256114	Minus	50715-50833
	406378	9256142	Minus	126408-126800
	406413	9256407	Plus	43858-44003,46993-47136
	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880

406603 8272659 Minus 39506-39694

5 TABLE 31A: ABOUT 1884 GENES UP-REGULATED IN IPF COMPARED TO NSIP

Table 31A lists about 1884 genes whose expression levels are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with non-specific interstitial pneumonia (NSIP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" non-specific interstitial pneumonia sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" non-specific interstitial pneumonia level was set to the 90th percentile amongst non-specific interstitial pneumonia samples.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of IPF (idiopathic pulmonary fibrosis) to NSIP (non-specific interstitial pneumonia)

Pkey	ExAccn	Unigene ID	Unigene Title	R1
450478	AW451709	Hs.271200	ESTs	20.2
405654				16.1
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
403637				11.2
431548	AI834273	Hs.9711	novel protein	10.8
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	10.4
439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
403574				10.1
416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.3
441233	AA972965	Hs.135568	ESTs	9.1
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	8.4
432437	W07088	Hs.293685	ESTs	8.3
407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	8.2
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	8.1
403329				8.0
429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	8.0
441519	AA972740	Hs.127092	ESTs	7.9
453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	7.8
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	7.7
416379	N38857	Hs.203933	ESTs	7.7
428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	7.5
407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	7.2
434683	AW298724	Hs.202639	ESTs	7.2
441802	AA968636	Hs.127877	ESTs	6.9
431242	AA987742	Hs.251278	KIAA1201 protein	6.9
442377	AA993807	Hs.167367	ESTs	6.9
420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	6.8
428908	AW303529	Hs.144955	ESTs	6.8
445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.7
457673	AA551569	Hs.272034	hypothetical protein PRO2822	6.7
458771	AW295151	Hs.163612	ESTs	6.6
426800	AA385085		gb:EST98959 Thyroid Homo sapiens cDNA 5'	6.6
440504	AI948966	Hs.130017	ESTs, Weakly similar to JN0908 H+-transp	6.6
415025	AW207091	Hs.72307	ESTs	6.5
438557	AW364104	Hs.143509	hypothetical protein FLJ21924	6.5
416128	AA173632	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	6.4
457242	AA457011		gb:aa90c11.r1 Stratagene fetal retina 93	6.3
423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	6.3
404793				6.2
435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	6.2
415672	N53097	Hs.193579	ESTs	6.2
455488	AA102322		gb:z190f03.r1 Stratagene colon (937204)	6.2
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	6.1
412282	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	6.1
431622	AW979271	Hs.293184	ESTs	6.1
405523				6.0
424693	BE169810	Hs.47557	ESTs	6.0
436397	AA715013	Hs.169835	ESTs	6.0
456476	AA256753		gb:zs22b12.r1 NCI_CGAP_GCB1 Homo sapiens	5.9
434784	AA649051	Hs.164007	ESTs	5.9
422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	5.9
442849	R10099	Hs.269805	ESTs	5.9
451519	AI800600	Hs.209573	ESTs	5.8
412474	AI791451		gb:ni50c09.y5 NCI_CGAP_Ov2 Homo sapiens	5.8
457081	AA916785	Hs.180610	splicing factor proline/glutamine rich (5.8
444827	R09764	Hs.20416	ESTs	5.8
404822				5.7
402430				5.7
457900	AW976692	Hs.291665	ESTs	5.7
400292	AA250737	Hs.72472	ESTs	5.7
410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
440172	AA868584	Hs.126154	ESTs	5.7

5	431374	BE258532	Hs.251871	CTP synthase	5.7
	409816	AW500954		gb:UL-HF-BP0p-air-h-12-0-ULr1 NIH_MGC_5	5.6
	447613	AL041057	Hs.33363	DKFZP434N093 protein	5.6
	417919	AI928203	Hs.86379	ESTs	5.6
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.6
10	439063	AF085922	Hs.113968	ESTs	5.6
	406053				5.5
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
	451830	H18433	Hs.21542	KIAA1035 protein	5.5
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.5
15	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	5.5
	459458	AW270957	Hs.254577	ESTs, Weakly similar to B34087 hypotheti	5.5
	416154	Z46122		gb:HSC0VB031 normalized infant brain cDN	5.5
	404561				5.4
	428895	AA437124	Hs.187247	ESTs	5.4
20	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	5.4
	440925	AW511090	Hs.130419	ESTs	5.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
	448477	BE612572		gb:601452090F1 NIH_MGC_66 Homo sapiens c	5.4
25	454039	AW079064	Hs.245540	ESTs	5.3
	459664				5.3
	401497				5.3
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	5.3
30	456680	AL137758	Hs.116072	Homo sapiens mRNA; cDNA DKFZp434H245 (fr	5.3
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	5.2
	411402	BE297855	Hs.69855	NRAS-related gene	5.2
	404957				5.2
	436445	AA922213	Hs.121735	ESTs	5.2
35	442617	AW340093	Hs.130538	ESTs	5.2
	416045	H15990	Hs.31403	ESTs	5.2
	425178	H16097	Hs.161027	ESTs	5.2
	441918	AI733373	Hs.128119	ESTs	5.2
	455464	AW983901		gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.2
40	420929	AI694143	Hs.296251	programmed cell death 4	5.2
	448844	AI581519	Hs.177164	ESTs	5.2
	430686	NM_001942	Hs.2633	desmoglein 1	5.2
	405229				5.1
	417641	AA205015	Hs.54617	hypothetical protein FLJ20060	5.1
45	434167	AA626334	Hs.116153	ESTs	5.1
	450438	AI696071	Hs.253800	ESTs	5.1
	456394	W28506		gb:48f1 Human retina cDNA randomly prime	5.0
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
	417420	T85150	Hs.268814	ESTs	5.0
50	409545	BE296182	Hs.19002	hypothetical protein MGC4675	5.0
	426750	AA383950		gb:EST97403 Thymus II Homo sapiens cDNA	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
	408959	AW890878	Hs.211610	CUG triplet repeat, RNA-binding protein	4.9
	454482	BE147919		gb:RC3-HT0230-160200-016-a08 HT0230 Homo	4.9
55	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	4.9
	452046	AB018345	Hs.27657	KIAA0802 protein	4.9
	407415	AF073328		gb:Homo sapiens tetracycline transporter-	4.9
	450090	AW448940	Hs.202259	ESTs	4.9
	406333				4.9
60	434188	AI765848	Hs.281680	peroxisomal trans 2-enoyl CoA reductase;	4.8
	403344				4.8
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	4.8
	405455				4.8
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	4.8
65	426097	BE327369	Hs.112238	ESTs	4.8
	427768	T78402	Hs.174880	ESTs	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
	415257	F03016	Hs.27513	ESTs	4.8
	441107	AA917075	Hs.190520	ESTs	4.8
70	419519	AI198719	Hs.176376	ESTs	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
	424188	AW954552	Hs.142634	zinc finger protein	4.8
	456987	AI557290	Hs.173536	ESTs	4.8
75	405303				4.8
	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.8
	451620	AW449888	Hs.257224	ESTs	4.7
	421948	L42583	Hs.334309	keratin 6A	4.7
	424780	U39576	Hs.153058	butyrophilin, subfamily 1, member A1	4.7
80	443271	BE568568	Hs.195704	ESTs	4.7
	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	402230				4.7
	422246	AA461032	Hs.5306	hypothetical protein DKFZp586F1122 simil	4.7
	431508	NM_012481	Hs.182979	ribosomal protein L12	4.7
	415236	R41400		gb:yf94b12.s1 Soares infant brain 1N1B H	4.7
	413101	BE065215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo	4.6
	444774	AW052174	Hs.196030	ESTs	4.6

5	444414	AW293214	Hs.8752	transmembrane protein 4	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	436853	BE328074	Hs.148661	ESTs	4.6
	445334	AI610081	Hs.9475	glucose transporter protein 10	4.6
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	4.6
10	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	404638				4.6
	447617	AI400762	Hs.176675	ESTs	4.6
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	4.6
	442360	AI374621	Hs.29055	ESTs	4.6
15	411738	AW859353		gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
	444157	AI125785	Hs.153351	ESTs	4.5
	401365				4.5
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF I [4.5
	436269	AA707472	Hs.190760	ESTs	4.5
20	459448	AA416773	Hs.275012	EST	4.5
	452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	4.5
	414899	AW975433	Hs.36288	ESTs	4.5
	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	4.5
	444898	AI201548	Hs.308338	ESTs	4.5
25	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.5
	428528	AI004034	Hs.98638	ESTs	4.5
	405605				4.5
	457982	AW856093	Hs.183617	ESTs	4.5
	427731	AA411750	Hs.20943	ESTs	4.4
30	420691	AA829433	Hs.275343	ESTs	4.4
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	4.4
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	4.4
	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
	435747	AI079519	Hs.134398	ESTs	4.4
35	453824	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	4.4
	458865	T05095	Hs.19597	KIAA1694 protein	4.4
	459037	AW439497	Hs.290656	EST	4.4
	403310				4.4
	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
40	427500	AW970017	Hs.293948	ESTs, Weakly similar to S65657 alpha-1C-	4.4
	432020	AJ251509	Hs.272345	phosphodiesterase 11A	4.4
	453043	AW136440	Hs.224277	ESTs	4.4
	456293	AW131715	Hs.311561	ESTs, Weakly similar to CYA7_HUMAN ADENY	4.4
	447879	BE503405	Hs.170437	ESTs, Weakly similar to PRP4_HUMAN SALIV	4.4
45	426646	AA382787	Hs.122713	ESTs	4.4
	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	4.4
	404898				4.4
	435434	AA680387	Hs.187850	ESTs	4.4
	443314	AW771701	Hs.54646	ESTs	4.3
50	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	4.3
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	4.3
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	4.3
	404767				4.3
	445189	AI936450	Hs.147482	ESTs	4.3
55	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	428740	AA433838		gb:zw53e12.r1 Soares_total_fetus_Nb2HF8_	4.3
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H	4.3
	410615	AW772721		gb:hl95c01.x1 NCI_CGAP_Thy8 Homo sapiens	4.3
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.3
60	406073				4.3
	405692				4.3
	436033	H75391	Hs.255748	ESTs	4.3
	410733	D84284	Hs.66052	CD38 antigen (p45)	4.3
	455587	BE007829		gb:QV0-BN0147-280400-213-d03 BN0147 Homo	4.3
65	459084	H01699	Hs.27289	CGI-125 protein	4.3
	401189				4.3
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-heregulin	4.3
	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
70	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	436659	AI217900	Hs.144464	ESTs	4.3
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	4.3
	439481	AF086294	Hs.125844	ESTs	4.3
75	405287				4.3
	405784				4.3
	436461	AW511956	Hs.293261	ESTs	4.3
	437636	AA764781	Hs.291844	ESTs	4.2
	409629	AW449589	Hs.279724	ESTs	4.2
80	412999	BE046255		gb:hn38g10.x2 NCI_CGAP_RDF2 Homo sapiens	4.2
	403281				4.2
	427531	AA405097	Hs.97957	ESTs	4.2
	451882	AI821324	Hs.100445	ESTs	4.2
	418856	AA362858		gb:EST72900 Ovary II Homo sapiens cDNA 5	4.2
	405494				4.2
	456027	BE327387	Hs.13913	KIAA1577 protein	4.2
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	4.2

5	421106	AA877124	Hs.172844	ESTs	4.2
	409076	N57559	Hs.82273	hypothetical protein	4.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	4.2
	411688	AW953440		gb:EST365510 MAGE resequenes, MAGB Homo	4.1
	416614	T83391	Hs.111849	ESTs	4.1
10	454434	AA083558	Hs.261286	ESTs	4.1
	404526	AI912555	Hs.157195	peptide YY, 2 (seminalplasmin)	4.1
	446393	AW014174	Hs.301956	zinc finger protein	4.1
	405302				4.1
	432669	AL043482	Hs.267115	ESTs	4.1
15	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	430484	D82880	Hs.241548	RAS p21 protein activator 2	4.1
	403895				4.1
20	420457	AA482280	Hs.191656	ESTs	4.1
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	458421	AI279978	Hs.22547	ESTs	4.1
	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.1
	411382	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	4.1
25	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	4.1
	430749	AJ242956	Hs.25960	v-myc avian myelocytomatosis viral relat	4.1
	403625				4.1
	401887				4.1
	403667				4.1
30	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	432792	AA448114	Hs.278950	protocadherin beta 1	4.0
	405443				4.0
35	431169	AW971240		gb:EST383329 MAGE resequenes, MAGL Homo	4.0
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens	4.0
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.0
	448324	AI571356	Hs.34174	ESTs, Moderately similar to ALU8_HUMAN A	4.0
	456536	AW135986	Hs.257859	ESTs	4.0
40	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.0
	449327	AI638743	Hs.224672	ESTs	4.0
	426062	N57014	Hs.75874	pregnancy-associated plasma protein A	4.0
45	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	4.0
	434849	AW292765	Hs.8053	ESTs	4.0
	400268				4.0
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	4.0
	445414	AV653692	Hs.146105	ESTs	4.0
50	406470				3.9
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (3.9
	453098	Z25935	Hs.86379	ESTs	3.9
	402867				3.9
	431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
55	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	419091	T85332	Hs.178294	ESTs	3.9
	422591	L07648	Hs.118630	MAX-interacting protein 1	3.9
	426076	AW962714		gb:EST374787 MAGE resequenes, MAGG Homo	3.9
60	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	3.9
	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogen	3.9
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	3.9
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.9
65	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
	455993	BE179085		gb:RC0-HT0613-140300-021-d06 HT0613 Homo	3.9
	420111	AA255662		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	403956	W28077	Hs.79389	nel (chicken)-like 2	3.9
70	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru	3.9
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	3.9
	430140	AW296771	Hs.221999	ESTs	3.8
	457042	AI382130	Hs.97703	ESTs	3.8
	450236	AW162998	Hs.24684	KIAA1376 protein	3.8
75	417706	T90797	Hs.268623	ESTs	3.8
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	413071	BE064032		gb:QV3-BT0296-010300-111-b08 BT0296 Homo	3.8
	437354	AA749215	Hs.291886	ESTs	3.8
	403381				3.8
80	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens	3.8
	459429	AA278779	Hs.335696	EST	3.8
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	3.8
	430757	AI458623		gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	3.8
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	433887	AW204232	Hs.279522	ESTs	3.8
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.8
	404043				3.8

5	431333	AA708488	Hs.120127	Homo sapiens cDNA: FLJ22769 fis, clone K	3.8
	451073	AI758905	Hs.206063	ESTs	3.8
	417663	R07483	Hs.180461	ESTs	3.8
	432363	AA534489		gb:nf76g11.s1 NCL_CGAP_Co3 Homo sapiens	3.8
	436975	AA740723	Hs.212644	ESTs	3.8
10	405959				3.8
	400631	AF173937	Hs.109494	secreted protein of unknown function	3.7
	425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3.7
	446158	AI277603	Hs.145990	ESTs, Weakly similar to I38022 hypotheti	3.7
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.7
15	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.7
	436020	AA778177	Hs.121724	ESTs	3.7
	424989	AA985520	Hs.23575	ESTs	3.7
	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.7
	441416	AI990139	Hs.148609	ESTs	3.7
20	456443	AW967500	Hs.133543	ESTs	3.7
	402112	R58624	Hs.2186	eukaryotic translation elongation factor	3.7
	404453				3.7
	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
	421037	AI684808	Hs.197653	ESTs	3.7
25	427088	AA398085	Hs.142390	ESTs	3.7
	453375	AI990114	Hs.240091	ESTs	3.7
	453530	AW021633		gb:df26c02.y1 Morton Fetal Cochlea Homo	3.7
	406964	M21305		gb:Human alpha satellite and satellite 3	3.7
	432291	AK001108	Hs.274274	hypothetical protein FLJ10246	3.7
30	449623	C00719	Hs.120440	EST	3.7
	419691	W03298	Hs.193521	ESTs	3.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.7
	403271				3.7
	453123	AI953718	Hs.221849	ESTs	3.7
35	400462				3.7
	449804	AI535663	Hs.39379	ESTs	3.7
	443305	AI050693	Hs.133318	ESTs	3.7
	411186	AW821257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.6
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	3.6
40	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	403296				3.6
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.6
	436026	AI349764	Hs.217081	ESTs	3.6
	429864	AA480039	Hs.286	ribosomal protein L4	3.6
45	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	3.6
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.6
	446304	AW104432	Hs.149761	ESTs	3.6
	441216	BE299830	Hs.192908	ESTs	3.6
	421494	AI763322	Hs.152104	ESTs	3.6
50	404476				3.6
	416327	R99822	Hs.36172	ESTs	3.6
	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.6
	417401	AA426026	Hs.187615	ESTs	3.6
	401200				3.6
55	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.6
	426306	AA447310	Hs.164059	Homo sapiens cDNA FLJ13338 fis, clone OV	3.6
	437918	AI761449	Hs.121629	ESTs	3.6
	447917	AL048037	Hs.164588	ESTs, Moderately similar to neuronal thr	3.6
	421328	BE466506	Hs.3981	ESTs	3.6
60	447290	AI476732	Hs.263912	ESTs	3.6
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	403515				3.6
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (fr	3.6
65	435554	AF208502	Hs.185708	early B-cell factor	3.6
	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	3.6
	410500	R09442		gb:ylf26c09.r1 Soares fetal liver spleen	3.6
	439326	W07140	Hs.54721	ESTs	3.6
	426296	R14454	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.6
70	411311	AW836491		gb:PM3-LT0032-281299-002-f02 LT0032 Homo	3.6
	418019	R68911	Hs.176275	ESTs	3.6
	417490	AA203335		gb:zx56g02.r1 Soares_fetal_liver_spleen_	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	416575	W02414	Hs.38383	ESTs	3.5
75	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	418405	AI868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
	450350	T97817	Hs.174880	ESTs	3.5
	451704	AI755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.5
80	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRN	3.5
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	430533	AA480895	Hs.201552	ESTs, Weakly similar to T17288 hypotheti	3.5
	457141	AA521410	Hs.41371	ESTs	3.5
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	3.5
	440737	AI375167	Hs.132221	hypothetical protein FLJ12401	3.5
	452728	AI915676	Hs.239708	ESTs	3.5
	423266	AA323875	Hs.193574	ESTs	3.5

5	413543	AA130228	Hs.324611	ESTs, Moderately similar to ALU8_HUMAN A	3.5
	454447	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	3.5
	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	415549	F11942		gb:HSC33F061 normalized infant brain cDN	3.5
10	420910	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (f	3.5
	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	453211	W84829		gb:zh53f04.r1 Soares_fetal_liver_spleen_	3.5
	418717	AI334430	Hs.86984	ESTs	3.5
	400641				3.5
15	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	3.5
	418007	M13509	Hs.83169	matrx metalloproteinase 1 (interstitial	3.5
	440364	AA910460	Hs.128626	ESTs	3.5
	458340	AI457102	Hs.6986	Human glucose transporter pseudogene	3.5
	412281	AI810054	Hs.14119	ESTs	3.5
20	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	3.5
	416616	H68270		gb:yr81h09.r1 Soares fetal liver spleen	3.5
	444338	AI937026	Hs.146642	ESTs	3.4
	436946	AW137748	Hs.125956	ESTs	3.4
	413632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fis, clone HE	3.4
25	403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	3.4
	422093	AF151852	Hs.111449	CGI-94 protein	3.4
	428816	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	3.4
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
	405970				3.4
30	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.4
	416100	H18700	Hs.268799	ESTs	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
	440388	AI693520	Hs.223000	ESTs	3.4
35	421072	AI215069	Hs.89113	ESTs	3.4
	424578	AK001973	Hs.150890	hypothetical protein	3.4
	436331	AI239495	Hs.120189	ESTs	3.4
	444063	AI122614		gb:qa96b05.x1 Soares_fetal_heart_NbHH19W	3.4
	444453	AW379394	Hs.145126	ESTs	3.4
40	404196				3.4
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	3.4
	409555	AW410788	Hs.256185	ESTs	3.4
	417659	T99898		gb:ye68g01.r1 Soares fetal liver spleen	3.4
	416057	AI927382	Hs.29857	ESTs	3.4
45	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	3.4
	447738	AI871000	Hs.161330	ESTs	3.4
	430664	AW969834	Hs.303303	ESTs	3.4
	411377	AW841462		gb:RC6-CN0014-080300-012-B09 CN0014 Homo	3.4
	415769	H94186	Hs.5912	F-box only protein 7	3.4
50	429382	AI791249	Hs.278054	ESTs, Weakly similar to I38022 hypothe	3.4
	431474	AL133990	Hs.190642	ESTs	3.4
	456908	AI953671	Hs.220994	hypothetical protein FLJ14129	3.4
	442826	AI018777	Hs.131241	ESTs	3.4
	400608				3.4
55	436111	AI803082	Hs.157212	ESTs	3.4
	452807	AA028933	Hs.162434	ESTs	3.4
	436577	W84774	Hs.17643	ESTs	3.4
	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	3.4
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	3.4
60	423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	3.4
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.4
	409623	AW449185		gb:UI-H-BI3-akg-e-05-0-UI.s1 NCL_CGAP_Su	3.4
	416182	NM_004354	Hs.79069	cyclin G2	3.4
	420854	AW296927		gb:UI-H-BW0-ajc-c-07-0-UI.s1 NCL_CGAP_Su	3.4
65	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
	432404	AA535246	Hs.50852	ESTs	3.4
	458695	AV660159	Hs.282284	ESTs, Weakly similar to I38022 hypothe	3.4
	440727	AI073991	Hs.134268	ESTs, Weakly similar to Z109260A B cell	3.3
	428766	AA477989	Hs.98800	ESTs	3.3
70	439567	AI056618	Hs.134314	ESTs	3.3
	456231	H73183	Hs.129885	ESTs, Weakly similar to 2004399A chromos	3.3
	454318	AW367764	Hs.7857	erythrocyte membrane protein band 4.1-li	3.3
	411966	AA099113	Hs.118609	ESTs	3.3
	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	3.3
75	437037	T63804		gb:yc21e09.r1 Stratagene lung (937210) H	3.3
	407664	AW063476	Hs.279080	ESTs	3.3
	405780				3.3
	426567	AA381579	Hs.182962	ESTs	3.3
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	3.3
80	403356				3.3
	404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	3.3
	413581	BE150618		gb:RC3-HT0272-110100-013-c06 HT0272 Homo	3.3
	429875	AI091815		gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi	3.3
	433785	BE044593	Hs.112704	ESTs	3.3
	437876	AA770151	Hs.126424	ESTs	3.3
	444870	AI200621	Hs.148504	ESTs	3.3
	453324	W26592	Hs.232089	ESTs	3.3

	437963	BE396279		gb:601309785F1 NIH_MGC_44 Homo sapiens c	3.3
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	3.3
	408813	AI580090	Hs.48295	RNA helicase family	3.3
5	426692	AK001751	Hs.171835	hypothetical protein FLJ10889	3.3
	407456	AJ237589		gb:Homo sapiens mRNA for T-box transcript	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	438456	AA913381	Hs.190513	ESTs	3.3
10	453242	T98327	Hs.18343	ESTs	3.3
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.3
	412040	D86519	Hs.73086	neuropeptide Y receptor Y6 (pseudogene)	3.3
	435070	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	3.3
	444443	AI149286	Hs.55099	rab6 GTPase activating protein (GAP and	3.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	3.3
15	454145	AA046872	Hs.62798	ESTs	3.3
	405264				3.3
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	3.3
	416816	T71168	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	3.3
20	435325	AI038388	Hs.119309	ESTs	3.3
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	428356	AL046991	Hs.10338	ESTs	3.3
	429216	AI369472	Hs.65407	ESTs	3.3
	429106	AA446612		gb:zw85g07.s1 Soares_total_fetus_Nb2HF8_	3.3
25	405720				3.3
	400889				3.3
	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	422094	AF129535	Hs.272027	F-box only protein 5	3.3
	425374	AI904013		gb:MR-BT041-220199-104 BT041 Homo sapien	3.3
30	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
	427374	AI150033	Hs.143686	ESTs	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
	457604	AI004397	Hs.334552	Homo sapiens cDNA FLJ14930 fis, clone PL	3.3
35	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.3
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	3.3
	458885	AA411303	Hs.30022	ESTs, Weakly similar to NAH6_HUMAN SODIU	3.3
	429608	U49250	Hs.210862	T-box, brain, 1	3.2
	437454	AL390159	Hs.269812	Homo sapiens mRNA; cDNA DKFZp761M0415 (f	3.2
40	430503	AA533574	Hs.152274	ESTs	3.2
	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	3.2
	421698	T89677	Hs.324323	ESTs	3.2
	412321	AW936913		gb:RC1-DT0029-030200-012-f08 DT0029 Homo	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
45	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	441705	AI087052	Hs.55993	ESTs	3.2
	403619				3.2
	435608	AW183971	Hs.250896	ESTs	3.2
	426701	AI968103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.2
50	401132				3.2
	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
	409425	U40462	Hs.54452	zinc finger protein, subfamily 1A, 1 (lk	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	443603	BE502601	Hs.134289	ESTs, Weakly similar to KIAA1063 protein	3.2
55	419936	AI792788		gb:cl91d05.y5 NCL_CGAP_Kid5 Homo sapiens	3.2
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	3.2
	406592				3.2
	446530	AV658909	Hs.282642	ESTs	3.2
	454466	AA984138	Hs.155101	ATP synthase, H+ transporting, mitochond	3.2
60	401449				3.2
	431196	AW974436	Hs.154929	ESTs	3.2
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	459459	AA460445		gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_	3.2
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.2
65	427335	AA448542	Hs.251677	G antigen 7B	3.2
	455236	AW875972		gb:CM3-PT0014-071299-051-b05 PT0014 Homo	3.2
	425156	AA351364		gb:EST59099 Infant brain Homo sapiens cD	3.2
	404588				3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
70	444910	AI201849		gb:qs76g04.x1 NCL_CGAP_Pr28 Homo sapiens	3.2
	426660	NM_002719	Hs.171734	protein phosphatase 2, regulatory subuni	3.2
	438315	R56795	Hs.82419	ESTs	3.2
	425523	AB007948	Hs.158244	KIAA0479 protein	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
	425636	AK001243	Hs.158370	hypothetical protein FLJ10381	3.2
75	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	447375	AI376660	Hs.257822	ESTs	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
80	410536	N39533		gb:yv27d04.s1 Soares fetal liver spleen	3.2
	448495	AW136516	Hs.208515	ESTs	3.2
	405634				3.2
	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoadenylate	3.2

	421581	U89331	Hs.105932	short stature homeobox	3.1
	440633	AI140686	Hs.263320	ESTs	3.1
	453264	AA034137	Hs.271955	ESTs	3.1
5	411656	AW855576		gb:CM4-CT0278-221099-027-d01 CT0278 Homo	3.1
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	3.1
	426591	AA431127	Hs.98685	ESTs	3.1
	446966	C01448	Hs.300511	ESTs	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
10	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.1
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.1
	423657	AL045128	Hs.1691	glucan (1,4-alpha-), branching enzyme 1	3.1
	400816				3.1
	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
15	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
	400315	U46120	Hs.193392	Human expressed unknown mRNA	3.1
	411965	BE467339	Hs.280115	ESTs	3.1
	416316	H58721	Hs.271628	ESTs	3.1
	400613				3.1
20	414819	BE177320	Hs.156148	hypothetical protein FLJ13231	3.1
	434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.1
	418693	AI750878	Hs.87409	thrombospondin 1	3.1
	416258	N45661	Hs.90011	adenylosuccinate synthase	3.1
	405093				3.1
25	415273	Z39840	Hs.22229	ESTs	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	422654	AA314316	Hs.163725	ESTs	3.1
	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	3.1
30	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.1
	402790				3.1
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	3.1
	447524	D80449	Hs.45177	ESTs	3.1
	448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
35	415979	H16427	Hs.271501	ESTs, Weakly similar to I54374 gene NF2	3.1
	434479	AI138213	Hs.162035	olfactory receptor, family 52, subfamily	3.1
	426724	AA383623	Hs.293616	ESTs	3.1
	418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	3.1
	405608				3.1
40	406506				3.1
	421216	AV649282	Hs.102664	vesicle-associated membrane protein 4	3.1
	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti	3.1
	404288				3.1
	429878	AA460188	Hs.127263	ESTs	3.1
45	439834	AI754576	Hs.124523	ESTs	3.1
	454564	AW807573		gb:MR1-ST0088-021299-004-g01 ST0088 Homo	3.1
	450491	BE045604	Hs.202301	ESTs	3.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	3.1
	400579				3.1
50	402953				3.1
	404285				3.1
	426890	AA393167	Hs.41294	ESTs	3.1
	457770	BE065030	Hs.124179	ESTs	3.1
	435477	BE218708	Hs.117270	hypothetical protein FLJ14345	3.1
55	436391	AJ227892	Hs.146274	ESTs	3.1
	456083	U46922	Hs.77252	fragile histidine triad gene	3.1
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.1
	430101	AF110002	Hs.233363	guanylate cyclase activator 1C	3.1
	449238	AA428229	Hs.331561	muscle-specific RING-finger protein 3	3.1
60	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	3.1
	456323	AW752389	Hs.87296	Homo sapiens cDNA FLJ20269 fis, clone HE	3.1
	429828	AB019494	Hs.225767	IDN3 protein	3.1
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	3.1
	452762	AW501435	Hs.278582	v-akt murine thymoma viral oncogene homo	3.1
	401344				3.1
65	455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	3.1
	455280	AW886156		gb:RC5-OT0078-150300-021-E08 OT0078 Homo	3.1
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.1
	423600	AI633559	Hs.310359	ESTs	3.1
70	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	3.0
	407257	AB006834		gb:Homo sapiens mRNA for HRV Fab N6-VH,	3.0
	457041	AA399018	Hs.250835	ESTs	3.0
	421482	AL135462	Hs.104715	inversin	3.0
	459062	AA059246	Hs.110293	ESTs	3.0
75	436475	R58806	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
	411622	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFp564B176 (fr	3.0
	417489	AW953341	Hs.22573	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
	409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo	3.0
80	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	3.0
	443741	AW451759	Hs.145420	ESTs	3.0
	405090				3.0
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
	445409	AI949081	Hs.147862	ESTs	3.0

	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.0
	406364				3.0
5	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	3.0
	448405	AW207634	Hs.170849	ESTs	3.0
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.0
10	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	3.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.0
	426424	BE081745	Hs.272188	Homo sapiens cDNA FLJ12090 fis, clone HE	3.0
	419505	AA243660	Hs.143061	ESTs	3.0
	403743				3.0
15	415452	F09134	Hs.12839	ESTs	3.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	400227				3.0
20	436219	AK001695	Hs.146589	hypothetical protein FLJ10701	3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439693	AI741816	Hs.125897	ESTs	3.0
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.0
	403513				3.0
25	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.0
	440122	AI733011	Hs.127678	ESTs	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	3.0
	448130	AW271635	Hs.170717	ESTs	3.0
30	420288	AW071225	Hs.245556	ESTs	3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	3.0
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
	404513				3.0
35	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	3.0
	407762	AW235638	Hs.29475	ESTs	3.0
	403396				3.0
	436938	AW139680	Hs.161393	ESTs	3.0
40	458090	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	3.0
	400706				2.9
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.9
	444600	R41398	Hs.6996	ESTs	2.9
	403786				2.9
45	430187	AI799909	Hs.158989	ESTs	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.9
	457503	AW970244	Hs.162188	ESTs	2.9
	446251	AW867156	Hs.282589	ESTs, Weakly similar to I38022 hypotheti	2.9
	406327				2.9
50	434671	R34758		gb:yg61g02.r1 Soares infant brain 1NIB H	2.9
	430175	AA468724		gb:ne09a06.s1 NCI_CGAP_Co3 Homo sapiens	2.9
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	2.9
	449459	BE546846	Hs.195048	ESTs	2.9
55	435934	R19382	Hs.117869	ESTs	2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	414514	BE327365	Hs.280187	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
60	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.9
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	2.9
	456186	W26642		gb:34b8 Human retina cDNA randomly prime	2.9
	412222	AA528283	Hs.292737	ESTs	2.9
65	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.9
	435579	AI332373	Hs.156924	ESTs	2.9
	417027	AA192306	Hs.23926	triadin	2.9
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.9
70	445909	BE262656	Hs.32603	hypothetical protein MGC3279 similar to	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Brn52 Homo sapien	2.9
	403341				2.9
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
75	453830	AA534296	Hs.20953	ESTs	2.9
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.9
	407676	AW064111	Hs.279823	ESTs	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
80	457049	AW631495	Hs.27135	B-cell receptor-associated protein BAP29	2.9
	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	2.9
	456189	H91010	Hs.44940	ESTs	2.9
	441874	AA970389	Hs.128055	ESTs	2.9
	416483	H58311	Hs.165077	ESTs	2.9

	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
	446447	AI300402	Hs.202250	ESTs	2.9
	439953	AA918129	Hs.124638	ESTs	2.9
5	400643				2.9
	436594	AI419982	Hs.156189	ESTs	2.9
	438402	D16902	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.9
	451353	N21043	Hs.42932	ESTs	2.9
	419791	AI579909	Hs.105104	ESTs	2.9
10	415628	F13080		gb:HSC3ID041 normalized infant brain cDN	2.9
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	454747	AW818535		gb:RC1-ST0278-140300-016-f05 ST0278 Homo	2.9
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.9
	457178	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	2.9
15	401526				2.9
	408751	N91553	Hs.258343	ESTs	2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
20	444125	AI124882	Hs.118121	ESTs	2.9
	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.9
	421847	NM_014717	Hs.108884	KIAA0390 gene product	2.8
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.8
	422225	BE245652	Hs.118281	zinc finger protein 266	2.8
25	403011				2.8
	405170				2.8
	435878	R08330	Hs.20152	ESTs	2.8
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	2.8
	400394	AF040257	Hs.283818	Homo sapiens TNF receptor homolog mRNA,	2.8
30	411244	AW833768		gb:QV4-TT0008-130100-077-e06 TT0008 Homo	2.8
	441817	AW969706	Hs.293332	ESTs	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.8
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.8
35	402131				2.8
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	2.8
	438160	AA779332	Hs.122671	ESTs	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
	417877	AI025829	Hs.86320	ESTs	2.8
40	439235	N45513	Hs.46608	ESTs	2.8
	451257	AA016255	Hs.31856	ESTs, Weakly similar to KIAA1453 protein	2.8
	437113	AA744693		gb:ny26c10.s1 NCL_CGAP_GCB1 Homo sapiens	2.8
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.8
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
45	410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.8
	417827	T79366	Hs.108258	actin binding protein; macrophin (microf	2.8
	420206	M91463	Hs.95958	solute carrier family 2 (facilitated glu	2.8
	449676	AW380579	Hs.209657	ESTs	2.8
50	454778	AW820199		gb:QV2-ST0296-190100-029-a07 ST0296 Homo	2.8
	451203	AW070604	Hs.46517	ESTs	2.8
	450180	AW449644	Hs.257182	ESTs	2.8
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.8
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
55	450003	AA777809	Hs.191995	ESTs	2.8
	401602				2.8
	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.8
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.8
	415652	T79213	Hs.272073	ESTs	2.8
60	404076				2.8
	409416	AW388359	Hs.10667	ESTs	2.8
	420814	AA721156	Hs.190440	ESTs	2.8
	426960	AA393713		gb:zt71h04.r1 Soares_testis_NHT Homo sap	2.8
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.8
65	448597	BE613250	Hs.98265	KIAA1877 protein	2.8
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	2.8
	433077	AA314262	Hs.301917	YDD19 protein	2.8
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	447410	AI470235	Hs.172698	EST	2.8
70	414652	AI620599	Hs.72068	ESTs	2.8
	430454	AW469011	Hs.105635	ESTs	2.8
	412417	AA102268	Hs.158622	ESTs	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430660	R11884	Hs.100826	ESTs	2.8
75	401098				2.8
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	2.8
	403549				2.8
	414394	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.8
80	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	2.8
	433513	AI566356	Hs.171437	ESTs	2.8
	446677	AI800311	Hs.156291	ESTs	2.8
	457756	AA126136	Hs.38125	interferon-induced protein 75, 52kD	2.8
	450895	N66727	Hs.10957	ESTs	2.8
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.8

	449358	AA001229	Hs.131436	ESTs	2.8
	422816	AA323586	Hs.93235	ESTs	2.8
	420756	AA411800	Hs.189900	ESTs	2.8
5	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
	451206	H86228	Hs.271780	ESTs, Weakly similar to I38022 hypothe	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
10	458023	AW978161	Hs.268555	5'-3' exoribonuclease 2	2.8
	422260	AA315993	Hs.105484	regenerating gene type IV	2.8
	429638	AI916662	Hs.211577	kineclin 1 (kinesin receptor)	2.8
	408936	AL138043	Hs.293549	ESTs	2.8
	411762	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	2.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
15	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	406992	S82472		gb:beta-pol=DNA polymerase beta (exon a	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	445611	AW418497	Hs.145583	ESTs	2.7
20	445747	AI820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	445017	AI205493	Hs.176860	ESTs	2.7
	411726	AW858612		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	2.7
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	2.7
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
25	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
	427134	AA398409	Hs.173561	EST	2.7
	435689	AA694284		gb:zi35c02.s1 Soares_fetal_liver_spleen_	2.7
	429282	N27596	Hs.21342	ESTs	2.7
	435731	AA699581	Hs.186811	ESTs	2.7
30	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
	421274	BE160327	Hs.104572	ESTs	2.7
	403776				2.7
	409526	BE298751	Hs.55014	hypothetical protein FLJ10206	2.7
	410201	AA126129		gb:zm78c07.r1 Stratagene neuroepithelium	2.7
35	427839	AA608823	Hs.98244	ESTs	2.7
	447884	H29505		gb:ym60d10.r1 Soares infant brain 1NIB H	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	422988	AW673847	Hs.97321	ESTs	2.7
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.7
40	434890	AF161345	Hs.283930	Homo sapiens HSPC082 mRNA, partial cds	2.7
	412400	AW948066		gb:RC0-MT0012-290300-031-h10 MT0012 Homo	2.7
	413998	AW103807	Hs.243933	ESTs	2.7
	403677				2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
45	430698	AA492071		gb:ne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	2.7
	432591	AA643238	Hs.146144	ESTs	2.7
	446800	AI341635	Hs.156486	ESTs	2.7
	454938	AW846134		gb:QV0-CT0179-091199-049-d02 CT0179 Homo	2.7
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
50	445233	AV653034	Hs.297559	ESTs	2.7
	448756	AI739241	Hs.171480	ESTs	2.7
	418379	AA218940	Hs.137516	fidgetin-like 1	2.7
	435068	H16262	Hs.31415	ESTs	2.7
	406092				2.7
55	422036	AA302647	Hs.271891	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.7
	441541	AA938663	Hs.199828	ESTs	2.7
	451395	AI082419	Hs.114761	ESTs	2.7
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7
60	423949	AI014546	Hs.130912	ESTs	2.7
	435420	AI928513	Hs.59203	ESTs	2.7
	439418	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	2.7
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	2.7
	447453	AW608645	Hs.18800	hypothetical protein FLJ20281	2.7
65	454767	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	2.7
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	2.7
	402429				2.7
	403760				2.7
	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
70	435448	H17132	Hs.27085	ESTs	2.7
	445706	AA305520	Hs.108812	hypothetical protein FLJ22004	2.7
	422171	U50529	Hs.112434	Novel human gene mapping to chromosome 13	2.7
	459023	AW968226	Hs.60798	ESTs	2.7
	443246	T75157	Hs.337603	ESTs, Weakly similar to T08680 hypothe	2.7
	404569				2.7
75	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	422897	AA679784	Hs.4290	ESTs	2.7
	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.7
	449880	AI673006	Hs.231948	ESTs	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
80	415268	R53935	Hs.287827	ESTs, Highly similar to MDR3_HUMAN MULTI	2.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.7
	452512	AW363486	Hs.337635	ESTs	2.7
	440728	AW086077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	2.7

	419481	AI879195	Hs.90606	15 kDa selenoprotein	2.7
	454352	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo	2.7
	422831	R02504	Hs.332943	ESTs	2.7
5	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.7
	426872	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapie	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	2.7
	446002	AI346468	Hs.145789	ESTs	2.7
10	454716	AW850684		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.7
	406664	L34041	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	2.7
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	2.7
	408691	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	2.7
	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	2.7
15	439451	AF086270	Hs.278554	heterochromatin-like protein 1	2.7
	445225	AI216555	Hs.202398	ESTs	2.7
	427175	H06924	Hs.23782	hypothetical protein FLJ12847	2.7
	411816	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.7
	438135	AI253025	Hs.190426	ESTs	2.7
20	405981				2.7
	406005				2.7
	430762	AI343652	Hs.105667	ESTs	2.7
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.7
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.7
25	434684	AA737282	Hs.190911	ESTs	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
	400844				2.6
	415725	BE219771	Hs.237146	hypothetical protein FLJ12752	2.6
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.6
30	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	430052	AF102850	Hs.227933	Alg5, S. cerevisiae, homolog of	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	417252	AA195014	Hs.85971	ESTs	2.6
35	427167	AI239607	Hs.99196	hypothetical protein MGC11324	2.6
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.6
40	442240	AI791883	Hs.292719	ESTs	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
	410238	N94320	Hs.144225	ESTs	2.6
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	2.6
	440801	AA906366	Hs.190535	ESTs	2.6
45	440274	R24595	Hs.7122	scrapie responsive protein 1	2.6
	411597	AW852925		gb:PM0-CT0248-131099-001-f10 CT0248 Homo	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
	425176	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcr	2.6
50	425492	AL021918	Hs.158174	zinc finger protein 184 (Krueppel-like)	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	426098	NM_014906	Hs.166351	KIAA1072 protein	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
55	445550	AI242754	Hs.137306	ESTs	2.6
	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.6
	436407	T88803	Hs.271507	ESTs, Weakly similar to TIM_HUMAN PROBAB	2.6
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	2.6
60	418282	AA215535	Hs.98133	ESTs	2.6
	442757	AI739528	Hs.28345	ESTs	2.6
	413470	N20934		gb:yx54c11.s1 Soares melanocyte 2NbHM Ho	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	441209	AA922939	Hs.135742	ESTs	2.6
65	458679	AW975460	Hs.143563	ESTs	2.6
	442279	AW867006	Hs.159970	ESTs	2.6
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.6
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	2.6
	404845				2.6
70	411693	AW857271		gb:CM0-CT0307-210100-158-g09 CT0307 Homo	2.6
	438298	H23542	Hs.181788	ESTs	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
	457630	AI680803	Hs.112627	ESTs	2.6
75	424015	N95696	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	2.6
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.6
	413174	AA723564	Hs.191343	ESTs	2.6
	438875	AA827640	Hs.189059	ESTs	2.6
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	2.6
80	423257	AW161039	Hs.125878	synapsin III	2.6
	431086	AI829692	Hs.211561	ESTs	2.6
	409337	H71289	Hs.220535	ESTs	2.6
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	2.6
	410004	AI298027	Hs.5057	carboxypeptidase D	2.6

	455935	BE158687	gb:CM0-HT0395-280100-169-b09 HT0395 Homo	2.6
	403273			2.6
	445955	AA332209	Hs.158196 transcriptional adaptor 3 (ADA3, yeast h	2.6
5	425626	AI537536	Hs.173519 ESTs	2.6
	451531	AA018311	Hs.114762 ESTs	2.6
	428085	AA421081	Hs.12388 ESTs	2.6
	429761	AI276780	Hs.135173 ESTs	2.6
	437958	BE139550	Hs.121668 ESTs, Moderately similar to PC4259 ferri	2.6
10	442666	W74633	Hs.303720 ESTs	2.6
	413088	BE064962	gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	419107	AW085152	Hs.292987 ESTs	2.6
	435766	R11673	Hs.186498 ESTs	2.6
	452879	AW905328	Hs.180842 ribosomal protein L13	2.6
15	440400	AA994364	Hs.125594 ESTs, Weakly similar to T25472 hypotheti	2.6
	440460	H92571	Hs.234478 Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	424146	AA705092	Hs.202368 ESTs	2.6
	439950	AW937417	Hs.293561 ESTs	2.6
	410366	AI267589	Hs.302689 hypothetical protein	2.6
20	417485	AA203304	Hs.32826 CGI-130 protein	2.6
	412566	AW962574	gb:EST374647 MAGE resequences, MAGG Homo	2.6
	416498	U33632	Hs.79351 potassium channel, subfamily K, member 1	2.6
	440397	AA884448	Hs.157239 ESTs	2.6
	451236	AI767406	Hs.207026 ESTs, Weakly similar to B56205 transcrip	2.6
25	411819	AW947884	gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.6
	430357	AW976789	Hs.165607 ESTs	2.6
	432869	AW974094	gb:EST386197 MAGE resequences, MAGM Homo	2.6
	427506	AK000134	Hs.179100 hypothetical protein FLJ20127	2.6
	401614			2.6
30	404531	Z25884	Hs.121483 chloride channel 1, skeletal muscle (Th	2.6
	426698	AA394104	Hs.97489 ESTs	2.6
	440479	AA886461	Hs.208161 ESTs	2.6
	443160	AI467915	Hs.36053 ESTs	2.6
	419323	AI092379	Hs.135275 ESTs	2.5
35	442813	AI018435	Hs.270970 ESTs	2.5
	436196	AK001084	Hs.333498 Homo sapiens cDNA FLJ10222 fis, clone HE	2.5
	433561	BE540937	Hs.20104 hypothetical protein FLJ00052	2.5
	434059	AA649162	Hs.236456 ESTs	2.5
	454836	AW833711	gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
40	458589	AV654623	Hs.288141 hypothetical protein MGC3156	2.5
	459716			2.5
	436340	R42246	Hs.21606 ESTs	2.5
	428020	L19058	Hs.181581 glutamate receptor, ionotropic, kainate	2.5
	416951	AA190926	Hs.190785 ESTs, Moderately similar to S65657 alpha	2.5
	401078			2.5
45	410644	AW902125	gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.5
	411660	AW855718	gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
	425201	AA352111	gb:EST60061 Activated T-cells XX Homo sa	2.5
	455252	AW876627	gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
50	439096	AA830185	Hs.269680 ESTs	2.5
	442627	AI027990	Hs.132303 ESTs	2.5
	457799	AF220188	Hs.236510 uncharacterized hypothalamus protein HTM	2.5
	428799	AI478619	Hs.104677 ESTs	2.5
	450402	BE218027	Hs.89969 ESTs	2.5
55	411156	AW819939	Hs.273629 ESTs	2.5
	431673	AW971302	Hs.293233 ESTs	2.5
	415706	BE182587	Hs.57485 ESTs	2.5
	412882	BE006919	Hs.134106 ESTs	2.5
	441300	R35063	Hs.181536 ESTs	2.5
60	413257	BE075035	gb:PM3-BT0584-260300-002-g05 BT0584 Homo	2.5
	434662	AA641957	gb:ns18d08.r1 NCI_CGAP_GCB1 Homo sapiens	2.5
	455255	AW877139	gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.5
	417137	U46265	Hs.81281 mitochondrial ribosomal protein S21	2.5
	417909	R35614	gb:yg66e08.r1 Soares infant brain 1N1B H	2.5
65	458043	AW979009	Hs.326108 ESTs	2.5
	417006	AW673606	Hs.80758 aspartyl-tRNA synthetase	2.5
	442006	AW975183	Hs.292663 ESTs, Weakly similar to S72482 hypotheti	2.5
	455756	BE079307	gb:RC1-BT0623-120200-011-g09 BT0623 Homo	2.5
	454032	W31790	Hs.194293 ESTs, Weakly similar to I54374 gene NF2	2.5
70	444963	AI916973	Hs.213603 ESTs	2.5
	443526	AW792804	Hs.134002 ESTs	2.5
	454532	AA344685	Hs.58831 regulator of Fas-induced apoptosis	2.5
	428832	AA578229	Hs.324239 ESTs, Moderately similar to ZN91_HUMAN Z	2.5
	442003	AW297497	Hs.201891 ESTs	2.5
75	452768	AW069459	Hs.61539 ESTs	2.5
	411355	AW838479	Hs.22692 ESTs	2.5
	458890	AW865523	gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.5
	400074			2.5
	405241			2.5
80	413096	BE065209	gb:RC1-BT0314-310300-015-b12 BT0314 Homo	2.5
	414349	BE512968	gb:601172296F1 NIH_MGC_15 Homo sapiens c	2.5
	422884	AW860975	Hs.13256 ESTs	2.5
	429515	AL031228	Hs.204370 DNA segment on chromosome 6 (unique, pse	2.5
	431925	AK000890	gb:Homo sapiens cDNA FLJ10028 fis, clone	2.5

	442653	BE269247		gb:601185486F1 NIH_MGC_8 Homo sapiens cD	2.5
	401882				2.5
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hig	2.5
	405336				2.5
5	439492	AF086310	Hs.103159	ESTs	2.5
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.5
	436359	Z83806		gb:H.sapiens mRNA for axonemal dynein he	2.5
	429322	D86984	Hs.199243	KIAA0231 protein	2.5
10	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	2.5
	437107	AA745598	Hs.291840	ESTs, Weakly similar to I78885 serine/th	2.5
	441953	H11695	Hs.322901	disrupter of silencing 10	2.5
	442777	AW341541	Hs.271153	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
15	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
	457824	R84938		gb:yf65f04.r1 Soares retina N2b4HR Homo	2.5
	428550	AW297880	Hs.98661	ESTs	2.5
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.5
	456359	AI967991	Hs.93574	homeo box D3	2.5
20	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.5
	452528	AA742457	Hs.291479	ESTs	2.5
	408444	AW661839	Hs.253204	ESTs	2.5
	440327	R12581	Hs.191146	ESTs	2.5
	410406	AI969703	Hs.1466	glycerol kinase	2.5
25	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.5
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	2.5
	435427	AA682573	Hs.188982	ESTs, Weakly similar to organic anion tr	2.5
	427791	AA412446	Hs.98138	ESTs	2.5
	403509	AF231919	Hs.18759	KIAA0539 gene product	2.5
30	436590	AI393115	Hs.127655	ESTs	2.5
	455556	AW995423		gb:QV0-BN0042-010400-183-g08 BN0042 Homo	2.5
	405869				2.5
	408274	R17315		gb:yg12g11.r1 Soares infant brain 1NIB H	2.5
	448015	AI458065	Hs.23196	ESTs	2.5
35	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
	436154	AA764950	Hs.119898	ESTs	2.5
	406377				2.5
	437030	AA742577	Hs.303781	EST	2.5
	420815	AA280684	Hs.270584	ESTs	2.5
40	418421	R58620	Hs.85050	phospholamban	2.5
	423638	AI003521	Hs.130310	Homo sapiens mRNA for cyclin B3 isoform	2.5
	415425	F08365		gb:HSCZSA121 normalized infant brain cDN	2.5
	404577				2.5
	403568				2.5
45	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.5
	449899	AI610700	Hs.103280	ESTs	2.5
	451078	AI927694	Hs.204470	ESTs	2.5
	453343	AA905353	Hs.121622	ESTs	2.5
	428728	NM_016625	Hs.191381	hypothetical protein	2.5
50	409642	AW450809	Hs.257347	ESTs	2.5
	426235	AI631964	Hs.34447	ESTs	2.5
	452043	H86231		gb:y03f02.r1 Soares retina N2b5HR Homo	2.5
	401992				2.5
55	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	2.5
	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	449311	AI657014		gb:tt49a12.x1 NCL_CGAP_GC6 Homo sapiens	2.5
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
60	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.4
	421583	AA293333		gb:ztl53c09.r1 Soares ovary tumor NbHOT H	2.4
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.4
	454437	AI248173	Hs.191460	hypothetical protein MGC12936	2.4
	419187	AA234852	Hs.44693	ESTs	2.4
65	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypot	2.4
	405547				2.4
	454086	AW885909	Hs.6975	PRO1073 protein	2.4
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	2.4
	416277	W78765	Hs.180145	HSPC030 protein	2.4
70	420976	AI924940	Hs.108082	ESTs, Weakly similar to T31636 hypotheti	2.4
	406468				2.4
	408617	R61736	Hs.124128	ESTs	2.4
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	2.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
75	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypotheti	2.4
	455328	AW896438		gb:PM1-NN0047-040400-001-d09 NN0047 Homo	2.4
	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	2.4
	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.4
	419511	AA429750	Hs.75113	general transcription factor IIIA	2.4
80	437980	R50393	Hs.278436	KIAA1474 protein	2.4
	439999	AA115811	Hs.6838	ras homolog gene family, member E	2.4
	403501				2.4
	446845	AI343645	Hs.156108	ESTs	2.4
	401775				2.4

	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411836	AW901879	Hs.314453	ESTs	2.4
	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo	2.4
5	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypotheti	2.4
	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	428945	AW192803	Hs.98974	ESTs, Weakly similar to S65824 reverse t	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
10	435256	AF193766	Hs.13872	cytokine-like protein C17	2.4
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.4
	458239	BE439877	Hs.283389	ESTs	2.4
	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	2.4
	441262	AI809130	Hs.176906	ESTs	2.4
	402076				2.4
15	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.4
	400587				2.4
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	2.4
	411203	AW872430	Hs.273743	ESTs	2.4
20	447849	AI538147	Hs.164277	ESTs	2.4
	454201	AB023191	Hs.44131	KIAA0974 protein	2.4
	424131	AA335714	Hs.199665	ESTs	2.4
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	2.4
	440385	AA884283	Hs.192136	ESTs	2.4
25	417976	BE565892	Hs.83077	interleukin 18 (interferon-gamma-inducin	2.4
	447179	AW015633	Hs.157299	ESTs	2.4
	412977	AA125910	Hs.191461	ESTs	2.4
	436958	AA740322	Hs.293539	Homo sapiens mRNA for KIAA1758 protein,	2.4
	401361				2.4
30	403891				2.4
	408419	AW250092	Hs.305953	zinc finger protein 83 (HPF1)	2.4
	417002	T79613	Hs.14613	ESTs	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	458570	AW971698	Hs.12627	TJ6 protein	2.4
35	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	459344	AW499533	Hs.257976	ESTs	2.4
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.4
	412114	AW893891	Hs.240833	ESTs, Weakly similar to I38022 hypotheti	2.4
	423296	AW957193	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	2.4
40	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	2.4
	428268	AA424957	Hs.294132	ESTs	2.4
	450947	AI745400	Hs.204662	ESTs	2.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.4
	438142	T90309	Hs.269651	ESTs	2.4
45	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	2.4
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
	433868	AA612960	Hs.337300	ESTs	2.4
	401645				2.4
50	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.4
	453393	AW956392	Hs.110376	ESTs	2.4
	436054	AI076262	Hs.119813	ESTs	2.4
	425433	AA357471		gb:EST66274 LNCAP cells I Homo sapiens c	2.4
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.4
55	420639	AI683116	Hs.25328	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	453369	BE551550	Hs.232630	ESTs	2.4
	405017				2.4
	405385				2.4
60	435633	AI248152	Hs.270047	ESTs	2.4
	457128	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.4
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	2.4
	434544	C05875	Hs.91575	ESTs	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	455219	AW879403		gb:PM0-OT0019-150300-002-d01 OT0019 Homo	2.4
65	458734	AI554946	Hs.158794	ESTs	2.4
	442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	2.4
	444313	AI140494	Hs.197955	KIAA0704 protein	2.4
	440448	AA885428	Hs.125646	ESTs	2.4
	441498	AI379248	Hs.58742	ESTs	2.4
70	438205	AA780365	Hs.122161	ESTs	2.4
	402615				2.4
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.4
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.4
	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
75	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
	449007	AI620433	Hs.193201	EST, Weakly similar to NIP2_HUMAN BCL2/A	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	2.4
	418857	D10216	Hs.89394	POU domain, class 1, transcription facto	2.4
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	2.4
80	458914	BE327696	Hs.280922	ESTs	2.4
	435061	AI651474	Hs.163944	ESTs	2.4
	416458	AA180511		gb:zp53f03.r1 Stratagene NT2 neuronal pr	2.4
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, I	2.4

	403003			2.4
	405347			2.4
	406091			2.4
5	428402	AW237531	Hs.326876	Homo sapiens SOX6 mRNA, complete cds
	438762	AW844412	Hs.65450	reticulon 4
	455780	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo
	457024	AA397546	Hs.119151	ESTs
	404249			2.4
10	443921	AI091310	Hs.134848	ESTs
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir
	417154	AI674701	Hs.21388	ESTs
	419720	AA249131	Hs.337778	hypothetical protein FLJ11068
	405230			2.4
	405935			2.4
15	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon
	419233	AA458873	Hs.178306	ESTs
	414277	BE269910		gb:601186291F1 NIH_MGC_8 Homo sapiens cD
20	452092	BE245374	Hs.27842	hypothetical protein FLJ11210
	453736	AL118674	Hs.34871	zinc finger homeobox 1B
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo
	434239	AF119910	Hs.283047	hypothetical protein PRO2964
	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapi
25	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p
	445688	AI248205	Hs.153244	ESTs
	451656	BE327088	Hs.212752	ESTs
	423956	W28203	Hs.136169	Homo sapiens clone 25215 mRNA sequence,
	413445	BE141022		gb:MR0-HT0067-201099-002-d10 HT0067 Homo
30	436149	AI754308	Hs.159452	ESTs
	405629			2.3
	432702	AW973953	Hs.293744	ESTs
	433377	AI752713	Hs.43845	ESTs
	444711	AI188739	Hs.148488	ESTs
35	445621	AI733818	Hs.145549	ESTs
	456432	AW966931	Hs.179662	nucleosome assembly protein 1-like 1
	449236	AJ403126	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H
	459024	AA020799	Hs.262869	plasminogen-like
	441037	AA913360	Hs.126468	ESTs
40	431577	T34523	Hs.302040	Homo sapiens DNA sequence from PAC 43401
	438782	AA828380	Hs.126733	ESTs
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo
	429044	AI261490	Hs.145527	ESTs
45	431655	AW971119		gb:EST383206 MAGE resequences, MAGL Homo
	439642	W81441	Hs.153967	ESTs
	441721	AI288259	Hs.127652	ESTs
	443482	AW188093	Hs.250385	ESTs
	403416	AI744626	Hs.151385	KIAA0564 protein
50	416443	N69469	Hs.194225	ESTs
	419714	AA758751	Hs.98216	ESTs
	415511	AI732617	Hs.182362	ESTs
	412344	AW938384	Hs.264190	vacuolar protein sorting 35 (yeast homol
	449264	AI637649	Hs.196105	ESTs
55	451664	AA889081	Hs.153952	5' nucleotidase (CD73)
	441269	AW015206	Hs.178784	ESTs
	402333			2.3
	453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)
	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S
60	404367			2.3
	403696			2.3
	441622	AW450957	Hs.224864	ESTs
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo
	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo
65	428548	AA430058	Hs.98649	EST
	404059			2.3
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H
	413640	BE158118		gb:MR2-HT0378-240200-205-d09 HT0378 Homo
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin
70	435338	AA678071	Hs.194300	ESTs, Weakly similar to I38022 hypotheti
	442710	AI015631	Hs.23210	ESTs
	444206	AW301017	Hs.146492	ESTs
	451250	AA491275	Hs.236940	hypothetical protein FLJ12542
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo
75	458455	AV648310	Hs.213488	ESTs
	458521	AI651039	Hs.148559	ESTs
	407938	AA905097	Hs.85050	phospholamban
	439546	AF088056		gb:Homo sapiens full length insert cDNA
	441274	AW593781	Hs.131357	ESTs
80	454314	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo
	409660	AW452065	Hs.258905	ESTs
	428532	AF157326	Hs.184786	TBP-interacting protein
	411384	AW842115		gb:RC0-CN0026-090200-031-e11 CN0026 Homo
	453687	T55674	Hs.283108	hemoglobin, gamma G

	410140	AL134435	Hs.22269	neurexin 3	2.3
	422443	NM_014707	Hs.116753	histone deacetylase 7B	2.3
	409071	AW316932	Hs.181982	ESTs	2.3
5	421253	AI188102	Hs.31028	ESTs	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3
	448458	AW614367	Hs.171054	ESTs	2.3
	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.3
	443718	AI083580	Hs.221373	ESTs	2.3
10	445568	H00918	Hs.268744	KIAA1796 protein	2.3
	400582				2.3
	411262	AW834480		gb:MR2-TT0014-151199-011-b07 TT0014 Homo	2.3
	401145				2.3
	407440	AF227135		gb:Homo sapiens candidate taste receptor	2.3
15	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo	2.3
	459077	N20370	Hs.235883	ESTs	2.3
	448117	H49129	Hs.172982	ESTs	2.3
	453331	AI240665	Hs.8895	ESTs	2.3
	443751	AI285839	Hs.153324	EST	2.3
20	402038				2.3
	402176				2.3
	456605	AI827786	Hs.259044	ESTs	2.3
	432479	AL042844	Hs.275675	katanin p80 (WD40-containing) subunit B	2.3
	402527				2.3
25	449272	AW137656	Hs.197645	ESTs	2.3
	411024	BE062590		gb:QV1-BT0260-281099-023-f05 BT0260 Homo	2.3
	455608	BE011437		gb:CM4-BN0220-080500-170-f03 BN0220 Homo	2.3
	458818	AI523857	Hs.232257	ESTs	2.3
	419875	AA853410	Hs.93557	proenkephalin	2.3
30	405521				2.3
	436517	BE080932	Hs.135225	ESTs	2.3
	456801	AW961886	Hs.138263	Homo sapiens clone 24528 mRNA sequence	2.3
	430444	AW296421	Hs.121035	ESTs	2.3
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.3
35	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
	419337	AW291112	Hs.209978	ESTs	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypotheti	2.3
	454456	AW850984		gb:IL3-CT0220-150200-068-H08 CT0220 Homo	2.3
40	454633	AW811380		gb:IL3-ST0143-290999-019-D05 ST0143 Homo	2.3
	457028	AW449838	Hs.97562	ESTs	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.3
	430850	BE144152		gb:MR0-HT0165-060200-006-e02 HT0165 Homo	2.3
45	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	2.3
	421227	R78581	Hs.266308	mosaic serine protease	2.3
	426902	AI125334	Hs.97408	ESTs	2.3
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	2.3
	447475	AI380797	Hs.158992	ESTs	2.3
50	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.3
	430712	AW044647	Hs.196284	ESTs	2.3
	458103	AW780192	Hs.267596	ESTs	2.3
	420959	AA282119	Hs.88975	ESTs	2.3
	444098	AV647969	Hs.109694	KIAA1451 protein	2.3
55	445641	AI245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	2.3
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
	459497	AA825742	Hs.87517	ESTs	2.3
60	412852	BE004117	Hs.37415	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	437539	AA974673	Hs.121419	ESTs	2.3
	421813	BE048255		gb:tz49b05.y1 NCL_CGAP_Brn52 Homo sapien	2.3
	411994	R67298	Hs.109087	Homo sapiens cDNA: FLJ22845 fis, clone K	2.3
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	2.3
65	452463	R36452	Hs.300817	ESTs	2.3
	404936				2.3
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.3
	440836	AW370882	Hs.222080	ESTs	2.3
	405120				2.3
70	400238				2.3
	407809	AW082279	Hs.244106	ESTs	2.3
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	441417	AI733297	Hs.144474	ESTs	2.3
75	445117	AI208754	Hs.147369	ESTs	2.3
	431162	AW971180		gb:EST383268 MAGE resequences, MAGL Homo	2.2
	437036	AI571514	Hs.133022	ESTs	2.2
	455849	BE146866		gb:QV4-HT0222-211099-014-f06 HT0222 Homo	2.2
	447624	AI640326	Hs.62713	ESTs	2.2
80	439780	AL109688		gb:Homo sapiens mRNA full length insert	2.2
	405706				2.2
	447732	AI758398	Hs.161318	ESTs	2.2
	440625	BE539853	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	2.2
	404257				2.2

	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypotheti	2.2
	449133	AI631655	Hs.197919	ESTs	2.2
	456555	AW592167	Hs.293299	ESTs	2.2
5	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiester	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	446096	AI276454		gb:ql71a12.x1 Soares_NhHMPu_S1 Homo sapi	2.2
10	448106	AI800470	Hs.171941	ESTs	2.2
	450232	BE300815	Hs.201326	ESTs	2.2
	436134	AK000618	Hs.123784	ESTs	2.2
	448466	AI522109	Hs.171066	ESTs	2.2
	420678	AW593288	Hs.3530	TLS-associated serine-arginine protein 2	2.2
15	430692	X80240		gb:H.sapiens endogenous retrovirus HERV-	2.2
	446453	AV658469	Hs.188646	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	423611	AB011163	Hs.129908	KIAA0591 protein	2.2
	444050	AW138295	Hs.135024	ESTs	2.2
	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
20	422669	H12402	Hs.119122	ribosomal protein L13a	2.2
	403388				2.2
	403780				2.2
	419423	D26488	Hs.90315	KIAA0007 protein	2.2
	424719	H90452		gb:yv01c03.r1 Soares fetal liver spleen	2.2
25	431453	AW753917		gb:RC0-CT0299-291199-031-F02 CT0299 Homo	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	2.2
	427119	AW880562	Hs.114574	ESTs	2.2
	400486				2.2
30	448482	AW294078	Hs.171092	ESTs	2.2
	402621				2.2
	408363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	2.2
	424584	H10692	Hs.13310	ESTs	2.2
35	445061	AI253094	Hs.145227	ESTs	2.2
	431065	AA491286	Hs.128792	ESTs	2.2
	411908	L27943	Hs.72924	cytidine deaminase	2.2
	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
40	422677	AL046388	Hs.208206	hypothetical protein FLJ21162	2.2
	455534	AW991925		gb:PM3-BN0011-130100-002-b07 BN0011 Homo	2.2
	400163				2.2
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	409206	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	2.2
45	410556	R32158		gb:yh67a07.s1 Soares placenta Nb2HP Homo	2.2
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	2.2
	439482	W70045	Hs.58089	ESTs	2.2
	447877	AI435184	Hs.164252	ESTs	2.2
	418297	R91254		gb:yp94e12.s1 Soares fetal liver spleen	2.2
50	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	414000	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.2
	432762	NM_014099	Hs.278924	PRO1768 protein	2.2
	437606	AA761594	Hs.122440	ESTs	2.2
55	438550	AW976002	Hs.258402	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
	444540	AI693927	Hs.265165	ESTs	2.2
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.2
	456481	AA258033	Hs.108110	DKFZP547E2110 protein	2.2
60	435138	BE314734		gb:601152976F1 NIH_MGC_19 Homo sapiens c	2.2
	412887	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.2
	454204	AW816498		gb:QV0-ST0236-171299-075-b02 ST0236 Homo	2.2
	408253	AW807476	Hs.21051	Homo sapiens mRNA for FLJ00012 protein,	2.2
	432887	AI926047	Hs.162859	ESTs	2.2
65	448063	AI459108	Hs.159818	ESTs	2.2
	416171	H23896	Hs.125790	leucine-rich repeat-containing 2	2.2
	433098	AW190593	Hs.151143	ESTs	2.2
	409781	AW812266	Hs.15220	zinc finger protein 106	2.2
	423441	R68649	Hs.278359	absent in melanoma 1 like	2.2
70	423646	H02364		gb:yj35d06.r1 Soares placenta Nb2HP Homo	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
75	437334	AL353947	Hs.283780	hypothetical protein DKFZp761N1814	2.2
	431917	D16181	Hs.2868	peripheral myelin protein 2	2.2
	400843				2.2
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.2
80	449560	AA001767	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	408940	M58583	Hs.662	cerebellin 1 precursor	2.2
	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.2
	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.2
	459495	BE544158		gb:601076707F1 NIH_MGC_12 Homo sapiens c	2.2
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	2.2

	444547	AV650207	Hs.282437	ESTs, Weakly similar to I38022 hypotheti	2.2
	417156	N49476	Hs.166563	replication factor C (activator 1) 1 (14	2.2
	416761	H85422	Hs.108556	ESTs	2.2
5	408867	AA437199	Hs.656	cell division cycle 25C	2.2
	406748	AW339106	Hs.217493	annexin A2	2.2
	427443	AA402713	Hs.97872	ESTs	2.2
	452843	AI796769	Hs.208320	ESTs	2.2
	427473	AW274439	Hs.252709	ESTs	2.2
10	433919	AA746311		gb:oa56d12.r1 NCL_CGAP_GCB1 Homo sapiens	2.2
	431058	AW968865		gb:EST380941 MAGE resequences, MAGJ Homo	2.2
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	2.2
	415250	F02614	Hs.27319	ESTs	2.2
	440253	AI651329	Hs.160289	ESTs	2.2
15	434470	AA634818	Hs.298138	ESTs	2.2
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	2.2
	432463	AA548518	Hs.186733	ESTs	2.2
	400861				2.2
	407287	AI678812		gb:tu59d08.x1 NCL_CGAP_Gas4 Homo sapiens	2.2
20	414817	AW902892	Hs.23782	hypothetical protein FLJ12847	2.2
	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	2.2
	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	2.2
	442952	AI743261	Hs.131860	ESTs	2.2
25	425187	AW014486	Hs.22509	ESTs	2.2
	408221	AA912183	Hs.47447	ESTs	2.2
	411480	AW848022		gb:IL3-CT0214-231299-053-A09 CT0214 Homo	2.2
	459681				2.2
	414784	NM_000344	Hs.288986	survival of motor neuron 1, telomeric	2.2
30	442726	AW136066	Hs.19145	ESTs	2.2
	450433	AW444538	Hs.231863	ESTs	2.2
	437642	AL079309		gb:Homo sapiens mRNA full length insert	2.2
	406298				2.2
	409723	AW885757	Hs.257862	ESTs	2.2
35	433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
	446534	AI307356	Hs.175225	ESTs	2.2
	403764				2.2
40	442735	R91949		gb:yq06h06.s1 Soares fetal liver spleen	2.2
	455221	AW867751		gb:MR0-SN0038-290300-001-a03 SN0038 Homo	2.2
	405965				2.2
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	2.2
45	441679	BE502267	Hs.65596	ESTs	2.2
	432781	NM_014133	Hs.278940	PRO0618 protein	2.2
	448470	AW026226	Hs.309479	ESTs	2.2
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.2
	443180	R15875	Hs.258576	claudin 12	2.2
	422213	AA306385	Hs.133160	ESTs	2.2
50	423119	AA322201	Hs.131976	ESTs	2.2
	450192	AA263143	Hs.24596	RAD51-interacting protein	2.2
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	2.2
	400734				2.2
	430499	AW969408	Hs.231991	ESTs	2.2
55	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.2
	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
60	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
	436640	AA724411	Hs.156065	ESTs	2.2
	436802	N34486	Hs.170504	ESTs	2.2
	443994	AI094805	Hs.135522	ESTs, Weakly similar to S38038 hypotheti	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	446412	AW135313	Hs.150098	ESTs	2.2
65	448390	AL035414	Hs.21068	hypothetical protein	2.2
	449939	T86420	Hs.272139	ESTs	2.2
	412700	BE222433	Hs.201262	ESTs, Weakly similar to I38022 hypotheti	2.2
	453125	AW779544	Hs.115497	hypothetical protein FLJ22655	2.2
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
70	452864	AA033714	Hs.287629	hypothetical protein FLJ14260	2.2
	452441	BE222078	Hs.113069	ESTs	2.2
	402395				2.2
	459659				2.2
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.2
75	438432	AW444990	Hs.258800	ESTs, Weakly similar to I38022 hypotheti	2.2
	409446	AI561173	Hs.67688	ESTs	2.2
	408764	BE087164	Hs.302415	ESTs	2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
80	436992	AA741074	Hs.120750	ESTs	2.2
	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
	444199	AI128931	Hs.260681	ESTs, Moderately similar to ALUF_HUMAN !	2.2
	446009	AI989885	Hs.231926	ESTs	2.2
	435510	BE143837		gb:MR0-HT0164-151299-012-b08 HT0164 Homo	2.1

	403691				2.1
	458333	AI000792	Hs.108209	ESTs	2.1
	454560	AW807281		gb:MR4-ST0062-240300-003-g01 ST0062 Homo	2.1
5	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.1
	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protei	2.1
	406941	X58140		(NONE)	2.1
	445712	AI458246	Hs.167451	ESTs	2.1
10	451270	AW341392	Hs.235795	ESTs	2.1
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	2.1
	437073	AI885608	Hs.94122	ESTs	2.1
	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	2.1
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.1
15	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence	2.1
	405233				2.1
	446512	H30351	Hs.207982	ESTs	2.1
	403188				2.1
	404443				2.1
20	433645	AI821746	Hs.190258	ESTs, Moderately similar to ALU6_HUMAN A	2.1
	414456	H74314		gb:yu56e10.r1 Soares fetal liver spleen	2.1
	433479	AW511459	Hs.249972	ESTs	2.1
	455482	AW948353		gb:RC0-MT0015-130400-031-d07 MT0015 Homo	2.1
	446364	AB006624	Hs.14912	KIAA0286 protein	2.1
25	452004	AI827815	Hs.277359	ESTs	2.1
	405059				2.1
	425457	AW964212		gb:EST376285 MAGE resequences, MAGH Homo	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
30	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	432774	AA564946	Hs.156280	ESTs	2.1
	436349	AI445255	Hs.115315	ESTs	2.1
	445532	BE138944	Hs.146200	ESTs	2.1
	456313	AA225741		gb:nc17b10.s1 NCI_CGAP_Pr1 Homo sapiens	2.1
35	412818	NM_003337	Hs.811	ubiquitin-conjugating enzyme E2B (RAD6 h	2.1
	450271	AI693900	Hs.200920	ESTs	2.1
	401521				2.1
	422880	AF228704	Hs.121524	glutathione reductase	2.1
	448871	BE616709	Hs.159265	kruppel-related zinc finger protein hckr	2.1
40	449233	BE048401	Hs.196511	ESTs	2.1
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	2.1
	457003	S78234	Hs.172405	cell division cycle 27	2.1
	417448	AA203135	Hs.130186	ESTs	2.1
	402103				2.1
45	450579	AW136774	Hs.48614	ESTs	2.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.1
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	2.1
	415333	H24415	Hs.13273	KIAA0592 protein	2.1
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotr	2.1
50	434985	AA658229	Hs.291228	ESTs	2.1
	414729	BE466928	Hs.281901	ESTs	2.1
	400510				2.1
	420844	AA595522		gb:nh22c09.s1 NCI_CGAP_Pr1 Homo sapiens	2.1
	427434	BE538374	Hs.301732	hypothetical protein MGC5306	2.1
55	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	2.1
	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.1
	453853	AL040600	Hs.188083	ESTs	2.1
	459108	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	2.1
	430118	AI377255	Hs.183287	ESTs	2.1
60	455964	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.1
	437981	AA774445	Hs.192095	ESTs, Weakly similar to KIAA1397 protein	2.1
	439957	AI453184	Hs.66357	ESTs	2.1
	423734	H02217		gb:yj38d11.r1 Soares placenta Nb2HP Homo	2.1
	450721	AI732271	Hs.25567	ESTs	2.1
65	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	2.1
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	2.1
	432919	AL079800		gb:DKFZp434O2330_r1 434 (synonym: htes3)	2.1
	434791	AA649235	Hs.116457	ESTs, Weakly similar to NIP3_HUMAN BCL2/	2.1
	445273	AI218441	Hs.153846	ESTs	2.1
	400514				2.1
70	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.1
	439391	AW975638	Hs.293490	ESTs, Weakly similar to I38022 hypotheti	2.1
75	428414	AL049980	Hs.184216	DKFZP564C152 protein	2.1
	429430	AI381837	Hs.155335	ESTs	2.1
	449689	AF228421	Hs.23889	DKFZP564A032 protein	2.1
	430909	AF034632	Hs.248126	G protein-coupled receptor 38	2.1
	453116	AI276680	Hs.146086	ESTs	2.1
80	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	2.1
	423019	AI640185	Hs.283626	ESTs	2.1
	414007	AI733895	Hs.103813	ESTs	2.1
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	2.1
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	2.1

	421279	AW664878	Hs.106645	ESTs	2.1
	443167	AI202009	Hs.132087	ESTs	2.1
	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.1
5	448078	AI460117	Hs.170464	ESTs, Highly similar to A53933 myosin I	2.1
	436858	BE545498		gb:601070344F1 NIH_MGC_12 Homo sapiens c	2.1
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.1
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.1
	407401	AF029325		gb:Homo sapiens laminin beta-4 chain pre	2.1
10	426336	AA375802		gb:EST88135 HSC172 cells II Homo sapiens	2.1
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	2.1
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens c	2.1
	406504				2.1
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	2.1
15	415186	AA160945	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.1
	416175	H24230	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	442095	AI733162	Hs.128470	ESTs	2.1
	451878	AI821027	Hs.8429	ESTs	2.1
20	449178	AI633748	Hs.197597	ESTs	2.1
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	2.1
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	2.1
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	2.1
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	2.1
25	441543	AI733014	Hs.269715	ESTs	2.1
	403065				2.1
	428811	AA436052	Hs.99487	ESTs	2.1
	451803	BE541174	Hs.252058	ESTs, Moderately similar to PC4259 ferri	2.1
	442906	AW296888	Hs.170939	ESTs	2.1
30	409171	R17126		gb:yg09c11.r1 Soares infant brain 1N1B H	2.1
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	2.1
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	2.1
	412039	AW887384		gb:RC0-OT0089-130300-021-d07 OT0089 Homo	2.1
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	2.1
35	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.1
	455022	AW850845		gb:IL3-CT0220-111199-028-D11 CT0220 Homo	2.1
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	2.1
	422942	AF054839	Hs.122540	tetraspan 2	2.1
	400451				2.1
40	406668	T62745	Hs.184411	albumin	2.1
	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	404834				2.1
	448732	BE614063	Hs.334689	KIAA1838 protein	2.1
	423453	AW450737	Hs.128791	CGI-09 protein	2.1
45	421447	AB005216	Hs.104481	Nck, Ash and phospholipase C binding pro	2.1
	408774	AW270899	Hs.254569	ESTs, Weakly similar to B34087 hypotheti	2.1
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.1
	405732				2.1
	417848	AA206581	Hs.39457	ESTs, Weakly similar to JC5314 CDC28/cdc	2.1
50	442875	BE623003	Hs.23625	Homo sapiens clone TCCTTA00142 mRNA sequ	2.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.1
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	2.1
	426953	AI769281	Hs.97439	ESTs	2.1
	440454	AI733037	Hs.129990	ESTs	2.1
55	433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D1	2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
	441963	AI733307	Hs.128002	ESTs	2.1
	439498	AA908731	Hs.58297	CLLL8 protein	2.1
60	456224	AW292905	Hs.128770	ESTs	2.1
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	2.1
	444702	AI220122	Hs.326560	hypothetical protein MGC2780	2.1
	417787	R14948	Hs.23883	ESTs	2.1
	400612				2.1
65	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	451067	BE172186		gb:MR0-HT0559-110300-005-h11 HT0559 Homo	2.1
	455032	AI830890	Hs.192422	ESTs	2.1
70	417945	R29072		gb:F1-101D 22 week old human fetal liver	2.1
	438268	AA782163	Hs.293502	ESTs	2.1
	424754	R09692		gb:yf23b12.r1 Soares fetal liver spleen	2.1
	404599				2.1
	459655				2.1
75	402455				2.1
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	2.1
	421987	AI133161	Hs.286131	CGI-101 protein	2.1
	400339	X57131	Hs.248209	H2A histone family, member F, pseudogene	2.1
	438206	AA780385	Hs.187885	ESTs	2.1
80	458451	AW297181	Hs.195922	ESTs	2.1
	447534	AW953935	Hs.30837	ESTs	2.1
	417687	AI828596	Hs.250691	ESTs	2.1
	412717	W00973	Hs.334728	ESTs	2.1
	405759				2.1

	406413				2.1
	442081	AA401863	Hs.22380	ESTs	2.1
	457938	AI373638	Hs.133900	ESTs	2.1
5	420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 fis, clone PL	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	2.1
	411421	BE272110	Hs.21177	ESTs	2.1
	437825	AA769123	Hs.291947	ESTs	2.1
10	437083	AW082597	Hs.244862	ESTs	2.1
	409466	AA436207	Hs.226666	ESTs, Moderately similar to I54374 gene	2.1
	433523	H29882	Hs.162614	ESTs	2.1
	446868	AV660737	Hs.135100	ESTs	2.1
	445882	AI948717	Hs.225155	ESTs, Weakly similar to A46302 PTB-assoc	2.1
15	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.1
	406817	AI936028		gb:wo47a09.x1 NCL_CGAP_Gas4 Homo sapiens	2.1
	410486	AW235094	Hs.69233	zinc finger protein	2.1
	411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
	412446	AI768015	Hs.92127	ESTs	2.1
20	457289	AW573204	Hs.137078	ESTs	2.1
	400335	Y13187	Hs.248067	Homo sapiens dmd gene, intron 11	2.0
	435959	AW296243	Hs.118375	ESTs	2.0
	448188	AW001835	Hs.13323	hypothetical protein FLJ22059	2.0
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	2.0
25	420430	AI703192		gb:wd92h04.x1 NCL_CGAP_Lu24 Homo sapiens	2.0
	445717	AW664658	Hs.149332	ESTs	2.0
	451862	H09260	Hs.32333	ESTs	2.0
	459686				2.0
	441996	BE349537	Hs.38383	ESTs	2.0
30	412194	AW900282	Hs.115412	hypothetical protein FLJ13881	2.0
	444229	AV648613	Hs.282397	ESTs	2.0
	441635	AI908538	Hs.133000	ESTs, Weakly similar to S26689 hypotheti	2.0
	421387	AF059566	Hs.103983	solute carrier family 5 (sodium iodide s	2.0
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.0
35	428209	AA424197	Hs.98947	ESTs, Weakly similar to S33496 trypsin [2.0
	443520	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	2.0
	409248	AB033035	Hs.51965	KIAA1209 protein	2.0
	444518	AI160278	Hs.146884	ESTs	2.0
	422237	M13149	Hs.1498	histidine-rich glycoprotein	2.0
40	409316	U28251	Hs.53237	ESTs, Highly similar to Z169_HUMAN ZINC	2.0
	402725				2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
45	425008	AW675764	Hs.174248	ESTs	2.0
	427271	AW195922	Hs.188758	connexin 59	2.0
	444102	AV647953	Hs.83077	interleukin 18 (interferon-gamma-inducin	2.0
	445829	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
50	457652	AF116656	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.0
	429540	M85776		gb:EST02297 Fetal brain, Stratagene (cat	2.0
	459456	AA486036	Hs.190124	ESTs	2.0
	409840	AW502122		gb:U1-HF-BR0p-ajr-c-08-0-UI.r1 NIH_MGC_5	2.0
	441025	AA913880	Hs.176379	ESTs	2.0
	457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.0
55	445627	AW818475	Hs.7363	ESTs	2.0
	440299	AI871778	Hs.250112	ESTs	2.0
	401236	H24185	Hs.92918	hypothetical protein	2.0
	429996	N90822	Hs.48969	ESTs	2.0
60	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	2.0
	411537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	2.0
	433449	AW772282		gb:hn71b05.x1 NCL_CGAP_Kid11 Homo sapien	2.0
	454197	BE140966		gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
	445297	BE544163	Hs.87128	hypothetical protein FLJ23309	2.0
	403977				2.0
65	458948	AI695359	Hs.280943	ESTs	2.0
	418663	AK001100	Hs.41690	desmocollin 3	2.0
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	2.0
	426536	AI949749	Hs.44441	ESTs	2.0
	442765	BE567353	Hs.99480	ESTs	2.0
70	400859				2.0
	405829				2.0
	411863	BE075244	Hs.12420	ESTs	2.0
	415258	AW752247	Hs.293853	ESTs	2.0
75	416093	R60685	Hs.268698	ESTs, Moderately similar to ALUC_HUMAN !	2.0
	416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
	457039	H29990	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.0
	444292	AI139794	Hs.146569	ESTs	2.0
80	431360	NM_000427	Hs.251680	loricrin	2.0
	407644	D16815	Hs.37288	nuclear receptor subfamily 1, group D, m	2.0
	412029	AW886238		gb:RC5-OT0078-280300-022-F01 OT0078 Homo	2.0
	438522	AA809431	Hs.258886	ESTs	2.0
	422634	NM_016010	Hs.118821	CGI-62 protein	2.0

	418790	H95693		gb:yl95d11.s1 Soares_pineal_gland_N3HPG	2.0
	442950	AI500417	Hs.46764	ESTs	2.0
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.0
5	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
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	408733	AW264812	Hs.254290	ESTs	2.0
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	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
10	418205	L21715	Hs.83760	tropoin I, skeletal, fast	2.0
	404604				2.0
	413627	BE182082	Hs.246973	ESTs	2.0
	402341				2.0
	438090	AA777534	Hs.191992	ESTs	2.0
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	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.0
	401986				2.0
	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0
	417756	Z43056		gb:HSC12B021 normalized infant brain cDN	2.0
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	433755	AW085934	Hs.120868	ESTs	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
	435648	H24347	Hs.27524	ESTs	2.0
	447555	AI391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	2.0
25	458175	AW296024	Hs.150434	ESTs	2.0
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.0
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	2.0
	447678	BE385257	Hs.336457	Homo sapiens dopamine receptor interacti	2.0
	448150	AI472167	Hs.302739	ESTs	2.0
30	453445	AL036532	Hs.91453	ESTs	2.0
	444420	AI148157	Hs.146766	ESTs	2.0
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	2.0
	413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo	2.0
	428231	U17989	Hs.183105	nuclear autoantigen	2.0
35	455873	BE152239		gb:QV4-HT0316-091199-028-f12 HT0316 Homo	2.0
	430970	AI018210	Hs.144083	ESTs	2.0
	412277	BE277592	Hs.73799	guanine nucleotide binding protein (G pr	2.0
	413025	AA805265	Hs.291646	ESTs	2.0
	424083	AF055018	Hs.139137	Homo sapiens clone 24442 mRNA sequence	2.0
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	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.0
	423942	AF209704	Hs.135723	glycolipid transfer protein	2.0
	430340	AA476777		gb:zw94g11.r1 Soares_total_fetus_Nb2HF8_	2.0
	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.0
45	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.0
	400285				2.0
	405966				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
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	434531	AA642007	Hs.116369	ESTs	2.0
	447153	AA805202	Hs.315562	ESTs	2.0
	447185	AW377092	Hs.99601	hypothetical protein FLJ12553	2.0
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	400617	AF151064	Hs.36069	hypothetical protein	2.0
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	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	2.0
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	439509	AF086332	Hs.58314	ESTs	2.0
	430203	L36140	Hs.235069	RecQ protein-like (DNA helicase Q1-like)	2.0
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	2.0
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	407528	X64990		gb:H.sapiens mRNA HTPCRX16 for olfactory	2.0
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	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	2.0
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	422600	BE143586	Hs.87	retinoblastoma-like 1 (p107)	2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.0
	433153	AA578512		gb:nh22e11.s1 NCL_CGAP_Pr1 Homo sapiens	2.0
75	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
	435373	AW665538	Hs.117689	ESTs	2.0
	442988	AI026130	Hs.131683	ESTs	2.0
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.0
80	454423	AW603985		gb:RC4-CN0048-140100-011-a04 CN0048 Homo	2.0

Table 31B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

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	409206	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659
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	409699	1149033_1	BE154650 BE154785 AW468343 BE154816 BE154667
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	409840	1156071_1	AW502122 AW502125 AW501663 AW501720
	410201	118365_1	AA126129 AA126033 AA082561
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	410536	1207322_1	N39533 AW753094 AW753093
	410556	1208157_1	R32158 AW754055 AW754054 AW754053 AW754045 AW857320
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	420430	193538_1	AI703192 AW901259 AA278523 AA262062
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	421583	204220_1	AA293333 AI820910 AA293403
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	423841	232507_1	AW753967 AA370795 AA331630 AW962550
	423867	232732_1	AA331886 AW962659 AW962655 T89841
	423871	232749_1	AA331906 AA332484
	424719	242889_1	H90452 AA345767 AW964302 H90399
	424754	243305_1	R09692 R09414 AA346353
	424872	244505_1	AA347923 AA347928 AW961769

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	428679	294049_1	AA431765 AA432015
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	429875	310034_1	AI091815 AA460162 AA460761
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	430340	316229_1	AA476777 T86049
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
	430553	319868_1	AW392821 AW392809 AW843258 AW843049 AW603156 BE165656 AW821728
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	430757	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
	430850	324651_1	BE144152 AA937952 AA487799
	431058	327401_1	AW968865 AA491199 C17148
	431071	327550_1	AA491379 H86020 AW969148
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	431169	328799_1	AW971240 AA493843 AA493723
	431453	333457_1	AW753917 BE152926 AA505333 BE155673
	431655	336189_1	AW971119 AA574265 AA513268
	431822	338082_1	AA516049 AW004922
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	432363	345469_1	AA534489 AW970240 AW970323
	432779	354024_1	AW979241 AA565006 AA847102
	432869	355475_1	AW974094 AA569074 AA602574
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	433153	359936_1	AA578512 AA595535 BE177533
	433347	36388_1	AF023130 AF181250 AA984703 AA694303 AA351792
	433449	366532_1	AW772282 AA592974
	433919	377243_1	AA746311 AA927492 AA617995
45	434098	380006_1	AA625499 AA625269 AA625184
	434138	380572_1	AA625804 AW418787 AW074833 AI675642 AI393368
	434662	390415_1	AA641957 AW749897 AW749866 AW749887 AW749890
	434671	390655_1	R34758 AA642317
	435079	399783_1	AA664192 H60250 T71388
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	435689	409755_1	AA694284 H68267 H68264
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	436858	428095_1	BE545498 AA830720 AI873015 AA732679
	437037	431828_1	T63804 T63768 AA742849
	437113	433234_1	AA744693 AW750059
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	438005	447553_1	BE151746 BE336853 D63271 T94955 AA774994
	438993	467651_1	AA828995 AA834879 AI926361
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	442735	550247_1	R91949 AI016237 BE072329
	443764	579650_1	F23283 AI084941 F35774
	444063	590989_1	AI122614 AW869134
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	451067	85759_1	BE172186 AA059279 AA020815 AA013437
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	453211	95527_1	W84829 AA033900 AW573557
	453530	97021_1	AW021633 AA036730 AI866854
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5	454190	1049996_1	AW177821 AW177896 AW177867
	454197	1050392_1	BE140966 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969 BE141673 BE141650 BE141674 BE141550 BE141688 AW178241 BE140994 BE141666 BE140998 BE141008 BE140988 BE141011 BE140975 BE141667 BE141675 BE141657 BE141681 BE141656 BE141672 BE141680 AW178237 BE141012 BE140990 BE141658 BE141648 BE141013 BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646 BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671 AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141556
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	454352	1129667_1	AW389668 AW389657 AW609198 AW389649
	454423	1183079_1	AW603985 AW854350
	454447	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
	454456	1207088_1	AW850984 AW752836 M86124
	454482	1215087_1	BE147919 AW794884 BE147847
20	454560	1223940_1	AW807281 AW807092 AW807425 AW807330 AW807174 AW807171 AW807274 AW807278 AW807367
	454564	1224407_1	AW807573 AW807566 AW807572
	454566	1224432_1	AW807605 AW807690 AW807839 AW807752 AW807673 AW807667 AW807955 AW807760 AW807615 AW807898 AW807849 AW807821 AW807832 AW807842 AW807827 AW807822 AW807829 AW807830 AW807825 AW807603 AW807612 AW807908 AW807595 AW807617 AW807678 AW807687 AW807918 AW807921 AW807596 AW807602 AW807688 AW807609 AW807684 AW807770 AW807593 AW807754 AW807679 AW807957 AW807683 AW807763 AW807902 AW807840 AW807819 AW807836 AW807769 AW807685 AW807847 AW807674 AW807686 AW807670 AW807917 AW807677 AW807680 AW807900 AW807669 AW807952 AW807907 AW807846 AW807756 AW807835 AW807608 AW807753 AW807601 AW807956
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	454716	1230503_1	AW850684 AW850150
	454747	1233006_1	AW818535 AW818588 AW818651
	454754	1233580_1	AW819191 AW819252 AW819183 AW819175 AW819177 AW819186 AW819180 BE158470 AW819242 AW819269 AW819244 AW819190 AW819265 AW819268 AW819246 BE152602 AW819249 AW819251 AW819263 AW819194
35	454767	1234028_1	BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202 AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784
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	454790	1234752_1	AW820852 AW820773 AW821088
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	454864	1237929_1	AW835775 AW845768 AW845764 AW845773 AW845757 AW845758 AW845780
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	455170	1256906_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
50	455201	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
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	455221	1261678_1	AW867751 AW867770 AW867763
	455236	1265662_1	AW875972 AW875983 AW875974 AW876000 AW875966 AW876050
	455252	1266222_1	AW876627 AW876630 AW876631 AW876625
55	455255	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	455275	1272255_1	AW977806 AW887923 AW886321
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	455310	1278158_1	AW893961 AW893998 AW894034 AW894019
	455328	1280063_1	AW896438 AW896534 AW896500 AW896540 AW896446
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	455556	1325658_1	AW995423 AW995373
	455571	1331885_1	BE003714 BE003721 BE003720 BE003716
	455587	1335046_1	BE007829 BE007815 BE007822 BE007996 BE007835 BE007837 BE007824 BE007836 BE007827
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70	455675	1349659_1	BE065984 BE065942 BE065955 BE066085
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	455696	1351077_1	BE067870 BE067866 BE165133 BE165334 BE165329 BE165332
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	455756	1358603_1	BE079307 BE079309
	455778	1364506_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
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 456407 184986_1 AW968614 AA243209 AA281411
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 457242 307984_1 AA457011 AI978850
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 458804 75803_1 AL157625 N72696 BE622492
 458890 812733_2 AW865523 AW865128 AW865467 AW865127 AW865466
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 459201 925883_1 AW391177 W45021

TABLE 31C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400451	8113550	Minus	82189-82320
400462	9929659	Minus	197610-197785
400486	8569885	Plus	181108-181605
400510	9796540	Minus	139633-139910,140469-140979
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
400579	9887603	Plus	21323-21526
400582	9887609	Plus	88642-88726,89716-89866
400587	9887626	Plus	25435-25588,25668-25747
400608	9887666	Minus	96756-97558
400612	9929646	Minus	151513-151662
400613	9864507	Plus	92278-92472
400641	8117693	Plus	4785-4992
400643	8117693	Plus	12818-13016
400706	7249204	Minus	78299-78686
400734	8118979	Plus	122853-123971
400816	8569993	Plus	161221-162078
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
400859	9757499	Minus	91888-92018,98131-98294,99474-99570
400861	9757506	Plus	163855-164016
400889	9958234	Minus	169782-170036
401078	3687273	Plus	105052-105171
401098	9965518	Minus	85632-86174
401132	8705350	Minus	85679-85795
401145	2547238	Plus	17599-17776
401189	9690246	Minus	90815-90929
401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
401344	9926411	Minus	82478-82602,86952-87110
401361	9958052	Plus	153093-154106
401365	9796180	Minus	119572-119672
401449	8574316	Minus	144928-145030
401497	7381770	Plus	92607-92813
401521	7705251	Plus	9127-9234
401526	7770561	Plus	91570-93177
401602	7689963	Plus	101096-101253
401614	7839924	Plus	17350-17735
401645	7657839	Minus	34986-35133
401694	3540172	Minus	64056-64168
401775	9966311	Minus	110228-110340
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401882	8139716	Plus	86466-87077
401887	7229981	Plus	93973-94120
401986	4406829	Minus	31137-31293
401992	4153858	Plus	31452-31649
402038	7684482	Minus	100751-100885
402048	8072512	Plus	43936-44078
402076	8117410	Plus	128316-128627
402103	7249203	Plus	14453-15414
402131	7704961	Minus	33114-33209,33496-33678
402176	7543687	Minus	10-750
402230	9966312	Minus	29782-29932
402333	8844110	Minus	165693-165856
402341	7656696	Plus	22583-23699
402395	9929693	Minus	131016-131998
402429	9796372	Minus	57622-57793,59282-59402,59624-59827
402430	9796372	Minus	62382-62552
402455	9796753	Minus	139640-139779,140568-140660
402527	9800806	Plus	4722-4916,17858-18037,19964-20140,24423-24605,26699-26881

	402615	9926801	Plus	131390-132157
	402621	9930950	Plus	130806-131036
	402674	8077108	Minus	39290-39502
5	402725	8979991	Plus	107231-107383
	402790	4835258	Minus	147744-147861
	402867	5596716	Plus	52806-53106,53500-53818
	402953	9408724	Minus	122603-122743
	403003	5441423	Minus	79403-79560,79712-80021
10	403011	6693597	Minus	3468-3623
	403065	8954197	Minus	71615-71773,73930-74144
	403188	9838289	Minus	157618-157755
	403271	7230852	Plus	134283-134485
	403273	8018055	Plus	133809-134099
15	403281	8072630	Minus	7521-7728
	403296	8096530	Minus	35913-36520
	403310	8139936	Minus	183883-184026
	403329	8516120	Plus	96450-96598
	403341	8569175	Plus	30699-30910
20	403344	8569726	Plus	70823-70990
	403356	8569930	Plus	92839-93036
	403381	9438267	Minus	26009-26178
	403388	9438331	Plus	112733-113001,114599-114735
	403396	9438367	Minus	952-1160
25	403501	7534005	Minus	108903-110438
	403513	7656757	Minus	155310-155436,158402-158535
	403515	7656757	Minus	173358-179553
	403534	8076917	Minus	46652-47332
	403549	8081591	Minus	137150-137362
30	403568	8101145	Minus	85509-85658
	403574	8101156	Plus	5542-6176
	403619	8569810	Plus	62501-62653
	403623	8569879	Minus	3519-5426
	403625	8569879	Plus	6551-7111
35	403637	8671936	Minus	142647-142771,145531-145762
	403667	6850483	Minus	1344-1442,1545-1697
	403677	7331517	Minus	55008-55083,62860-63051
	403691	7387384	Minus	88280-88463
	403696	3135242	Minus	143467-143634
40	403743	7652003	Minus	136463-136646
	403760	7712202	Minus	45910-46260,47563-47824
	403764	7717105	Minus	118692-118853
	403776	7770611	Minus	1414-1513,1624-1756
	403780	8076989	Plus	93160-93409
45	403786	8083636	Minus	73028-73217
	403891	7331467	Minus	191508-193220
	403895	7381715	Minus	3502-4002,4070-4308
	403977	7657840	Minus	115573-115820
	404043	9558573	Plus	29042-29135,46597-46699
50	404059	3548785	Plus	104326-106788
	404076	9931752	Minus	3848-3967
	404196	3805917	Minus	67928-68109
	404249	8655533	Plus	64270-64633
	404257	9367215	Plus	15262-16227
55	404285	2326514	Plus	32282-32416
	404288	2769644	Plus	3512-3691
	404367	9965011	Minus	114391-114628
	404443	7579073	Minus	87198-87441
	404453	7657714	Plus	27768-29179
60	404476	8080699	Plus	101841-102043
	404513	8151941	Minus	112837-113339
	404561	9795980	Minus	69039-70100
	404569	7249169	Minus	104257-104348,104822-104970
	404577	4020145	Plus	17991-18420
65	404588	6456726	Minus	40059-40210
	404599	8705107	Plus	110443-110733
	404604	9212537	Minus	72019-72509
	404638	9796751	Minus	99433-99528,100035-100161
	404767	7882827	Minus	23244-23759
70	404793	7232206	Minus	61087-61590
	404822	3810614	Plus	7541-8132
	404834	6911603	Minus	37948-38226
	404845	7958980	Minus	47174-47326,52928-53146,53312-53602
	404898	7331420	Minus	177015-177328
75	404936	6850774	Plus	191519-191664
	404957	7407927	Plus	147512-148011
	405017	6532084	Plus	35551-35690
	405059	7656683	Plus	349-822
80	405090	8072525	Minus	38552-39202
	405093	8072575	Plus	95878-96020
	405120	8099940	Plus	140176-140340
	405170	9966524	Plus	37047-37198
	405229	7249019	Plus	51081-51701
	405230	7249032	Minus	97493-97682

	405233	7249045	Plus	9588-10065
	405241	7249178	Minus	69927-70526
	405264	7329374	Plus	28556-28684
5	405287	3928029	Plus	89802-89999
	405302	2078453	Minus	121688-121840
	405303	2078453	Minus	130607-130802
	405336	6094635	Plus	33267-33563
	405347	2979602	Minus	977-1116
10	405385	6552772	Plus	48332-48454
	405443	7408143	Plus	90716-90887,101420-101577
	405455	7656675	Plus	134112-134671
	405494	8050952	Minus	70284-70518
	405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
15	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
	405547	1054740	Plus	124361-124520,124914-125050
	405605	5836195	Minus	117070-117270
	405608	5815499	Minus	66822-66925
	405629	4508116	Minus	101678-101866
20	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405706	4165003	Plus	44307-44431,49619-49802
	405720	9797144	Plus	13409-13861
	405732	7534017	Plus	146981-147316
25	405759	3288022	Minus	18283-18399
	405780	7248203	Minus	48204-48371
	405784	7417368	Minus	77798-78000
	405829	7109593	Minus	15628-16127
	405869	6758731	Minus	89867-90358
30	405935	6758795	Minus	163112-163652
	405959	6758815	Plus	1-642
	405965	8247786	Minus	179930-180373
	405966	8247788	Minus	51762-51978
	405970	8247789	Minus	45795-46295
35	405981	8247790	Plus	4771-5338
	406005	8247801	Minus	39912-40220
	406053	6758997	Plus	30921-31532
	406073	9119150	Plus	60495-60610
40	406091	9123919	Minus	197370-197935
	406092	9123919	Plus	251370-251797,252168-252882
	406298	5686278	Minus	30084-30770
	406327	9212407	Plus	168241-168492
	406333	9213235	Plus	64689-64798
	406364	9256114	Minus	50715-50833
45	406377	9256135	Plus	126826-126979,129755-129942
	406413	9256407	Plus	43858-44003,46993-47136
	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
	406470	9795562	Minus	15532-15697
50	406504	7711360	Minus	107068-107277
	406506	7711374	Minus	6843-8077F
	406592	4567182	Plus	352560-352963

55

Table 32A lists about 969 genes upregulated in lung fibrosis relative to normal body tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

60

Table 33A lists about 800 genes upregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

65

Table 34A lists about 703 genes upregulated in idiopathic pulmonary fibrosis (IPF) relative to hypersensitivity pneumonitis (HP) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

70

Table 35A lists about 323 genes upregulated in hypersensitivity pneumonitis (HP) relative to idiopathic pulmonary fibrosis (IPF) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

75

Table 36A lists about 52 genes upregulated in non-specific interstitial pneumonitis (NSIP) relative to hypersensitivity pneumonitis (HP) or idiopathic pulmonary fibrosis (IPF). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

80

Table 37A lists about 206 genes downregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 38A lists about 207 genes upregulated in lung fibrosis relative to normal tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

TABLE 32A: About 969 genes upregulated in lung fibrosis relative to normal body tissues

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.
 R2: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	22.45	28.63
406964	M21305		FGENES predicted novel secreted protein	16.10	7.65
431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	15.83	14.86
442275	AW449467	Hs.54795	ESTs	15.74	21.96
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	13.83	34.53
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	12.40	7.38
431089	BE041395		ESTs, Weakly similar to unknown protein	12.38	6.05
421110	AJ250717	Hs.1355	cathepsin E	11.86	6.49
457200	U33749	Hs.197764	thyroid transcription factor 1	11.38	9.79
425211	M18667	Hs.1867	progastricin (pepsinogen C)	10.89	15.94
443709	AI082692	Hs.134662	ESTs	10.84	8.27
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	10.06	8.92
445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	9.96	5.43
432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	9.90	7.87
421798	N74880		N-acylsphingosine amidohydrolase (acid c	9.38	8.35
400269			Eos Control	9.03	6.48
444325	AW152618	Hs.16757	ESTs	8.31	6.76
416402	NM_000715	Hs.1012	complement component 4-binding protein,	8.14	5.51
413048	M93221	Hs.75182	mannose receptor, C type 1	7.70	4.09
432985	T92363	Hs.178703	ESTs	7.56	7.83
443324	R44013	Hs.164225	ESTs	7.06	4.47
449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	6.90	2.89
408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88	4.00
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56	4.25
421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46	4.47
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.30	13.57
409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	6.28	3.38
441835	AB036432	Hs.184	advanced glycosylation end product-speci	5.99	13.26
446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.88	4.10
415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	5.88	3.35
442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	5.87	5.69
414812	X72755	Hs.77367	monokine induced by gamma interferon	5.84	3.34
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.72	5.90
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	5.59	6.89
436954	AA740151	Hs.130425	ESTs	5.58	4.72
446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	5.48	5.33
421340	F07783	Hs.1369	decay accelerating factor for complement	5.48	2.69
420656	AA279098	Hs.187636	ESTs	5.45	3.99
432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	5.38	3.65
408380	AF123050	Hs.44532	diubiquitin	5.37	3.11
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	5.30	3.98
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.29	4.00
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	5.28	2.48
442832	AW206560	Hs.253569	ESTs	5.20	3.78
407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	5.11	3.81
433293	AF007835	Hs.32417	hypothetical protein MGC4309	5.11	2.88
424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.07	3.46
428043	T92248	Hs.2240	uteroglobin	5.06	9.46
431745	AW972448	Hs.163425	ESTs	5.04	4.16
444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04	3.68
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	5.02	4.26
419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	4.97	3.35
428927	AA441837	Hs.90250	ESTs	4.92	3.15
432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.79	3.05
442994	AI026718	Hs.16954	ESTs	4.76	2.65
416030	H15261	Hs.21948	ESTs	4.76	4.26
438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.73	3.24
453142	AA033648	Hs.7473	ESTs	4.66	2.92
424917	AI636208	Hs.96901	hypothetical protein FLJ23049	4.64	4.88
439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	4.60	2.60
432810	AA863400		ESTs	4.54	2.42
418259	AA215404		ESTs	4.54	2.54
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	4.48	4.86
424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.46	3.62
423575	C18863	Hs.163443	intron of periostin(OSF-2os)	4.44	3.41
428667	AI375550	Hs.346868	nucleolar protein p40; homolog of yeast	4.42	3.41

	429228	AI553633		ESTs	4.32	2.98
	432435	BE218886	Hs.282070	ESTs	4.30	2.26
	446932	AA961459	Hs.125644	ESTs	4.30	2.81
5	408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30	2.39
	409435	AI810721	Hs.95424	ESTs	4.30	2.60
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	4.29	2.48
	452561	AI692181	Hs.49169	KIAA1634 protein	4.23	2.26
	427698	AW972594	Hs.335499	ESTs	4.22	3.49
10	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	4.22	13.34
	446608	N75217	Hs.257846	ESTs	4.20	3.62
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.18	3.14
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.16	2.64
	445885	AI734009	Hs.127699	KIAA1603 protein	4.16	3.99
15	430280	AA361258	Hs.237868	interleukin 7 receptor	4.13	2.79
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFp564K143 (fr	4.12	2.19
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	4.12	3.02
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.08	3.13
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.08	3.48
20	432731	R31178	Hs.287820	fibronectin 1	4.06	2.66
	439398	AA284267	Hs.221504	ESTs	4.06	2.86
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.05	3.51
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04	2.44
	436120	AI248193	Hs.119860	ESTs	4.04	3.11
25	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.03	2.69
	421462	AF016495	Hs.104624	aquaporin 9	4.00	2.51
	443257	AI334040	Hs.11614	HSPC065 protein	4.00	2.61
	421659	NM_014459	Hs.106511	protocadherin 17	4.00	3.00
	424273	W40460	Hs.144442	phospholipase A2, group X	3.98	2.30
30	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.97	3.36
	450656	AA010539	Hs.18912	ESTs	3.96	4.37
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.94	2.44
	424527	AW138558	Hs.334873	ESTs, Weakly similar to I54374 gene NF2	3.93	3.08
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.92	3.53
35	452416	AA026115	Hs.114777	ESTs	3.92	2.90
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	3.90	5.06
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ111041 fis, clone PL	3.90	2.00
	453204	R10799	Hs.191990	ESTs	3.90	2.22
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	3.81	3.82
40	422173	BE385828	Hs.250619	phorbol-like protein MDS019(CEM15)	3.80	2.23
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.78	2.86
	406672	M26041	Hs.198253	major histocompatibility complex, class	3.78	3.70
	457411	AW085961	Hs.130093	iroquois-class homeobox protein IRX2	3.76	2.56
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.76	2.76
45	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74	2.83
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.72	2.55
	428820	AA436187	Hs.172631	integrin, alpha M (complement component	3.71	2.25
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	3.70	2.26
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	3.69	7.71
50	417412	X16896	Hs.82112	interleukin 1 receptor, type I	3.68	2.17
	426174	AA547959	Hs.115838	ESTs	3.65	2.93
	408727	AL137259	Hs.47115	hypothetical protein DKFp434D0513	3.64	2.62
	435990	AI015862	Hs.131793	ESTs	3.62	2.27
	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	3.62	3.48
55	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	3.61	3.18
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.60	3.05
	426116	AA868729	Hs.144694	ESTs	3.60	2.80
	419235	AW470411	Hs.288433	neurotrimin	3.58	2.88
	424054	AA334511	Hs.26638	membrane-spanning 4-domains, subfamily A	3.56	2.58
60	422667	H25642		ESTs	3.55	2.44
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.54	3.98
	414142	AW368397	Hs.334485	hemicentin (fibulin 6)	3.54	3.30
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.54	3.11
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	3.53	2.38
65	417318	AW953937	Hs.240845	ESTs	3.52	2.02
	456034	AW450979		gb:UL-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	3.50	3.21
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.48	2.35
	430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo	3.48	2.13
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.47	2.93
70	424711	NM_005795	Hs.152175	calcitonin receptor-like	3.47	2.69
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.46	2.31
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	3.46	2.37
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.45	2.07
	447183	AI554733	Hs.173182	ESTs	3.42	2.01
75	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	3.40	3.49
	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFp761E2423 (f	3.40	2.42
	413714	AI560944	Hs.71428	ESTs	3.38	2.52
	407361	AA744622	Hs.292645	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.36	2.13
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36	2.41
80	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	3.36	2.06
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.35	2.42
	410606	AW418779	Hs.114889	ESTs	3.35	2.39
	450726	AW204600		retinoic acid receptor, alpha	3.34	6.35
	430573	AA744550	Hs.136345	ESTs	3.33	1.94

	421585	U95626	Hs.302043	chemokine (C-C motif) receptor-like 2(3.32	2.75
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.31	2.22
	454076	AW204712	Hs.61957	ESTs	3.31	1.95
5	452039	AI922988	Hs.172510	ESTs	3.30	2.95
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30	2.37
	430414	AW365665	Hs.120388	ESTs	3.30	2.48
	417958	AA767382	Hs.193417	ESTs	3.30	2.04
	423001	AA320014	Hs.208603	ESTs	3.29	2.62
10	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28	2.35
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	3.28	2.05
	424238	AA337401	Hs.137635	ESTs	3.28	2.45
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	3.27	2.63
	448869	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.26	2.67
15	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5	3.26	2.04
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22	2.36
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22	3.87
	422109	S73265	Hs.1473	gastrin-releasing peptide	3.20	2.79
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	3.20	2.30
20	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18	2.42
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.18	2.12
	438568	R98865	Hs.11135	major histocompatibility complex, class	3.18	3.86
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	3.18	2.99
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	3.17	2.02
25	446094	AK001760	Hs.13801	KIAA1685 protein	3.17	2.42
	442048	AA974603		gb:op34f05.s1 Soares_NFL_T_GBC_S1 Homo s	3.17	2.27
	406685	M18728		gb:Human nonspecific crossreacting anti	3.17	2.80
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.16	1.95
	424943	AU077260	Hs.153924	death-associated protein kinase 1	3.16	2.18
30	436805	AA731533	Hs.270751	ESTs	3.16	1.95
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.15	3.63
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	3.14	1.74
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.13	3.35
	420729	AW964897	Hs.290825	ESTs	3.12	2.09
35	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12	2.06
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	3.12	2.58
	451820	AW058357	Hs.199248	ESTs	3.10	2.26
	440028	AW473675		ESTs, Weakly similar to T17227 hypotheti	3.10	3.01
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10	2.32
40	437866	AA156781		metallothionein 1E (functional)	3.10	1.80
	428513	BE220806	Hs.184697	plexin C1	3.10	2.11
	438607	AW080237	Hs.252884	ESTs	3.10	2.20
	445034	AW293376	Hs.143659	ESTs	3.08	2.81
	458332	AI000341		ESTs	3.08	1.87
45	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.08	1.87
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08	1.94
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.07	2.12
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	3.07	2.16
	425509	AF079363	Hs.158213	sperm associated antigen 6	3.06	2.75
50	431087	H12723	Hs.290791	ESTs	3.06	2.41
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	3.06	2.64
	449328	AI962493		ESTs	3.06	2.78
	422900	AA641201	Hs.222051	ESTs	3.05	1.87
55	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.05	1.99
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	3.05	2.49
	437527	AI241019	Hs.145644	ESTs	3.04	2.17
	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	3.04	1.78
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	3.02	2.43
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	3.02	1.77
60	411252	AB018549	Hs.69328	MD-2 protein	3.02	1.95
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02	2.24
	420683	AA830168	Hs.271305	ESTs	3.01	2.14
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00	2.13
	410434	AF051152	Hs.63668	toll-like receptor 2	3.00	2.60
65	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	3.00	1.94
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.00	1.81
	435800	AI248285	Hs.118348	ESTs	3.00	1.89
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	3.00	2.08
	449057	AB037784	Hs.22941	KIAA1363 protein	3.00	2.18
70	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	2.99	2.46
	436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	2.99	2.76
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.99	2.16
	444020	R92962	Hs.35052	ESTs	2.98	2.21
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.98	2.08
75	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	2.98	2.40
	457675	AF119917	Hs.306574	Homo sapiens PRO3098 mRNA, complete cds	2.96	2.03
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	2.96	1.74
	429950	AW081608	Hs.105053	ESTs	2.96	2.40
	420394	AB023161	Hs.97403	KIAA0944 protein	2.95	2.46
	406698	X03068	Hs.73931	major histocompatibility complex, class	2.95	4.13
80	419038	AW134924	Hs.190325	ESTs	2.94	1.72
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94	2.93
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	2.94	1.94
	400880			NM_000611*:Homo sapiens CD59 antigen p18	2.94	1.74

5	430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypot	2.94	2.12
	419034	NM_002110	Hs.89555	hemopoietic cell kinase	2.93	2.25
	439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobin, fa	2.93	3.72
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.92	1.91
	419981	AA897581	Hs.128773	ESTs	2.92	2.18
10	400419	AF084545		Target	2.92	1.83
	435176	AA744875	Hs.189413	ESTs	2.91	2.15
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	2.90	2.25
	444339	T96555	Hs.31562	ESTs	2.90	3.16
	429272	W25140	Hs.110667	ESTs	2.90	2.43
15	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.90	2.29
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	2.90	2.40
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	2.88	2.47
	421554	AW137676	Hs.97775	ESTs	2.88	3.37
	422770	AL117544	Hs.120021	DKFZP434I092 protein	2.88	2.00
20	434658	AI624436	Hs.310286	ESTs	2.88	2.06
	440248	AA876138		ESTs	2.86	2.24
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.86	4.32
	430515	AA746503	Hs.283313	ESTs	2.86	2.96
	446063	AI720140	Hs.151079	ESTs	2.86	2.47
25	438177	BE327015		ESTs	2.86	1.70
	429083	Y09397	Hs.227817	BCL2-related protein A1	2.85	2.06
	417105	X60992	Hs.81226	CD6 antigen	2.85	3.00
	433230	AW136134	Hs.220277	ESTs	2.84	1.97
	438676	AA813745	Hs.123446	ESTs	2.84	2.62
30	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.82	4.33
	420252	AW270404	Hs.193161	ESTs	2.82	3.22
	415788	AW628686	Hs.78851	KIAA0217 protein	2.82	1.78
	428065	AI634046	Hs.157313	ESTs	2.81	2.47
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.81	2.67
35	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.78	3.39
	435517	AA928626	Hs.130177	ESTs	2.78	2.36
	439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	2.78	1.82
	434158	T86534	Hs.14372	ESTs	2.78	1.96
	428923	BE047698	Hs.188785	ESTs	2.78	2.07
40	413786	AW613780	Hs.13500	ESTs	2.78	1.97
	406387			Target Exon	2.77	4.22
	421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	2.76	3.24
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.76	2.11
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	2.76	1.94
45	417728	AW138437	Hs.24790	KIAA1573 protein	2.76	1.78
	435154	AA668764		ESTs	2.76	2.10
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.76	2.21
	423387	AJ012074		vasoactive intestinal peptide receptor 1	2.76	2.36
	432060	AW971364	Hs.324775	ESTs	2.75	2.02
50	434164	AW207019	Hs.148135	serine/threonine kinase 33	2.74	2.48
	423706	U95218	Hs.131924	G protein-coupled receptor 65	2.74	1.93
	442703	AL044949	Hs.116298	ESTs	2.74	1.89
	450247	AF123303	Hs.24713	hypothetical protein	2.74	1.73
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	2.74	2.85
55	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.74	1.88
	409196	NM_001874	Hs.334873	carboxypeptidase M	2.73	1.86
	422389	AF240635	Hs.115897	protocadherin 12	2.72	2.26
	444324	AI301330	Hs.143838	ESTs	2.72	1.74
	417831	H16423	Hs.82685	CD47 antigen (Rh-related antigen, integr	2.72	2.40
60	428769	AW207175	Hs.106771	ESTs	2.72	2.19
	404277			NM_019111:Homo sapiens major histocompa	2.72	3.12
	409653	AW451693	Hs.220826	ESTs	2.72	2.62
	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	2.72	2.25
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	2.72	2.09
65	444381	BE387335	Hs.283713	hypothetical protein BC014245	2.71	2.26
	443547	AW271273		hypothetical protein FLJ12666	2.71	1.74
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.70	2.39
	402674			Target Exon	2.70	1.95
	438068	AI927209	Hs.306210	Homo sapiens cDNA: FLJ23133 fis, clone L	2.70	2.23
70	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	2.69	2.11
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.69	2.28
	428656	AB037798	Hs.188790	KIAA1377 protein	2.68	1.91
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.68	3.95
	443951	F13272		ferritin, light polypeptide	2.68	2.66
75	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.68	1.74
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	2.68	1.78
	446423	AW139655	Hs.150120	ESTs	2.68	2.29
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.67	2.07
	431779	AW971178	Hs.268571	apolipoprotein C-I	2.67	3.00
80	458124	AW005548	Hs.124590	ESTs	2.67	3.78
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-ii	2.66	1.64
	445745	AB007924	Hs.13245	KIAA0455 gene product	2.66	1.64
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.65	1.92
	432231	AA339977	Hs.274127	CLST 11240 protein	2.64	4.23
	442200	AW590572	Hs.235768	ESTs	2.64	2.46
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	2.64	2.00
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.63	3.23

5	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.63	2.48
	411213	AA676939	Hs.69285	neuropilin 1	2.62	1.73
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.62	2.69
	446570	AV659177	Hs.127160	ESTs	2.61	2.44
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	2.60	3.39
10	434792	AA649253	Hs.132458	ESTs	2.60	1.74
	426782	R14614	Hs.33846	ESTs	2.60	2.36
	425371	D49441	Hs.155981	mesothelin	2.60	6.97
	447720	AL038765	Hs.161304	ESTs	2.59	3.06
	444623	AI183829	Hs.202111	ESTs	2.59	2.77
15	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	2.58	2.01
	444542	AI161293	Hs.280380	aminopeptidase	2.58	2.31
	439549	AW937885	Hs.137314	ESTs	2.58	2.37
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	2.58	2.56
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.56	2.47
20	433308	AA582718	Hs.291650	ESTs	2.56	2.01
	443885	H91806	Hs.15284	ESTs	2.55	1.71
	408170	AW204516	Hs.31835	ESTs	2.55	1.59
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.54	1.63
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.54	2.98
25	428791	AA435661	Hs.264750	ESTs	2.53	2.29
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.53	3.91
	447357	AI375922	Hs.159367	ESTs	2.52	2.83
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	2.52	1.90
	424105	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1	2.52	3.45
30	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	2.52	1.98
	438698	AW297855		ESTs, Weakly similar to I38022 hypotheti	2.52	1.98
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	2.52	2.41
	424049	AB014524	Hs.138380	KIAA0624 protein	2.51	2.19
	438543	AA810141	Hs.192182	ESTs	2.51	2.06
35	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	2.51	2.14
	424806	AA382523	Hs.105689	MSTP031 protein	2.51	2.11
	438580	AA811262	Hs.299202	ESTs	2.50	1.83
	434445	AI349306	Hs.11782	ESTs	2.50	3.13
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	2.50	1.76
40	413638	H71252		gb:ys12h12.s1 Soares fetal liver spleen	2.50	2.00
	421281	AI299139	Hs.17517	ESTs	2.50	2.40
	441384	AA447849	Hs.288660	retinoic acid induced 3	2.50	2.75
	436772	AW975688		metallothionein 1E (functional)	2.49	1.80
	433102	AI343966	Hs.158528	ESTs	2.49	2.25
45	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.48	2.09
	445612	N94126	Hs.12959	hypothetical protein	2.48	2.28
	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	2.48	1.87
	433854	AA610649	Hs.333239	ESTs	2.48	2.09
	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	2.48	2.75
50	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.48	2.01
	440594	AW445167	Hs.126036	ESTs	2.48	1.57
	450295	AI766732	Hs.210628	ESTs	2.48	1.99
	431316	AA502663	Hs.145037	ESTs	2.48	1.80
	438564	AA381553	Hs.198253	major histocompatibility complex, class	2.48	2.80
55	439593	BE073597	Hs.124863	ESTs	2.48	1.89
	422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	2.47	3.74
	453134	AA032211	Hs.118493	ESTs	2.46	2.72
	417169	R13550	Hs.21388	ESTs	2.46	1.88
	434411	AA632649	Hs.201372	ESTs	2.46	1.95
60	440381	AA917808	Hs.190495	ESTs	2.46	2.09
	448782	AL050295		KIAA0758 protein	2.46	2.69
	404240			NM_018950:Homo sapiens major histocompat	2.45	2.83
	450843	AI741483	Hs.205383	ESTs	2.44	2.25
	434137	AA907734	Hs.124895	ESTs	2.44	2.55
65	438315	R56795	Hs.82419	ESTs	2.44	1.94
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44	1.61
	439402	W02753	Hs.103002	ESTs	2.44	1.90
	445903	AI347487	Hs.132781	class I cytokine receptor	2.44	2.32
	437323	AA371145	Hs.194397	leptin receptor	2.44	1.70
70	433923	AI823453	Hs.146625	ESTs	2.44	1.58
	442201	AW516704	Hs.208726	ESTs	2.43	1.68
	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	2.43	3.22
	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	2.43	2.21
	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	2.43	2.13
75	406973	M34996	Hs.198253	major histocompatibility complex, class	2.43	2.68
	428055	AA420664	Hs.101760	ESTs	2.42	2.05
	428970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	2.42	2.79
	433138	AB029496	Hs.59729	semaphorin sem2	2.42	1.68
	415757	AA830854	Hs.187810	ESTs	2.42	2.02
80	438507	AA809052		ESTs	2.42	2.08
	450811	AI739486	Hs.245497	ESTs	2.42	1.97
	424027	AW337575	Hs.201591	ESTs	2.42	2.76
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.41	3.15
	435978	AF272899	Hs.135118	Homo sapiens PR-domain zinc finger prote	2.41	2.08
	426291	U58913	Hs.169191	small inducible cytokine subfamily A (Cy	2.40	1.76
	416370	N90470	Hs.203697	CD38 antigen (p45)	2.40	1.97
	415688	AA166963		gb:zo86d01.s1 Stratagene ovarian cancer	2.40	1.63

5	445633	AI453386	Hs.17287	ESTs, Weakly similar to S26689 hypotheti	2.39	1.99
	431300	AA502346		gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens	2.39	1.79
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	2.39	1.84
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.39	2.21
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	2.38	2.09
10	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.38	1.78
	437479	R61866	Hs.101277	ESTs	2.38	3.00
	445784	AI253155	Hs.146065	ESTs	2.38	1.61
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	2.38	2.25
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.37	1.55
15	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	2.37	2.41
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	2.37	1.61
	418262	Z38968		ESTs	2.37	2.05
	420943	AI718702	Hs.279930	major histocompatibility complex, class	2.37	2.00
	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.37	2.05
20	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.37	1.67
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.36	1.88
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.36	2.61
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	2.36	2.84
	427250	R35941	Hs.25418	ESTs	2.36	2.15
25	452194	AI694413		olfactory receptor, family 2, subfamily	2.36	3.41
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	2.36	3.05
	407242	M18728		gb:Human nonspecific crossreacting anti	2.35	2.34
	418875	W19971	Hs.233459	ESTs	2.35	1.95
	425023	AW956889	Hs.154210	EDG-1 (endothelial differentiation, sph	2.35	1.85
30	432608	AI492660	Hs.170935	ESTs	2.35	2.06
	408048	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2	2.35	1.91
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	2.35	2.34
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	2.35	2.13
	410577	X91911	Hs.64639	glioma pathogenesis-related protein	2.34	1.73
35	422099	AA156022	Hs.111518	hypothetical protein	2.34	1.80
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	2.34	2.24
	427541	AI798983	Hs.82921	solute carrier family 35 (CMP-sialic aci	2.33	2.62
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	2.32	2.52
	431848	AI378857	Hs.271605	ESTs, Highly similar to AF175283 1 zinc	2.32	2.50
40	446354	AW449650		ESTs	2.32	2.21
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.32	4.34
	423961	D13666	Hs.136348	perioslin(OSF-2os)	2.31	2.19
	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	2.31	2.34
	457250	AA811987	Hs.125779	ESTs	2.31	1.66
45	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	2.31	2.96
	426839	M74782	Hs.172689	interleukin 3 receptor, alpha (low affin	2.30	2.12
	422746	NM_004484	Hs.119651	glypican 3	2.30	2.16
	439920	H05430	Hs.288433	neurotrimin	2.30	4.06
	414942	C14898	Hs.192986	ESTs	2.30	2.02
50	419092	J05581	Hs.89603	mucin 1, transmembrane	2.29	3.08
	424878	H57111	Hs.221132	ESTs	2.29	1.84
	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.29	2.76
	411605	AW006831		ESTs	2.29	1.58
	416965	N26223	Hs.160436	ESTs	2.29	4.71
55	428713	AA432067		ESTs, Moderately similar to CYA4 RAT ADE	2.29	1.73
	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	2.28	1.90
	420380	AA640891	Hs.102406	ESTs	2.28	2.82
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.28	1.52
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28	2.09
60	447160	AA330310	Hs.24181	ESTs	2.28	1.71
	421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	2.27	1.98
	453686	AL110326	Hs.304679	ESTs, Moderately similar to Z195_HUMAN Z	2.27	1.91
	452114	N22687	Hs.8236	ESTs	2.27	1.88
	417355	D13168	Hs.82002	endothelin receptor type B	2.26	1.63
65	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.26	1.84
	442262	BE170651	Hs.8700	deleted in liver cancer 1	2.26	1.86
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	2.26	1.72
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26	1.70
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.26	1.56
70	414221	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCI_CGAP_Su	2.26	2.12
	435272	AA906415	Hs.110041	ESTs	2.25	2.15
	414991	C17898		gb:C17898 Human placenta cDNA (TFujiwara	2.24	3.58
	424623	AW963062	Hs.270737	ESTs	2.24	1.87
	424665	AW368576	Hs.139851	caveolin 2	2.24	2.15
75	422426	W79117	Hs.58559	ESTs	2.22	3.33
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.22	2.39
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.22	3.28
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.22	1.59
	446142	AI754693	Hs.145968	ESTs	2.22	1.88
80	410503	AW975746	Hs.188662	KIAA1702 protein	2.22	1.56
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.22	2.49
	437629	AW574774	Hs.121692	ESTs	2.22	1.70
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	2.21	1.64
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.20	2.73
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	2.20	2.58
	429496	AA453800	Hs.192793	ESTs	2.20	2.97
	425516	BE000707	Hs.29567	ESTs	2.20	1.58

5	422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (f	2.19	1.92
	423526	AB011086	Hs.129739	KIAA0514 gene product	2.19	2.85
	436485	X59135	Hs.156110	immunoglobulin kappa constant	2.19	2.01
	426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.19	2.53
	443441	AW291196	Hs.92195	ESTs	2.18	1.73
10	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	2.18	2.53
	408705	AA312135	Hs.48967	HSPCO34 protein	2.18	1.54
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.18	1.93
	430915	AA488953		gb:aa55e05.r1 NCI_CGAP_GCB1 Homo sapiens	2.18	1.57
	418791	AA935633	Hs.194628	ESTs	2.17	2.05
15	432620	AA777749	Hs.5978	LIM domain only 7	2.17	1.75
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	2.17	2.01
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.17	3.12
	424450	AL137526		dynein intermediate chain 2	2.17	4.14
	426410	BE298446	Hs.305890	BCL2-like 1	2.16	2.19
20	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.16	1.70
	421077	AK000061	Hs.101590	hypothetical protein	2.16	1.60
	424563	AA446932	Hs.151428	ret finger protein 2	2.16	1.83
	405102			C15001220*.gij4469558[gb]AAD21311.1] (AF	2.16	1.78
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	2.15	1.87
25	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	2.15	1.65
	418067	AI127958	Hs.83393	cystatin E/M	2.15	2.40
	436372	AW972301	Hs.310286	ESTs	2.15	2.35
	418728	AW970937	Hs.293843	ESTs	2.14	2.58
	450400	AI694722	Hs.279744	ESTs	2.14	2.06
30	409031	AA376836		ESTs	2.14	2.14
	435143	R12375	Hs.194600	ESTs	2.14	1.69
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	2.14	2.03
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	2.14	1.57
	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	2.14	1.68
35	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.14	2.04
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.13	1.72
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	2.13	1.68
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.13	2.47
	452353	C18825	Hs.29191	epithelial membrane protein 2	2.12	2.31
40	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.12	2.76
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	2.12	2.11
	437581	N59284	Hs.288010	ESTs	2.12	2.85
	410976	R36207	Hs.25092	hypothetical protein MGC10744	2.12	2.04
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.12	2.00
45	423069	W15613	Hs.1613	adenosine A2a receptor	2.12	1.72
	432860	AW974077	Hs.283349	ESTs	2.12	1.75
	449509	AA001615	Hs.84561	ESTs	2.12	1.84
	456062	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	2.11	4.42
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.11	1.65
50	459680	H96982	Hs.42321	ESTs	2.11	2.20
	449677	AA002071		gb:zh85d01.s1 Soares_fetal_liver_spleen_	2.10	2.12
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	2.10	2.48
	443021	AA368546	Hs.8904	Ig superfamily protein	2.10	2.42
	437838	AI307229		ESTs	2.10	1.67
55	429421	AL031658		Human DNA sequence from clone RP1-310O13	2.10	1.91
	407202	N58172	Hs.109370	ESTs	2.10	1.68
	443669	AI140462	Hs.134587	ESTs	2.10	1.64
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	2.10	1.71
	408410	AA447438	Hs.44697	ATPase, Class V, type 10C	2.10	2.05
60	436293	AI601188	Hs.120910	ESTs	2.10	2.01
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	2.10	1.66
	427876	AI494291		ESTs	2.10	2.48
	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	2.09	3.11
	434987	AW975114		ESTs	2.09	1.69
65	433735	AA608955	Hs.109653	ESTs	2.09	1.78
	433226	AW503733	Hs.9414	KIAA1488 protein	2.09	1.62
	425787	AA363867	Hs.155029	ESTs	2.09	1.85
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.08	3.41
	442369	AI565071		ESTs	2.08	1.60
70	430478	NM_014349	Hs.241535	apolipoprotein L, 3	2.08	2.39
	434421	AI915927	Hs.34771	ESTs	2.08	1.66
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.08	1.72
	431728	NM_007351	Hs.268107	multimerin	2.08	1.51
	444929	AI685841	Hs.161354	ESTs	2.08	3.14
75	408873	AL046017		calmodulin 2 (phosphorylase kinase, delt	2.08	2.09
	437634	AW293046	Hs.255158	ESTs	2.08	1.66
	400277			Eos Control	2.08	1.46
	443601	AI078554	Hs.42658	ESTs	2.08	1.87
	432212	AW137742		ESTs	2.08	2.84
80	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	2.07	1.48
	406122			Target Exon	2.06	2.75
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	2.06	1.66
	408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-102O5 from Y	2.06	1.70
	421057	T58283		Homo sapiens cDNA: FLJ22063 fis, clone H	2.06	1.78
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.06	2.30
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	2.06	2.31
	449444	AW818436		solute carrier family 16 (monocarboxylic	2.06	1.41

	421464	AA291553	Hs.190086	ESTs	2.06	2.61
	424831	H61453		ESTs	2.06	2.12
	434542	AA769310		hypothetical protein FLJ13164	2.06	1.44
5	418323	NM_002118	Hs.1162	major histocompatibility complex, class	2.05	2.61
	418836	AI655499	Hs.161712	ESTs	2.05	1.73
	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	2.05	1.99
	400750			Target Exon	2.05	1.75
	406851	AA609784		major histocompatibility complex, class	2.05	3.94
10	414936	C14774		gb:C14774 Clontech human aorta polyA mRNA	2.05	2.41
	453459	BE047032	Hs.257789	ESTs	2.04	1.86
	443450	N66045	Hs.133529	ESTs	2.04	2.46
	430015	AW768399		ESTs	2.04	1.63
	429399	AA452244	Hs.16727	ESTs	2.04	1.51
15	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	2.04	1.73
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	2.04	1.46
	421757	Z20897	Hs.296259	paraaxonase 3	2.04	2.13
	441942	AF182645	Hs.8024	IK cytokine, down-regulator of HLA II	2.04	1.82
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	2.04	1.67
20	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	2.04	3.23
	414154	AW205314	Hs.323060	ESTs	2.03	2.96
	449987	AW079749	Hs.184719	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.03	1.59
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	2.03	2.01
	406645	M57466	Hs.814	major histocompatibility complex, class	2.03	2.49
25	414516	AI307802		ESTs, Weakly similar to T43458 hypotheti	2.02	1.56
	417032	AA192469	Hs.271838	ESTs	2.02	1.48
	414875	H42679	Hs.77522	major histocompatibility complex, class	2.02	2.79
	414522	AW518944	Hs.76325	Immunoglobulin J chain	2.02	1.84
	410511	AA743475	Hs.285655	ESTs	2.02	1.87
30	423533	NM_014339	Hs.129751	interleukin 17 receptor	2.02	2.26
	437259	AI377755	Hs.120695	ESTs	2.02	2.34
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	2.02	1.86
	426722	U53823	Hs.171952	occludin	2.02	1.57
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	2.02	1.79
35	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.02	1.97
	447232	AW498834	Hs.327	interleukin 10 receptor, alpha	2.02	2.09
	449317	AW293413	Hs.132906	19A24 protein	2.02	1.84
	439556	AI623752	Hs.163603	ESTs	2.02	1.62
	443031	AW134696	Hs.49418	ESTs	2.01	1.58
40	444838	AV651680	Hs.208558	ESTs	2.01	1.69
	453108	AI311457	Hs.99472	ESTs	2.01	1.64
	432967	AA572949	Hs.207566	ESTs	2.01	1.83
	441390	AI692560	Hs.131175	ESTs	2.01	1.63
	448076	AJ133123	Hs.20196	adenylate cyclase 9	2.01	1.80
45	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.01	2.32
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	2.01	1.90
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.01	1.90
	415443	T07353	Hs.7948	ESTs	2.00	1.54
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	2.00	2.74
50	404394			ENSP00000241075:TRRAP PROTEIN.	2.00	2.99
	459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	2.00	1.89
	437204	AL110216		ESTs, Weakly similar to I55214 salivary	2.00	1.46
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	2.00	1.37
	440667	BE076969	Hs.7337	hypothetical protein FLJ10936	2.00	1.51
55	431193	AW749505	Hs.296770	KIAA1719 protein	1.99	2.01
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	1.99	2.11
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	1.98	1.79
	417072	BE243915	Hs.81118	leukotriene A4 hydrolase	1.98	2.47
	429073	AA446167	Hs.47385	ESTs	1.98	1.92
60	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.98	2.94
	420838	AW118210	Hs.42321	ESTs	1.98	1.67
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	1.97	2.10
	430702	U56979	Hs.278568	H factor 1 (complement)	1.97	1.84
	456804	AI421645	Hs.139851	caveolin 2	1.97	1.58
65	439195	H89360		gb:yw28d08.s1 Morton Fetal Cochlea Homo	1.97	1.93
	459299	BE094291	Hs.155651	hepatocyte nuclear factor 3, beta	1.97	2.28
	413836	W92003	Hs.70614	ESTs	1.97	1.80
	400417	X72475		Target	1.97	1.75
	427814	W28383	Hs.180900	Williams-Beuren syndrome chromosome regi	1.96	1.46
70	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	1.96	2.18
	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	1.96	2.06
	455615	BE045344	Hs.274923	ESTs, Moderately similar to unnamed prot	1.96	2.21
	414572	AU077174	Hs.288181	cathepsin H	1.96	2.65
	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	1.95	1.71
75	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	1.95	2.88
	451609	AL046019	Hs.209276	ESTs	1.94	3.26
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	1.94	2.94
	430887	N66801	Hs.260287	KIAA1841 protein	1.94	1.62
	414700	H63202	Hs.38163	ESTs	1.94	1.72
80	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	1.94	1.56
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	1.93	2.22
	425252	AW391162		calreticulin	1.92	2.14
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	1.92	2.19
	425810	AI923627	Hs.31903	ESTs	1.92	1.76

	433618	AA602539	Hs.345494	ESTs	1.92	1.84
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.92	2.27
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.92	1.76
5	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	1.92	1.72
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	1.91	1.83
	426780	BE242284	Hs.172199	adenylate cyclase 7	1.91	1.67
	452386	R12499	Hs.20468	ESTs	1.91	2.64
	438670	AI275803	Hs.123428	ESTs	1.91	3.12
10	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.91	1.82
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.90	2.06
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.90	1.85
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	1.90	1.65
	428166	AA423849	Hs.79530	M5-14 protein	1.90	1.70
15	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	1.89	3.22
	449271	AW338067	Hs.7869	Homo sapiens cDNA FLJ11946 fis, clone HE	1.88	2.07
	436576	AI458213	Hs.77542	ESTs	1.88	2.25
	437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.88	2.41
	449618	AI076459	Hs.15978	KIAA1272 protein	1.88	1.63
20	430634	AI860651	Hs.26685	calcyphosine	1.88	3.01
	440663	AW452976	Hs.247112	hypothetical protein FLJ10902	1.88	1.65
	440099	AL080058	Hs.6909	DKFZP564G202 protein	1.88	1.78
	414662	AL036058	Hs.76807	major histocompatibility complex, class	1.88	2.37
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	1.87	2.07
25	414464	AI870175	Hs.13957	ESTs	1.87	2.68
	427792	M63928	Hs.180841	tumor necrosis factor receptor superfam	1.87	2.25
	415801	R24219	Hs.278443	Fc fragment of IgG, low affinity Iib, re	1.87	2.05
	430027	AB023197	Hs.227743	KIAA0980 protein	1.87	1.70
	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.87	2.18
30	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	1.86	2.87
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	1.86	2.31
	420361	N92054	Hs.194718	zinc finger protein 265	1.86	1.63
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.86	2.13
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.85	1.77
35	442434	AA995787	Hs.129583	ESTs	1.85	2.15
	422735	AA169685	Hs.119529	Niemann-Pick disease, type C2 gene	1.85	2.77
	444083	AI123195		gb:oo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.84	1.73
	449679	AI823951	Hs.129700	tolloid-like 1	1.84	1.57
40	418183	NM_001772	Hs.83731	CD33 antigen (gp67)	1.84	2.02
	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.84	1.72
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	1.84	2.47
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	1.84	2.29
	455508	AW976165		gb:EST388274 MAGE resequences, MAGN Homo	1.84	1.69
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	1.83	2.12
45	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.83	1.59
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	1.83	1.57
	417086	AA194446		ESTs, Weakly similar to S55024 nebulin,	1.83	1.45
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	1.83	2.18
	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	1.83	1.75
50	438596	AA829427	Hs.243081	ESTs	1.83	2.83
	436486	AA742221	Hs.120633	ESTs	1.82	2.14
	433365	AF026944	Hs.293797	ESTs	1.82	2.50
	449943	AF104266	Hs.24212	latrophilin	1.82	2.08
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.82	2.37
55	421563	NM_006433	Hs.105806	granulysin	1.82	2.48
	449161	N53431	Hs.47647	ESTs, Weakly similar to T00057 hypotheti	1.81	2.81
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	1.81	2.66
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.81	2.50
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	1.81	2.05
60	432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	1.80	3.13
	428677	AI657119	Hs.120036	troponin I, cardiac	1.80	2.94
	409485	S80990	Hs.252136	ficolin (collagen/fibrinogen domain-cont	1.80	2.28
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.80	1.56
	425458	H89317	Hs.182889	ESTs	1.80	2.21
65	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	1.80	1.41
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	1.80	2.20
	430570	AI417881	Hs.292464	ESTs	1.80	1.62
	439425	AF086244	Hs.114659	ESTs	1.80	2.37
	408688	AI634522	Hs.152925	KIAA1268 protein	1.80	2.13
70	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	1.80	1.80
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PNO099 son3 prot	1.79	1.57
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.79	2.18
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.79	1.68
	403421			NM_016369*:Homo sapiens claudin 18 (CLDN	1.79	2.47
75	430423	AI190548	Hs.143479	ESTs, Weakly similar to hypothetical pro	1.79	2.92
	416384	AU076903	Hs.79283	selectin P ligand	1.79	1.87
	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	1.78	1.69
	422003	AA361760	Hs.296326	ESTs	1.78	2.05
80	412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140	1.77	1.82
	432987	AI864771	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	1.77	2.03
	441602	AI655043	Hs.133456	ESTs	1.77	2.01
	458194	AW383618		ESTs, Moderately similar to ALU2_HUMAN A	1.76	2.35
	432565	AA553477	Hs.152428	ESTs	1.76	2.63
	421071	AI311238	Hs.104476	ESTs, Weakly similar to CGHU1E collagen	1.75	2.59

	408989	AW361666	Hs.49500	KIAA0746 protein	1.75	1.66
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.75	1.54
	403903			C5001632*:gi10645308 gb AAG21430.1 AC00	1.75	3.20
5	421461	AW291023		ESTs, Weakly similar to A46010 X-linked	1.74	2.67
	430850	BE144152		gb:MR0-HT0165-060200-006-e02 HT0165 Homo	1.74	2.52
	424377	AF081675	Hs.146322	killer cell lectin-like receptor subfam1	1.74	2.15
	443884	N20617	Hs.194397	leptin receptor	1.74	1.51
	423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	1.74	1.63
10	448262	AW880830	Hs.186273	ESTs	1.73	2.57
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.73	1.87
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.73	2.21
	412896	AW804157	Hs.308026	major histocompatibility complex, class	1.72	2.37
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	1.72	2.16
15	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	1.72	1.52
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	1.71	1.55
	438606	NM_014859	Hs.6336	KIAA0672 gene product	1.71	1.57
	434795	BE620794	Hs.4147	translocating chain-associating membrane	1.71	2.21
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	1.71	1.46
20	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	1.71	2.49
	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	1.71	1.57
	423857	N48902	Hs.133481	Homo sapiens mRNA; cDNA DKFZp564O0862 (f	1.71	1.56
	408393	AW015318	Hs.23165	ESTs	1.70	1.43
	432409	AA806538	Hs.130732	KIAA1575 protein	1.70	1.54
25	440817	AI341423	Hs.288433	neurotrophin	1.70	2.17
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.69	2.54
	453691	H12235	Hs.226505	ESTs	1.69	2.07
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	1.68	1.54
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.68	2.29
30	434951	AF161442	Hs.191591	Homo sapiens HSPC324 mRNA, partial cds	1.68	2.24
	444301	AK000136	Hs.10760	asporin (LRR class 1)	1.68	1.44
	407775	NM_004914	Hs.38772	RAB36, member RAS oncogene family	1.68	2.03
	437119	AI379921	Hs.177043	ESTs	1.68	4.21
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1.68	2.28
35	453498	BE181412	Hs.23245	hypothetical protein FLJ11767	1.68	2.76
	428289	M26301	Hs.2253	complement component 2	1.67	2.40
	404854			Target Exon	1.67	1.76
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	1.67	2.32
	410048	W76467	Hs.343874	proline oxidase homolog	1.67	3.03
40	407857	AI928445	Hs.92254	synaptotagmin-like 2	1.66	1.51
	447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	1.66	2.01
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	1.66	2.05
	421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	1.66	2.20
	433350	BE563152	Hs.10362	Homo sapiens cDNA: FLJ20944 fis, clone A	1.66	2.11
45	417451	AW007280	Hs.115537	putative dipeptidase	1.65	2.11
	443791	N64458	Hs.143345	ESTs	1.65	2.11
	440475	AI807671	Hs.24040	potassium channel, subfamily K, member 3	1.65	2.04
	431743	AW972642	Hs.293055	ESTs	1.64	2.64
50	400328	X87344		transporter 2, ATP-binding cassette, sub	1.64	2.43
	451876	T63141		gb:yb99a12.s1 Stratagene lung (937210) H	1.64	2.02
	417321	N68722	Hs.191368	ESTs	1.64	2.53
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.64	2.01
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.63	2.17
	432176	AW090386	Hs.112278	arrestin, beta 1	1.63	2.04
55	450708	AA376654		eukaryotic translation initiation factor	1.62	2.05
	429570	BE242256	Hs.2441	KIAA0022 gene product	1.62	1.39
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	1.62	1.57
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	1.62	1.44
	452424	AI964028	Hs.48353	ESTs	1.62	2.53
60	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	1.62	1.38
	416316	H58721	Hs.271628	ESTs	1.62	1.39
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam1	1.62	2.67
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.62	2.45
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	1.62	1.51
65	438089	W05391		nuclear receptor subfamily 1, group I, m	1.61	1.45
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.61	1.52
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.61	2.40
	444009	AI380792	Hs.135104	ESTs	1.60	2.15
	436057	AJ004832	Hs.5038	neuropathy target esterase	1.60	2.60
70	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	1.60	2.57
	433614	W07475	Hs.277101	cytochrome c oxidase subunit IV isoform	1.60	3.30
	410494	M36564	Hs.64016	protein S (alpha)	1.59	1.42
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	1.59	2.02
	446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.59	2.52
75	419918	X80700	Hs.93728	pre-B-cell leukemia transcription factor	1.59	2.04
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	1.59	1.98
	434308	N51517	Hs.47282	ESTs	1.58	2.29
	447341	AF106941	Hs.18142	arrestin, beta 2	1.58	2.09
	454315	AW373564	Hs.251928	BANP homolog, SMAR1 homolog	1.58	2.10
80	423281	AJ271684	Hs.126355	C-type (calcium dependent, carbohydrate-	1.57	1.75
	433671	AW138797	Hs.132906	19A24 protein	1.57	2.05
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	1.57	2.71
	436906	H95990	Hs.181244	major histocompatibility complex, class	1.57	2.24
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	1.57	1.43

5	406825	AI982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.57	2.37
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.56	1.61
	423329	AF054910	Hs.127111	tektin 2 (testicular)	1.56	2.51
	424909	S78187	Hs.153752	cell division cycle 25B	1.55	2.00
	431921	N46466	Hs.58879	ESTs	1.54	3.04
10	437400	AB011542	Hs.5599	EGF-like-domain, multiple 5	1.54	1.44
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfam	1.54	3.04
	415078	AA311223	Hs.283091	found in inflammatory zone 3	1.53	2.61
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.53	2.18
	401854			Target Exon	1.53	2.08
15	406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.52	1.52
	433815	AI696602	Hs.112757	ESTs	1.52	2.57
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.52	1.36
	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	1.51	1.43
	414763	U97276	Hs.77266	quiescin Q6	1.50	2.07
20	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	1.50	1.46
	412870	N22788	Hs.82407	CXC chemokine ligand 16	1.50	2.83
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.50	2.04
	432894	AW167668	Hs.279772	brain specific protein	1.50	2.25
	457941	AI004525	Hs.14587	ESTs, Weakly similar to AF151859 1 CGI-1	1.49	2.22
25	442743	AI801351	Hs.302110	ESTs, Weakly similar to MUC2_HUMAN MUCIN	1.49	2.09
	419542	AA366037	Hs.90911	solute carrier family 16 (monocarboxylic	1.49	2.40
	433124	U51712	Hs.13775	hypothetical protein SMAP31	1.49	1.39
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.49	1.39
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.48	1.76
30	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.48	1.41
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	1.48	1.44
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.47	1.31
	427872	AA835058		Human DNA sequence from clone RP1-261G23	1.47	2.50
	449853	AF006823	Hs.24040	potassium channel, subfamily K, member 3	1.47	2.21
35	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (1.47	1.50
	415149	X12451	Hs.78056	cathepsin L	1.46	1.84
	447217	BE465754	Hs.17778	neuropilin 2	1.46	1.40
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid melaph	1.46	2.16
	445672	AI907438	Hs.282862	ESTs	1.46	2.01
40	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.46	2.10
	458208	AI380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	1.46	1.60
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	1.45	1.40
	419577	L36531	Hs.91296	integrin, alpha 8	1.45	1.40
	439620	AA838727	Hs.124405	ESTs, Weakly similar to A46010 X-linked	1.45	1.57
45	423804	AW403448	Hs.16725	interferon-stimulated transcription fact	1.45	2.10
	424658	NM_002406	Hs.151513	mannosyl (alpha-1,3)-glycoprotein beta-	1.44	2.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	1.44	1.45
	431573	AW971070	Hs.291160	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.44	1.40
	409524	AW402151	Hs.54673	tumor necrosis factor (ligand) superfami	1.43	2.01
50	406787	AW090702	Hs.240615	tubulin alpha 1	1.42	1.86
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.42	1.95
	406422			Target Exon	1.41	2.02
	421341	AJ243212		deleted in malignant brain tumors 1	1.41	1.47
	421195	BE464560	Hs.133017	ESTs	1.41	2.42
55	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	1.41	2.05
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.41	1.34
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	1.40	2.10
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.40	3.64
	411880	AW872477		gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens	1.40	3.24
60	432133	AB033088	Hs.272567	KIAA1262 protein	1.40	2.78
	428833	AI928355		ESTs	1.40	2.02
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.39	1.55
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	1.39	2.09
	427732	NM_002980	Hs.2199	secretin receptor	1.38	2.44
65	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	1.38	1.85
	407568	AA740964	Hs.62699	ESTs	1.38	3.13
	422573	AW297985	Hs.295726	integrin, alpha V(vitronectin receptor	1.38	1.38
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	1.37	1.12
	457918	AL359590	Hs.162604	hypothetical protein DKFZp762M186	1.36	2.01
70	423696	Z92546	Hs.131819	Sushi domain (SCR repeat) containing	1.36	2.54
	416700	AW498958	Hs.343475	cathepsin D (lysosomal aspartyl protease	1.36	2.04
	407244	M10014		fibrinogen, gamma polypeptide	1.36	1.29
	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	1.35	1.34
	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	1.35	2.47
75	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	1.34	1.66
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	1.34	1.92
	436982	AB018305	Hs.5378	spondin 1, (F-spondin) extracellular mat	1.34	1.86
	427507	AF240467	Hs.179152	toll-like receptor 7	1.34	2.11
	446967	AI699629	Hs.156781	ESTs	1.34	3.75
80	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.34	2.18
	456637	AW161450	Hs.109201	CGI-86 protein	1.33	1.78
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.33	1.95
	417785	X59812	Hs.82568	cytochrome P450, subfamily XXVIIA (stero	1.32	2.05
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unnamed protein	1.32	2.08
	436986	AA740983	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.32	2.06
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	1.32	2.08
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	1.31	1.29

5	429500	X78565	Hs.289114	hexabrachion (lenascin C, cytotoxic)	1.30	1.25
	413474	T86312	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.30	1.92
	406659	AA663985	Hs.277477	major histocompatibility complex, class	1.30	2.22
	451049	AA013353		gb:ze28h10.s1 Soares retina N2b4HR Homo	1.30	2.12
	436494	AA720997	Hs.128295	ESTs	1.29	2.30
	438374	AA321866	Hs.6193	hypothetical protein FLJ14590	1.28	2.34
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	1.28	2.39
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.28	1.69
10	428458	AA428820	Hs.251399	neurogranin (protein kinase C substrate,	1.27	2.00
	443180	R15875	Hs.258576	claudin 12	1.26	1.25
	421764	AI681535	Hs.148135	serine/threonine kinase 33	1.26	2.01
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.26	1.21
	433283	BE041135	Hs.175622	ESTs	1.24	3.05
15	426759	AI590401	Hs.21213	ESTs	1.23	1.20
	436446	AW016809	Hs.119021	ESTs	1.23	1.20
	421467	AA291590	Hs.97252	ESTs	1.22	1.54
	431353	AA828032		ESTs	1.22	3.00
	427403	AA402107	Hs.257146	ESTs, Moderately similar to I38022 hypot	1.22	1.91
20	453037	AA045175	Hs.17914	ESTs	1.22	2.40
	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.22	2.26
	439941	AI392640	Hs.18272	amino acid transporter system A1	1.22	1.22
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	1.21	1.49
	400496			ENSP00000224716*:GTP-binding protein SAR	1.20	1.25
25	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	1.20	1.44
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.19	2.06
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.18	2.02
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2B (p1	1.17	1.14
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	1.14	1.16
	440555	D31292	Hs.6853	hypothetical protein FLJ22167	1.14	2.19
30	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.13	1.12
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.12	2.43
	432798	AA565309	Hs.194015	ESTs	1.10	2.23
	411274	NM_002776	Hs.69423	kallikrein 10	1.10	1.09
35	438856	N40027	Hs.7473	ESTs	1.09	1.52
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	1.09	1.07
	448253	H25899	Hs.201591	ESTs	1.08	2.10
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.08	2.08
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.06	1.58
40	449321	AA001150	Hs.132937	ESTs	1.06	2.06
	418693	AI750878	Hs.87409	thrombospondin 1	1.06	1.02
	402333			Target Exon	1.03	1.03
	421814	L12350	Hs.108623	thrombospondin 2	1.02	1.02
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	2.36
45	458158	AW296778	Hs.144734	Human DNA sequence from clone RP3-416F21	1.00	2.73
	406517			nel (chicken)-like 2	1.00	2.07
	442526	AW277221		ESTs	1.00	2.21
	446164	AW273539		hypothetical protein FLJ23577	1.00	2.52
	449122	AI631310	Hs.196955	ESTs	1.00	2.23
50	438038	AI732629		ESTs, Weakly similar to TA2R HUMAN, BETA	1.00	2.04
	429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	1.00	2.02
	453672	U73531	Hs.34526	G protein-coupled receptor	1.00	2.57
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	1.00	2.64
	438909	AF085839		gb:Homo sapiens full length insert cDNA	1.00	2.23
55	423609	AA328348	Hs.218289	ESTs	1.00	2.19
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	1.00	2.28
	436284	AA708016	Hs.190389	ESTs	1.00	2.22
	440932	AI801509	Hs.182080	ESTs	1.00	1.66
	403420			Target Exon	1.00	1.86
60	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	1.00	2.02
	425916	NM_006786	Hs.162200	urotensin 2	1.00	2.11
	419721	NM_001650		aquaporin 4	1.00	2.26
	421761	AL120297	Hs.108043	Friend leukemia virus integration 1	1.00	1.86
	425781	AF001622	Hs.159523	class-I MHC-restricted T cell associated	1.00	1.96
65	415094	D59513	Hs.330778	ESTs	1.00	2.32
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	2.26
	420727	H75701	Hs.99886	complement component 4-binding protein,	1.00	1.84
	430049	AW277085	Hs.99619	ESTs	1.00	1.87
	446868	AV660737		ESTs	1.00	1.79
70	418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	1.00	1.44
	436391	AJ227892	Hs.146274	ESTs	1.00	1.30
	413059	BE151498		gb:RCO-HT0295-291199-031-E11 HT0295 Homo	1.00	1.42
	427739	AW196755	Hs.98105	NYD-SP14 protein	1.00	2.41
	452788	AW294571	Hs.136040	ESTs	1.00	2.23

TABLE 32B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826

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		AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664
		H91240 R60548 N41701
		BI826340 BI868674 R12615 AW887767 BF439409 AI424995 BG059893 AA417003 AI220270 AA418740 AI190974 Z39070 AA742556 AA835058
		AA694436 R20520 AA418795 BG460307 BI560147
		AI990640 AI380016 BM273298 BM273060
		NM_007329 AF159456 AJ243212 AJ297935 AA295769 NM_017579 AJ243224 AI492875 AI796676 AI749838 AA918144 AI814590 AI923531
		BF513992 AI720725 AI150879 AI279072 AW612904 AI492104 AI284510 AI141231 AA613554 AW662148 AW769047 AA565985 AW612888
		AU100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569 T89953 BE934311
		BE088101 T05990 AW872477
		AI928355 AI709178 AA436447 AI431274 BF946000
		BE091833 BE091874 BE091871
		W92422 AA013353
		AW977507 AA503803 AA767137 AA828032 AA828033
		AA019761 AA017656 AA017374
		AF150283 AW182000 AW277221 AV735848
		AK026817 AI559708 AW273539 AW892986
		AI732629 AI732831 AA776249
		AF085839 R69254 R69137 AW188788
		AW971240 AA493723 AA493843
		AK026728 AL138136 BF059437 AI657037 AL600872 C15206 C14676 AA001003 AL157562 BG706081 H24162 BF841047 H15952 Z45355
		AL157565 AV721762 AW953127 AA324171 BF476417 R52508 N54211 R46734 BG485659 BF810747 BE766227 AL538364 R19964 T15657
		AW197333 R16235 R40826 BG152309 AV729035 R45066 AA016969 BE504976 BF593783 N51085 R61284 BE702264 AI216994 Z41068 N72577
		R37645 AW237014 AW197630 AI359402 AA707906 AL119885 H23480 T16037 AI950756 T62597 T91664 R40195 D60186 H23014 T89715 H05749
		H24054 AA001565 H15041 C15205 D59987 R13787 R61283 H23479 H07874 R14070 R52555 R21139 H05856 AA348655 AL120460 T62525
		AV725241 AA046875 AI361912 H13341 BG150438 AL119338 Z42792 F05895 H07966 F06492 R59866 D31594 H09436 R35726 BI917845
		BG704196 BF735198 AL036526 BG569879 AW195713 R59867 AA016968 H09087 BE841173 AW893631
		AK074473 BC017997 BI831060 BF971101 AI886394 AI082824 AV708785 W86073 W07772 AV660737 AI816793 R52250 BG183529 AA633473
		AI191256 R44763 R19947 BF571346 W86257
		BE063078 BE151503 BE151498

TABLE 32C:

65

Pkey:

Ref:

Strand:

Nt_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) [Nature](#) 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

70

Pkey

Ref

Strand

Nt_position

400880

9931121

Plus

29235-29336,36363-36580

402474

7547175

Minus

53526-53628,55755-55920,57530-57757

406387

9256180

Plus

116229-116371,117512-117651

404277

1834458

Minus

91665-91946

75

402674

8077108

Minus

39290-39502

404240

5002624

Minus

116132-116407,116653-116922

405102

8076881

Minus

120922-121296

406122

9144087

Minus

30940-31386

400750

8119067

Plus

198991-199168,199316-199548

80

404394

3135305

Minus

37121-37205,37491-37762,41053-41140,4132

403421

9665041

Minus

126609-126773,139986-140205

403903

7710671

Minus

101165-102597

404854

7143420

Plus

14260-14537

401854	7770538	Plus	151483-151637,151902-152008,152146-15231
406422	9256411	Plus	163003-163311
400496	9743564	Plus	41515-41695
402333	8844110	Minus	165693-165856
406517	7711431	Plus	7151-7402
403420	9664969	Plus	159835-159938

10 TABLE 33A: About 800 genes upregulated in lung fibrosis relative to normal lung

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of lung fibrosis Als divided by 90th percentile of normal lung Als, where the minimum value for the numerator and denominator was set to 50

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
20	406964	M21305		FGENES predicted novel secreted protein	16.10
	431089	BE041395		ESTs, Weakly similar to unknown protein	12.38
	421110	AJ250717	Hs.1355	cathepsin E	11.86
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	11.62
25	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.90
	444381	BE387335	Hs.283713	hypothetical protein BC014245	8.58
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	8.26
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	8.24
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.72
	408380	AF123050	Hs.44532	diubiquitin	7.24
30	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	7.15
	456034	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCI_CGAP_Su	7.12
	453355	AW295374	Hs.31412	myopodin	6.96
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88
35	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.83
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	6.72
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	6.72
	438089	W05391		nuclear receptor subfamily 1, group I, m	6.62
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56
40	421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	6.32
	439195	H89360		gb:yyw28d08.s1 Morton Fetal Cochlea Homo	6.29
	444301	AK000136	Hs.10760	asporin (LRR class 1)	6.28
	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	6.13
45	423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	6.11
	430702	U56979	Hs.278568	H factor 1 (complement)	6.10
	424878	H57111	Hs.221132	ESTs	6.00
	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	6.00
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	5.94
50	408491	AI088063	Hs.7882	ESTs	5.94
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	5.92
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	5.92
	407857	AI928445	Hs.92254	synaptotagmin-like 2	5.90
55	433230	AW136134	Hs.220277	ESTs	5.86
	412719	AW016610	Hs.816	ESTs	5.86
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.82
	426759	AI590401	Hs.21213	ESTs	5.72
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.72
	421814	L12350	Hs.108623	thrombospondin 2	5.71
60	430887	N66801	Hs.260287	KIAA1841 protein	5.70
	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	5.62
	436954	AA740151	Hs.130425	ESTs	5.58
	411573	AB029000	Hs.70823	KIAA1077 protein	5.55
	432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	5.38
65	410606	AW418779	Hs.114889	ESTs	5.38
	410800	BE280421	Hs.94499	ESTs	5.32
	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	5.28
	406687	M31126		matrix metalloproteinase 11 (stromelysin	5.26
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	5.22
70	412622	AW664708	Hs.171959	ESTs	5.22
	439941	AI392640	Hs.18272	amino acid transporter system A1	5.18
	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	5.15
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	5.13
	425177	AF127577	Hs.155017	nuclear receptor interacting protein 1	5.12
75	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	5.11
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04
	452239	AW379378		protein tyrosine phosphatase, receptor t	4.97
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	4.96
	443884	N20617	Hs.194397	leptin receptor	4.94
	444040	AF204231	Hs.182982	golgin-67	4.94
80	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	4.93
	440687	AL080222	Hs.7358	hypothetical protein FLJ13110	4.92
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	4.92
	432435	BE218886	Hs.282070	ESTs	4.92

	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	4.90
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	4.90
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.90
5	415992	C05837	Hs.145807	hypothetical protein FLJ13593	4.82
	430027	AB023197	Hs.227743	KIAA0980 protein	4.78
	408393	AW015318	Hs.23165	ESTs	4.76
	449509	AA001615	Hs.84561	ESTs	4.72
	416205	AW206248	Hs.111092	hypothetical protein FLJ22332	4.72
10	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	4.72
	433226	AW503733	Hs.9414	KIAA1488 protein	4.68
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	4.68
	442994	AI026718	Hs.16954	ESTs	4.66
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	4.66
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.66
15	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	4.65
	433586	T85301		gb:yd78d06.s1 Soares fetal liver spleen	4.64
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	4.64
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	4.64
20	418113	AI272141	Hs.83484	SRV (sex determining region Y)-box 4	4.62
	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	4.62
	450086	AW016343	Hs.233301	ESTs	4.61
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	4.60
	442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	4.59
25	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.58
	418259	AA215404		ESTs	4.54
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.54
	432810	AA863400		ESTs	4.54
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.53
30	436100	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	4.52
	412652	AI801777		ESTs	4.52
	438899	AF085833	Hs.135624	ESTs	4.52
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	4.52
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	4.52
35	443324	R44013	Hs.164225	ESTs	4.51
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	4.51
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.51
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	4.50
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	4.50
40	436865	AW880358	Hs.339808	hypothetical protein FLJ10120	4.46
	452561	AI692181	Hs.49169	KIAA1634 protein	4.46
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	4.45
	442048	AA974603		gb:op34f05.s1 Soares_NFL_T_GBC_S1 Homo s	4.44
	436120	AI248193	Hs.119860	ESTs	4.44
45	423575	C18863	Hs.163443	intron of periostin (OSF-2os)	4.44
	429697	AW296451	Hs.24605	ESTs	4.44
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	4.43
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	4.43
	414462	BE622743	Hs.301064	araplatin 1	4.42
50	428698	AA852773	Hs.334838	KIAA1866 protein	4.42
	420838	AW118210	Hs.42321	ESTs	4.41
	458584	AF217518	Hs.8360	PTD012 protein	4.40
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	4.40
	400076			Eos Control	4.38
55	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	4.38
	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (f	4.36
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.36
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.36
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.34
60	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	4.34
	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	4.33
	409342	AI077058	Hs.54089	BRCA1 associated RING domain 1	4.33
	429228	AI553633		ESTs	4.32
	426458	D83032	Hs.169984	nuclear protein	4.30
65	408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30
	432476	T94344	Hs.326263	ESTs	4.29
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.28
	436446	AW016809	Hs.119021	ESTs	4.27
	439556	AI623752	Hs.163603	ESTs	4.26
70	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-li	4.26
	428411	AW291464	Hs.10338	ESTs	4.26
	434936	AI285970	Hs.183817	ESTs	4.23
	413048	M93221	Hs.75182	mannose receptor, C type 1	4.23
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.22
75	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	4.22
	409977	AW805510	Hs.97056	hypothetical protein FLJ21634	4.22
	441297	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.21
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	4.20
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	4.20
80	423578	AW960454	Hs.222830	ESTs	4.20
	446608	N75217	Hs.257846	ESTs	4.20
	424238	AA337401	Hs.137635	ESTs	4.19
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	4.18
	420674	NM_000055	Hs.1327	butyrylcholinesterase	4.18

	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.18
	439593	BE073597	Hs.124863	ESTs	4.17
	442369	AI565071		ESTs	4.16
5	445885	AI734009	Hs.127699	KIAA1603 protein	4.16
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.16
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	4.16
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	4.15
	407347	AA829847		gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens	4.14
10	409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.13
	430168	AW968343	Hs.145582	DKFZP434I1735 protein	4.12
	451184	T87943		transcription factor 7-like 2 (T-cell sp	4.12
	426174	AA547959	Hs.115838	ESTs	4.12
	431562	AI884334	Hs.11637	ESTs	4.12
15	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.12
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.12
	449437	AI702038	Hs.100057	Homo sapiens cDNA: FLJ22902 f1s, clone K	4.12
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homolog	4.10
	444020	R92962	Hs.35052	ESTs	4.10
20	439424	AI478667	Hs.118183	hypothetical protein FLJ22833	4.10
	416987	D86957	Hs.80712	KIAA0202 protein	4.10
	457121	AI743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	4.09
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	4.09
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.08
25	431193	AW749505	Hs.296770	KIAA1719 protein	4.08
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	4.08
	433308	AA582718	Hs.291650	ESTs	4.08
	445756	AA290690	Hs.300776	ESTs	4.08
	431745	AW972448	Hs.163425	ESTs	4.08
30	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	4.07
	440099	AL080058	Hs.6909	DKFZP564G202 protein	4.06
	439398	AA284267	Hs.221504	ESTs	4.06
	432731	R31178	Hs.287820	fibronectin 1	4.06
	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	4.05
35	433626	AF078859	Hs.86347	hypothetical protein	4.05
	428055	AA420564	Hs.101760	ESTs	4.04
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04
	413243	AA769266	Hs.193657	ESTs	4.02
	431214	AA294921	Hs.348024	v-rat simian leukemia viral oncogene hom	4.02
40	453753	BE252983	Hs.35086	ubiquitin specific protease 1	4.02
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	4.02
	434404	AW445034	Hs.256578	ESTs	4.02
	407604	AW191962		collagen, type VIII, alpha 2	4.02
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	4.02
45	436772	AW975688		metallothionein 1E (functional)	4.00
	443257	AI334040	Hs.11614	HSPC065 protein	4.00
	450187	AA736788	Hs.78521	KIAA1717 protein	3.98
	433913	AI694106	Hs.72325	ESTs, Weakly similar to I38022 hypotheti	3.98
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	3.98
50	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	3.98
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 f1s, clone PL	3.98
	426818	AA554827	Hs.292996	DKFZp434A0131 protein	3.98
	440118	AB040893	Hs.6968	KIAA1460 protein	3.98
	413836	W92003	Hs.70614	ESTs	3.97
55	442647	AL038436	Hs.31388	ESTs	3.96
	449188	AW072939	Hs.347187	myotubularin related protein 1	3.96
	450656	AA010539	Hs.18912	ESTs	3.96
	410817	AI262789	Hs.93659	protein disulfide isomerase related prot	3.94
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.94
60	408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypotheti	3.94
	407879	AA045464	Hs.6557	zinc finger protein 161	3.93
	438146	Z36842	Hs.57548	ESTs	3.93
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.93
	429355	AW973253	Hs.292689	ESTs	3.92
65	437210	AA311443	Hs.293563	Homo sapiens mRNA; cDNA DKFZp586E2317 (f	3.92
	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	3.92
	452416	AA026115	Hs.114777	ESTs	3.92
	413873	AI310151	Hs.173524	ESTs	3.91
	400196			Eos Control	3.91
70	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.90
	453204	R10799	Hs.191990	ESTs	3.90
	454076	AW204712	Hs.61957	ESTs	3.90
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.90
	437158	AW090198		KIAA1150 protein	3.90
	443970	AI280341	Hs.166571	ESTs	3.90
75	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	3.90
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 f1s, clone PL	3.90
	444057	AA316896	Hs.257267	FYVE and coiled-coil domain containing 1	3.89
	411495	AP000693	Hs.70359	KIAA0136 protein	3.88
80	438452	AI220911	Hs.288959	hypothetical protein FLJ20920	3.88
	410297	AA148710		lumican	3.88
	427698	AW972594	Hs.335499	ESTs	3.88
	436769	AA748675		ESTs	3.86
	417819	AI253112	Hs.133540	ESTs	3.86

5	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ly	3.86
	425838	NM_014071	Hs.159613	nuclear receptor coactivator RAP250; per	3.86
	422173	BE385828	Hs.250619	phorbol-like protein MDS019 (CEM15)	3.86
	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109260A B cell	3.85
	445693	AW800444	Hs.76507	LPS-induced TNF-alpha factor	3.85
10	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	3.85
	412636	NM_004415		desmoplakin (DPI, DPII)	3.84
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	3.84
	418876	AA740616		gb:ny97f11.s1 NCL_CGAP_GCB1 Homo sapiens	3.84
	436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypotheti	3.84
15	430317	AB020645	Hs.239189	glutaminase	3.84
	442806	AW294522	Hs.149991	ESTs	3.84
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.82
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	3.82
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	3.82
20	430573	AA744550	Hs.136345	ESTs	3.82
	453394	AW960474	Hs.40289	ESTs	3.81
	431266	AW149321	Hs.105411	ESTs	3.80
	434987	AW975114		ESTs	3.80
	452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	3.79
25	435176	AA744875	Hs.189413	ESTs	3.78
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	3.77
	430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo	3.77
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.76
	441989	AA306207	Hs.286241	protein kinase, cAMP-dependent, regulato	3.76
30	417228	AL134324	Hs.7312	ESTs	3.76
	418546	AA224827		gb:nc32g04.s1 NCL_CGAP_Pr2 Homo sapiens	3.76
	450779	AW204145	Hs.156044	ESTs	3.75
	412408	D51103	Hs.73851	ATP synthase, H transporting, mitochondr	3.75
	443879	Z28462	Hs.9927	Homo sapiens mRNA; cDNA DKFZp564D156 (fr	3.75
35	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.75
	429494	AA769365	Hs.126058	ESTs	3.75
	447118	AB014599	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro	3.75
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	3.74
	419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	3.74
40	448121	AL045714	Hs.128653	hypothetical protein DKFZp564F013	3.74
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.73
	414883	AA926960		CDC28 protein kinase 1	3.72
	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.72
45	452250	BE618654	Hs.28607	hypothetical protein A-211C6.1	3.72
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	3.72
	438607	AW080237	Hs.252884	ESTs	3.72
	408221	AA912183	Hs.47447	ESTs	3.72
	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.70
50	419900	AI469960	Hs.170698	ESTs	3.70
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	3.70
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	3.70
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.70
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	3.70
55	447846	AA324057	Hs.77955	Homo sapiens cDNA: FLJ23527 fis, clone L	3.70
	436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	3.70
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.69
	408495	W68796	Hs.237731	ESTs	3.69
	424452	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypotheti	3.68
60	448479	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphorylas	3.68
	431974	AW972689	Hs.200934	ESTs	3.68
	416354	NM_000633	Hs.79241	B-cell CLL/lymphoma 2 (BCL2)	3.68
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	3.68
	413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	3.67
65	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	3.67
	419111	AA234172	Hs.137418	ESTs	3.67
	423979	AF229181	Hs.136644	CS box-containing WD protein	3.66
	418875	W19971	Hs.233459	ESTs	3.66
	451690	AW451469	Hs.209990	ESTs	3.66
70	423032	AI684746	Hs.119274	RAS p21 protein activator (GTPase activa	3.66
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.66
	428347	AI264161	Hs.183773	golgi autoantigen, golgin subfamily a, 4	3.66
	426779	AA384577	Hs.93714	ESTs, Weakly similar to T00365 hypotheti	3.66
	435335	AI693150	Hs.137928	ESTs	3.66
75	410577	X91911	Hs.64639	glioma pathogenesis-related protein	3.66
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	3.65
	429105	D87077	Hs.196275	KIAA0240 protein	3.64
	407813	AL120247	Hs.40109	KIAA0872 protein	3.64
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	3.64
80	451678	AA374181	Hs.26799	DKFZP564D0764 protein	3.64
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.64
	452408	AA306477	Hs.29379	hypothetical protein FLJ10687	3.64
	441466	AW673081	Hs.54828	ESTs	3.63
	414013	AA766605	Hs.47099	hypothetical protein FLJ21212	3.62
	420056	AW043684	Hs.99804	ESTs	3.62
	424886	H88584	Hs.96900	hypothetical protein; KIAA1830 protein	3.62
	431774	BE348813	Hs.268561	hypothetical protein FLJ10726	3.62

	435990	AI015862	Hs.131793	ESTs	3.62
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	3.62
	414715	AA587891	Hs.904	amylase-1,6-glucosidase, 4-alpha-glucanot	3.62
5	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	3.62
	417008	AA191708	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	3.62
	413823	AI341417	Hs.29406	ESTs	3.61
	435354	AA678267	Hs.117115	ESTs	3.60
	427832	AF038362	Hs.180930	TBP-associated factor 172	3.60
10	427846	AW499770	Hs.180948	KIAA0729 protein	3.60
	426116	AA868729	Hs.144694	ESTs	3.60
	457635	AV660976	Hs.3569	hypothetical protein	3.60
	443998	AI620661	Hs.296276	ESTs	3.60
	417867	AW952547	Hs.194603	ESTs, Moderately similar to I38022 hypot	3.58
	418182	AW016405	Hs.16648	ESTs	3.58
15	434941	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	3.58
	424831	H61453		ESTs	3.58
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.58
	421823	N40850	Hs.28625	ESTs	3.58
20	414781	D50917	Hs.77293	KIAA0127 gene product	3.57
	427393	AB029018	Hs.177635	KIAA1095 protein	3.57
	415664	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.56
	425465	L18964	Hs.1904	protein kinase C, iota	3.56
	417124	BE122762	Hs.25338	ESTs	3.56
25	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	3.56
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	3.55
	421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	3.55
	410390	AA876905	Hs.125286	ESTs	3.54
	442073	AW973443	Hs.8086	RNA (guanine-7-) methyltransferase	3.54
30	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	3.54
	441499	AW298235	Hs.101689	ESTs	3.54
	453256	AI565587	Hs.32556	KIAA0379 protein	3.54
	414142	AW368397	Hs.334485	hemiscentin (fibulin 6)	3.54
	438023	AF204883	Hs.6048	FEM-1 (C.elegans) homolog b	3.54
35	412245	AI952669	Hs.22893	ESTs, Weakly similar to I38022 hypothe	3.54
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.53
	446682	AW205632	Hs.211198	ESTs	3.52
	431392	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	3.52
	433430	AI863735		ESTs	3.52
40	420394	AB023161	Hs.97403	KIAA0944 protein	3.52
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.52
	443547	AW271273		hypothetical protein FLJ12666	3.52
	420676	AI434780	Hs.4248	vav 2 oncogene	3.51
	410690	AA322979	Hs.130266	ESTs	3.50
45	459645	AA074346		ESTs	3.50
	401403			Target Exon	3.50
	451166	T98171	Hs.185675	ESTs	3.50
	418836	AI655499	Hs.161712	ESTs	3.50
	421462	AF016495	Hs.104624	aquaporin 9	3.50
50	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	3.50
	432401	NM_013330	Hs.274479	NME7	3.49
	408392	U28831	Hs.44566	KIAA1641 protein	3.49
	425836	AW955696	Hs.90960	ESTs	3.48
	452327	AK000196	Hs.29052	hypothetical protein FLJ20189	3.48
55	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.48
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	3.48
	422960	AW890487		cadherin 13, H-cadherin (heart)	3.48
	430570	AI417881	Hs.292464	ESTs	3.48
	406387			Target Exon	3.47
60	416585	X54162	Hs.79386	leiomodulin 1, smooth muscle (LMOD1) (Thy	3.46
	432340	AA534222		gb:nj21d02.s1 NCL_CGAP_AA1 Homo sapiens	3.46
	412240	H72176		hypothetical protein FLJ13159	3.46
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.46
	443634	H73972	Hs.134460	ESTs	3.46
65	422963	M79141	Hs.13234	ESTs	3.46
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	3.46
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	3.46
	425100	AF051850	Hs.154567	supervillin	3.45
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.45
70	444250	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	3.44
	428386	R17298	Hs.295923	seven in absentia (Drosophila) homolog 1	3.44
	447764	NM_003776	Hs.19500	nuclear localization signal deleted in v	3.44
	411251	R19774	Hs.22835	HHGP protein	3.44
	432648	AA557952		gb:n17c05.s1 NCL_CGAP_HSC1 Homo sapiens	3.44
75	428708	NM_014897	Hs.190386	KIAA0924 protein	3.44
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	3.43
	451743	AW074266	Hs.23071	ESTs	3.42
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	3.42
	448705	H05072	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	3.42
80	414489	AI620677	Hs.73105	ESTs	3.42
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.41
	435841	R28522	Hs.186937	ESTs	3.41
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	3.40
	451198	AW964541		hypothetical protein FLJ21127	3.40

	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	3.40
	436023	T81819	Hs.302251	ESTs	3.40
	449656	AA002008	Hs.188633	ESTs	3.40
5	437739	AW579216	Hs.264610	ESTs, Moderately similar to Ibd1 [H.sapi	3.40
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	3.40
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	3.40
	456505	AA504595		ESTs	3.40
	439867	AA847510	Hs.161292	ESTs	3.40
10	442113	BE622187		ESTs, Weakly similar to I38022 hypotheti	3.40
	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (f	3.40
	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	3.40
	421263	AB020638	Hs.103000	KIAA0831 protein	3.40
	410300	AW903988	Hs.62119	hypothetical protein FLJ14800	3.39
15	440028	AW473675		ESTs, Weakly similar to T17227 hypotheti	3.39
	454070	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	3.38
	432572	AI660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN !!!!	3.38
	442426	AI373062	Hs.332938	hypothetical protein MGC5370	3.38
	428412	AA428240	Hs.126083	ESTs	3.38
20	448772	AW390822	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.38
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.38
	413714	AI560944	Hs.71428	ESTs	3.38
	415663	AW296841	Hs.313332	ESTs	3.38
	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	3.37
25	421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.37
	440214	AA247118	Hs.7049	hypothetical protein FLJ11305	3.37
	440980	AL042005	Hs.1117	tripeptidyl peptidase II	3.36
	411975	AI916058	Hs.144583	ESTs	3.36
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	3.36
30	414783	AW069569		inactive progesterone receptor, 23 kD	3.36
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.36
	411213	AA676939	Hs.69285	neuropilin 1	3.36
	420613	AI873871	Hs.7041	ESTs, Weakly similar to A47582 B-cell gr	3.35
35	417534	NM_004998	Hs.82251	myosin IE	3.35
	431698	AI92369		ESTs	3.35
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.35
	441623	AA315805		desmoglein 2	3.34
	420729	AW964897	Hs.290825	ESTs	3.34
40	440010	AA534930	Hs.127236	hypothetical protein FLJ12879	3.34
	448369	AW268962	Hs.111335	ESTs	3.34
	452820	N46161	Hs.35274	ESTs	3.34
	453271	AA903424	Hs.6786	ESTs	3.34
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.34
45	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.34
	443291	AA325633	Hs.136102	KIAA0853 protein	3.33
	418720	AI381687	Hs.39526	ESTs	3.33
	452107	AB020681	Hs.27973	KIAA0874 protein	3.33
	439943	AW083789	Hs.124620	ESTs	3.33
50	433282	BE539101		hypothetical protein	3.33
	410344	AW978436	Hs.62515	KIAA0494 gene product	3.33
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	3.32
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.32
	434210	AA665612		ESTs	3.32
55	431923	AI741770	Hs.292690	ESTs, Weakly similar to I38022 hypotheti	3.32
	453199	AI336266	Hs.32353	mitogen-activated protein kinase kinase	3.32
	419534	AA443691	Hs.90858	Homo sapiens clone 25023 mRNA sequence	3.32
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	3.32
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	3.32
60	422092	AB007883	Hs.111373	KIAA0423 protein	3.32
	412262	W26406		seven in absentia (Drosophila) homolog 1	3.32
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.32
	446094	AK001760	Hs.13801	KIAA1685 protein	3.32
	446493	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.32
65	420339	AW968259	Hs.186647	ESTs	3.31
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.31
	432331	W37862	Hs.274368	MSTP032 protein	3.31
	433697	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.31
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	3.31
70	430950	AA489525		ESTs	3.30
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	3.30
	417958	AA767382	Hs.193417	ESTs	3.30
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.30
	419543	AA244170		gb:nc05h02.s1 NCL CGAP_Pr1 Homo sapiens	3.30
75	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30
	452039	AI922988	Hs.172510	ESTs	3.30
	443798	R07848	Hs.188522	ESTs	3.29
	449378	AW664026	Hs.59892	ESTs	3.29
	455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	3.28
80	420126	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	3.28
	444291	AI598022	Hs.193989	TAR DNA binding protein	3.28
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	3.28
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	3.28
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28

	425657	T89839	Hs.119471	ESTs	3.28
	406672	M26041	Hs.198253	major histocompatibility complex, class	3.28
	419905	AW248229	Hs.93659	protein disulfide isomerase related prot	3.27
5	425332	AA633306	Hs.127279	ESTs	3.27
	418529	AW005695	Hs.250897	TRK-fused gene	3.27
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.27
	433618	AA602539	Hs.345494	ESTs	3.27
	408630	AA748009	Hs.173328	ESTs	3.26
10	415914	AA306033	Hs.78915	GA-binding protein transcription factor,	3.26
	415102	M31899	Hs.77929	excision repair cross-complementing rode	3.26
	432626	AA471098	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	3.26
	429493	AL134708	Hs.145998	ESTs	3.26
	445860	AA332145	Hs.13392	lethering factor SEC34	3.26
15	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	3.26
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.26
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	3.26
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	3.26
	436758	AW977167	Hs.155272	ESTs	3.26
20	438011	BE466173	Hs.145696	splicing factor (CC1.3)	3.26
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	3.25
	426860	U04953	Hs.172801	isoleucine-tRNA synthetase	3.25
	437830	AB020658	Hs.5867	KIAA0851 protein; suppressor of actin 1	3.25
	453368	W20296	Hs.288178	Homo sapiens cDNA FLJ11968 fis, clone HE	3.25
25	409939	AA463437	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	3.25
	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	3.24
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	3.24
	418283	S79895	Hs.83942	cathepsin K (pseudosostosis)	3.24
	414405	AI362533		KIAA0306 protein	3.24
30	445893	AI610702	Hs.202613	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.24
	434423	NM_006769	Hs.3844	LIM domain only 4	3.24
	408951	AW407227	Hs.227591	hypothetical protein FLJ11088	3.24
	408949	AF189011	Hs.49163	putative ribonuclease III	3.24
	410337	M83822	Hs.62354	cell division cycle 4-like	3.24
35	409010	AI648675		Homo sapiens, Similar to RIKEN cDNA 1700	3.24
	400419	AF084545		Target	3.24
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	3.24
	422461	NM_003417	Hs.117077	zinc finger protein 264	3.24
	441604	AI683049	Hs.201282	ESTs	3.24
40	411960	R77776	Hs.18103	ESTs	3.23
	414895	AW894856	Hs.116278	Homo sapiens cDNA FLJ13571 fis, clone PL	3.23
	430522	N75750	Hs.242271	KIAA0471 gene product	3.23
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	3.23
	405268			ENSP00000223174*:KIAA0783 PROTEIN.	3.23
45	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.22
	427196	AW967522	Hs.191593	ESTs	3.22
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	3.22
	417727	AL133623	Hs.82501	similar to mouse Xrn1 / Dhnm2 protein	3.22
	410853	H04588	Hs.30469	ESTs	3.22
50	411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	3.22
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22
	427480	BE148769	Hs.334477	hypothetical protein FLJ11328	3.22
	444623	AI183829	Hs.202111	ESTs	3.21
55	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	3.21
	435874	AA868688	Hs.93102	ESTs	3.20
	443801	AW206942	Hs.253594	intron of: trichorhinophalangeal syndro	3.20
	434982	AW975084		gb:EST387190 MAGE resequences, MAGN Homo	3.20
	430929	AA489166	Hs.156933	ESTs	3.20
60	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	3.20
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	3.20
	422109	S73265	Hs.1473	gastrin-releasing peptide	3.20
	451119	AA805417	Hs.64753	ESTs	3.20
	414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	3.20
65	432676	AI187366		gb:qf29c01.x1 Soares_testis_NHT Homo sap	3.19
	428820	AA436187	Hs.172631	integrin, alpha M (complement component	3.19
	422040	AA172106	Hs.110950	Rag C protein	3.18
	437838	AI307229		ESTs	3.18
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.18
70	420789	AI670057	Hs.199882	ESTs	3.18
	419135	R61448	Hs.106728	ESTs, Weakly similar to KIAA1353 protein	3.18
	446019	AI362520		histone deacetylase 3	3.18
	430848	AW021726	Hs.345490	gb:df27e02.y1 Morton Fetal Cochlea Homo	3.18
	425375	AA631977	Hs.155995	KIAA0643 protein	3.18
75	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.18
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18
	453111	AB014598	Hs.31720	hephaestin	3.18
	454042	H22570		hypothetical protein FLJ20093	3.18
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.18
80	447183	AI554733	Hs.173182	ESTs	3.18
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	3.18
	431831	AW023204	Hs.302743	ESTs	3.18
	420664	AI681270	Hs.99824	BCE-1 protein	3.18
	451582	AI963026	Hs.289958	ESTs, Weakly similar to putative p150 [H	3.17

	432954	AI076345		ESTs	3.17
	444990	AI912410	Hs.27475	Homo sapiens cDNA FLJ12749 fis, clone NT	3.17
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	3.17
5	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.17
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.17
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.16
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.16
	420623	BE245485	Hs.99437	Homo sapiens mRNA; cDNA DKFZp586G1924 (f	3.16
10	451475	T19093	Hs.26450	KIAA0725 protein	3.16
	452066	AA772149	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p	3.16
	429556	AW139399	Hs.98988	ESTs	3.16
	448514	AB020626	Hs.301866	KIAA0819 protein	3.16
	443732	AI188803	Hs.153944	ESTs	3.16
15	436805	AA731533	Hs.270751	ESTs	3.16
	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	3.16
	417511	AL049176	Hs.82223	chordin-like	3.16
	423595	R82826	Hs.220702	ESTs	3.16
	445837	AI261700	Hs.145544	ESTs	3.16
20	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	3.16
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.16
	414183	AW957446	Hs.301711	ESTs	3.16
	433194	AB040883	Hs.83243	KIAA1450 protein	3.16
	453915	AA588721	Hs.286218	ribosomal protein L44	3.15
25	407725	BE388094	Hs.21857	ESTs	3.15
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.14
	440937	AF202724	Hs.7531	KIAA0810 protein	3.14
	449057	AB037784	Hs.22941	KIAA1363 protein	3.14
	446126	AW085909		pleckstrin homology domain interacting p	3.14
30	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.14
	419145	N99638		gb:za39g11.r1 Soares fetal liver spleen	3.14
	418757	AI864193	Hs.169728	hypothetical protein FLJ13150	3.14
	430000	AW205931	Hs.99598	hypothetical protein MGC5338	3.14
	437296	AA350994	Hs.20281	KIAA1700	3.14
35	441381	H22195	Hs.31874	ESTs	3.14
	457250	AA811987	Hs.125779	ESTs	3.14
	422900	AA641201	Hs.222051	ESTs	3.14
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.14
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.14
40	419355	AA428520	Hs.90061	progesterone binding protein	3.14
	409509	AL036923	Hs.322710	ESTs	3.14
	417308	H60720	Hs.81892	KIAA0101 gene product	3.14
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	3.14
	429160	AW663083	Hs.144469	ESTs	3.14
45	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.14
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (U	3.14
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	3.14
	451518	AW340925	Hs.174918	ESTs	3.14
	435702	AI033647	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3.13
50	439208	AK000299	Hs.180952	dynactin 4 (p62)	3.13
	451838	AW005866	Hs.193969	ESTs	3.13
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zip	3.13
	446945	AI193115	Hs.16611	tumor protein D52-like 1	3.13
	453920	AI133148	Hs.36602	I factor (complement)	3.13
55	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.13
	417105	X60992	Hs.81226	CD6 antigen	3.12
	433854	AA610649	Hs.333239	ESTs	3.12
	408089	H59799	Hs.42644	thioredoxin-like	3.12
	453686	AL110326	Hs.304679	ESTs, Moderately similar to Z195_HUMAN Z	3.12
60	426167	AF039023	Hs.167496	RAN binding protein 6	3.12
	452195	AA994712	Hs.116878	ESTs	3.12
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	3.12
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12
	424001	W67883	Hs.137476	paternally expressed 10	3.12
65	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.12
	433401	AF039698	Hs.284217	serologically defined colon cancer antig	3.12
	409245	AA361037		tRNA isopentenylpyrophosphate transferas	3.12
	414290	AI568801	Hs.71721	ESTs	3.12
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	3.12
70	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	3.11
	448873	NM_003677	Hs.22393	density-regulated protein	3.11
	428471	X57348	Hs.184510	stratiffin	3.11
	436288	AI361722	Hs.192410	ESTs	3.10
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.10
75	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	3.10
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.10
	412340	AA101809	Hs.182685	ESTs	3.10
	438716	AA814903	Hs.155113	ESTs	3.10
	419440	AB020689	Hs.90419	KIAA0882 protein	3.10
80	433017	Y15067	Hs.279914	zinc finger protein 232	3.10
	428513	BE220806	Hs.184697	plexin C1	3.10
	437866	AA156781		metallothionein 1E (functional)	3.10
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	3.10
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10

	435445	AA737345	Hs.294041	ESTs	3.10
	420997	AK001214	Hs.100914	hypothetical protein FLJ10352	3.09
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	3.09
5	406122			Target Exon	3.09
	435272	AA906415	Hs.110041	ESTs	3.09
	410726	AI623859	Hs.15936	ESTs	3.09
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.08
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.08
10	417538	AW050865	Hs.275711	hypothetical protein MGC2452	3.08
	434938	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	3.08
	434733	AI334367	Hs.159337	ESTs	3.08
	434421	AI915927	Hs.34771	ESTs	3.08
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08
15	424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	3.08
	458332	AI000341		ESTs	3.08
	445034	AW293376	Hs.143659	ESTs	3.08
	446570	AV659177	Hs.127160	ESTs	3.08
	429920	AW473208	Hs.115572	ESTs, Weakly similar to I38022 hypotheti	3.08
20	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	3.06
	419038	AW134924	Hs.190325	ESTs	3.06
	451079	AI827988	Hs.240728	ESTs, Moderately similar to PC4259 ferri	3.06
	417386	AL037228	Hs.82043	D123 gene product	3.06
	453108	AI311457	Hs.99472	ESTs	3.06
25	449328	AI962493		ESTs	3.06
	428656	AB037798	Hs.188790	KIAA1377 protein	3.06
	425509	AF079363	Hs.158213	sperm associated antigen 6	3.06
	447957	NM_014821	Hs.20126	KIAA0317 gene product	3.06
	417226	AW505054	Hs.4283	ESTs	3.05
30	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	3.05
	426279	AI648520	Hs.169084	tubby like protein 3	3.05
	433814	AA609738	Hs.16525	ESTs	3.05
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	3.05
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	3.04
35	441789	D52059	Hs.7972	KIAA0871 protein	3.04
	456437	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.04
	438771	NM_016289	Hs.6406	MO25 protein	3.04
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	3.04
	416240	NM_001981	Hs.79095	epidermal growth factor receptor pathway	3.04
40	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	3.04
	424776	AI867931	Hs.164595	ESTs	3.03
	408409	AW838181	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.03
	429693	BE254962	Hs.211612	SEC24 (S. cerevisiae) related gene famil	3.03
	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	3.03
45	431625	AW750627	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	3.03
	451144	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	3.02
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.02
	408683	R58665	Hs.46847	TRAF and TNF receptor-associated protein	3.02
	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (3.02
50	440603	AL121733	Hs.7299	Novel human gene mapping to chromosome 1	3.02
	415443	T07353	Hs.7948	ESTs	3.02
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02
	406685	M18728		gb:Human nonspecific crossreacting antig	3.02
	446013	AI360167	Hs.152774	ESTs	3.02
55	433902	AW292820	Hs.144906	ESTs	3.02
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.02
	432505	AW274526	Hs.277721	KIAA0049	3.01
	440040	BE219431	Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.01
	433255	AI274270	Hs.96840	KIAA1527 protein	3.01
60	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.01
	417258	N58885		gb:yy60a09.s1 Soares_multiple_sclerosis_	3.00
	435800	AI248285	Hs.118348	ESTs	3.00
	444838	AV651680	Hs.208558	ESTs	3.00
	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	3.00
65	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	3.00
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.00
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	3.00
	410434	AF051152	Hs.63668	toll-like receptor 2	3.00
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00
70	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.98
	450247	AF123303	Hs.24713	hypothetical protein	2.98
	417865	AW086059	Hs.6529	ESTs, Weakly similar to I78885 serine/th	2.98
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.98
	438543	AA810141	Hs.192182	ESTs	2.98
75	415503	U36601	Hs.78473	N-deacetylase/N-sulfotransferase (hepara	2.98
	429138	AB020657	Hs.197298	NS1-binding protein	2.98
	447881	BE620886		GCN1 (general control of amino-acid synt	2.96
	425481	AW978162		ESTs	2.96
	453315	BE544203	Hs.24831	ESTs	2.96
80	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	2.95
	433208	AW002834	Hs.24095	ESTs	2.95
	442495	AI184717		ESTs	2.94
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.94
	408170	AW204516	Hs.31835	ESTs	2.94

5	430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypot	2.94
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94
	407361	AA744622	Hs.292645	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.94
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.93
	436005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 fis, clone OV	2.93
	449458	AI805078	Hs.208261	ESTs	2.93
	449317	AW293413	Hs.132906	19A24 protein	2.92
	411118	N27944	Hs.221476	ESTs, Weakly similar to AF108460 1 ubinu	2.92
10	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	2.91
	416311	D80529		gb:HUM081H05B Human fetal brain (TFujiwa	2.91
	433068	NM_006456	Hs.288215	sialyltransferase	2.90
	429272	W25140	Hs.110667	ESTs	2.90
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	2.90
15	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.88
	426782	R14614	Hs.33846	ESTs	2.88
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	2.88
	413882	AA132973	Hs.184492	ESTs	2.88
	421554	AW137676	Hs.97775	ESTs	2.88
20	446488	AB037782	Hs.15119	KIAA1361 protein	2.84
	421391	AW304350	Hs.191958	immunoglobulin superfamily receptor tran	2.84
	424527	AW138558	Hs.334873	ESTs, Weakly similar to I54374 gene NF2	2.82
	419284	AW820869	Hs.215658	ESTs, Moderately similar to ZN91_HUMAN Z	2.82
	415788	AW628686	Hs.78851	KIAA0217 protein	2.82
25	448481	W15284	Hs.74832	ESTs	2.82
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.80
	443441	AW291196	Hs.92195	ESTs	2.80
	422725	AA315703	Hs.199993	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.80
	431926	AW972724		gb:EST384816 MAGE resequences, MAGL Homo	2.80
30	420406	AA741024	Hs.88378	ESTs	2.79
	437678	AA829860	Hs.122834	ESTs	2.78
	440115	R41808	Hs.144924	ESTs, Weakly similar to B Chain B, Solut	2.78
	439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	2.78
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.77
35	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.76
	435154	AA668764		ESTs	2.76
	432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.75
	442703	AL044949	Hs.116298	ESTs	2.74
40	419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.74
	435861	AF254956	Hs.16608	candidate tumor suppressor protein	2.72
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.70
	438441	AW664960	Hs.205319	ESTs	2.70
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.67
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.66
45	416239	AL038450	Hs.48948	ESTs	2.62
	434792	AA649253	Hs.132458	ESTs	2.60
	424852	AI222779	Hs.144848	ESTs	2.58
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.57
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	2.56
50	450571	AF158240	Hs.60397	ESTs	2.56
	442435	AI986208	Hs.244760	ESTs, Highly similar to B34087 hypotheti	2.56
	424148	BE242274	Hs.1741	integrin, beta 7	2.56
	445784	AI253155	Hs.146065	ESTs	2.53
	408072	BE005566	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	2.52
55	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.52
	450295	AI766732	Hs.210628	ESTs	2.48
	440381	AA917808	Hs.190495	ESTs	2.46
	433923	AI823453	Hs.146625	ESTs	2.44
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44
60	429670	L01087	Hs.211593	protein kinase C, theta	2.44
	437908	AI082424		ESTs	2.43
	438676	AA813745	Hs.123446	ESTs	2.37
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28
	444969	AI203334	Hs.160628	ESTs	2.28
65	446423	AW139655	Hs.150120	ESTs	2.27
	435517	AA928626	Hs.130177	ESTs	2.27
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.00
	429073	AA446167	Hs.47385	ESTs	1.98
70	433834	AA620742	Hs.130786	ESTs	1.72
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	1.52
	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigen	1.30
	402550			Target Exon	1.09
75	TABLE 33B:				
	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
80	Pkey	CAT Number	Accession		
	431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826		
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	407192	2200202_1	AA602964 AA609200		

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409245	3199_2	AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857
30		AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R66856 H01374 BI257369 BI259630
		AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024
		BF093291 AW021929 H22650 AA459715 BG496341 BE697763 BI254209 BG499543 H42946 BI059780 BI086741 H87896 H87599 BF691752
		BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF909744 AW966003 AV714014 BI492868 BI495144 AA921845
35		AI693426 AI652147 AI435449 N47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897
		AW665247 AW340077 N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AI080245
		AA884954 AI125702 AI382934 AA931835 AI358631 AW439905 AI027833 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI768667
		AA948472 AI819214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AI492769 D56771 AA095911 BE222062
		D56772 AW372265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI492848
40	437866	HI6217 H21980 H22651 H88179 H87354 H44052 H25165 H44128
	34267_1	U52054 AL581000 AA158850 AW293839 BI335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161
		BM194134 AW966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF446960
		AA837481 AV755539 AW468444 AW468002 AA811830 AA581806 AI866686 AI572124 AA687333 D20160 AA812489 AU185248 AU186004
		AA156781 AI536733 BM144850 AI471883 AA040926 BF507639 AA043777 AW874142 BE832523 BE163972 BI022546 BI021204
45	458332	AI000341 AI766341 AW873274
	1139685_1	AV704062 BE162284 AI032946 BF360636
	417837_1	AI884781 AI652306 AI651694 AI638744 AI962493
	3030726_1	M18728
	406685	BG116781 BI914326 BI030196 N58885 N63406 AV683374 N58892 BG110501 AA333708 AA359583 AW963123 N95562 N95696 N95587
	0_0	AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261
	417258	AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119
50	447881	AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805
	44623_1	AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723
		BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
55	425481	AL520496 AW978162 AI610475 AI688890 AW470054 AA609426 AI167391 AA815231 AA358241
	334120_2	BG009500 AI376551 AA897445 T87714
	371165_1	AI184717 AW518883 AF121173
	442495	AA179446 AA357794 D81719 D80529 C14833
	928718_1	AW972724 AA877998 AA522631 AU185388
	416311	AW972063 AA668764 AA804491 AW665688 AA765069
	1280744_1	AI740586 AA771806 BE500996 AW204531 AI082424 AI033879 BF093176 AA771764 D38676
	431926	
	1237041_1	
	435154	
60	437908	
	126605_1	
	13268_11	

TABLE 33C:

65

Pkey:Unique number corresponding to an Eos probeset

Ref:Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) [Nature](#) 402:489-495.

Strand:Indicates DNA strand from which exons were predicted.

Nt_position:Indicates nucleotide positions of predicted exons.

70

Pkey	Ref	Strand	Nt_position
401403	7710966	Plus	146180-146294
406387	9256180	Plus	116229-116371,117512-117651
405268	4156151	Minus	24404-24521
406122	9144087	Minus	30940-31386
402550	7652009	Minus	80413-80673

75

80 TABLE 34A: About 703 genes upregulated in idiopathic pulmonary fibrosis relative to hypersensitivity pneumonitis or non-specific interstitial pneumonitis

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number
Unigene Title: Unigene gene title

R1: 90th percentile of IPF AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50

R2: 90th percentile of IPF AIs divided by 90th percentile of NSIP AIs, where the minimum value for the numerator and denominator was set to 50

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
5	405443			Target Exon	9.66	7.50
10	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.23	3.66
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.63	3.03
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	4.84	2.81
	406964	M21305		FGENES predicted novel secreted protein	4.73	5.69
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.34	4.34
15	407244	M10014		fibrinogen, gamma polypeptide	4.14	5.88
	421823	N40850	Hs.28625	ESTs	4.12	1.80
	419875	AA853410	Hs.93557	proenkephalin	3.90	2.01
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.88	2.90
	418310	AA814100	Hs.86693	ESTs	3.66	2.84
20	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	3.60	3.13
	438315	R56795	Hs.82419	ESTs	3.49	3.70
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.47	1.38
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	3.46	3.46
	434233	AF119903	Hs.138453	hypothetical protein PRO2834	3.28	2.51
25	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	3.26	3.26
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	3.19	2.12
	420185	AL044056	Hs.251385	ESTs	3.18	3.01
	420195	N44348		Homo sapiens cDNA FLJ11177 fis, clone PL	3.16	3.16
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	3.08	3.18
30	408221	AA912183	Hs.47447	ESTs	3.07	1.98
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.02	2.36
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.98	1.72
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.87	1.48
	422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (f	2.80	2.66
35	445745	AB007924	Hs.13245	KIAA0455 gene product	2.78	1.65
	407938	AA905097	Hs.85050	phospholamban	2.78	2.46
	423575	C18863	Hs.163443	intron of periostin (OSF-2os)	2.78	1.55
	446659	AI335361	Hs.226376	ESTs	2.74	1.56
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	2.74	1.85
40	437620	AW976930		ESTs	2.72	2.72
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.67	2.05
	416585	X54162	Hs.79386	leiomodulin 1, smooth muscle (LMOD1) (Thy	2.66	1.47
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.66	2.66
	430712	AW044647		ESTs	2.62	2.62
45	453111	AB014598	Hs.31720	hephaestin	2.61	1.72
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.59	1.27
	414290	AI568801	Hs.71721	ESTs	2.59	1.23
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.58	2.58
	412639	AW961284	Hs.203838	ESTs	2.58	2.29
50	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.57	1.74
	429757	AW452355	Hs.256037	ESTs	2.57	1.60
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57	1.00
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.56	1.12
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.56	1.25
55	411880	AW872477		gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens	2.54	2.54
	401645			C16001440:gil12330704[gb]AAG52890.1[AF3	2.53	3.38
	401673			C16001416:gil12743112[ref]XP_010131.2]	2.47	2.83
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.46	1.18
	416316	H58721	Hs.271628	ESTs	2.42	3.44
60	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.40	1.69
	451149	AL047586		RNA binding motif protein 8B	2.40	1.95
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.40	1.61
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	2.40	2.40
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.39	1.27
65	405120			C4001445:gil12697999[dbj]BAB21818.1[AB	2.38	2.38
	432224	AW189460	Hs.208358	ESTs	2.38	2.00
	418663	AK001100	Hs.41690	desmocollin 3	2.38	2.38
	412622	AW664708	Hs.171959	ESTs	2.37	1.63
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.37	1.52
70	442767	AI017208	Hs.131149	ESTs	2.36	1.22
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.35	1.79
	411800	N39342	Hs.103042	microtubule-associated protein 1B	2.35	1.18
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.34	2.34
	444009	AI380792	Hs.135104	ESTs	2.34	2.07
	435143	R12375	Hs.194600	ESTs	2.33	1.68
75	402333			Target Exon	2.33	3.15
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.33	1.10
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.32	1.30
	452242	R50956	Hs.159993	glycosyltransferase	2.32	1.45
	418693	AI750878	Hs.87409	thrombospondin 1	2.32	2.32
80	428411	AW291464	Hs.10338	ESTs	2.32	1.54
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.31	1.98
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.31	2.49
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.31	1.32

5	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.30	2.30
	456536	AW135986	Hs.257859	ESTs	2.28	2.28
	428166	AA423849	Hs.79530	M5-14 protein	2.27	1.88
	456936	M81349	Hs.1955	serum amyloid A4, constitutive	2.25	2.16
	417728	AW138437	Hs.24790	KIAA1573 protein	2.25	1.37
10	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.24	2.42
	409159	AW673312	Hs.50848	hypothetical protein FLJ20331	2.24	2.24
	404942			splicing factor, arginine/serine-rich 9	2.24	2.64
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.24	2.46
	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	2.24	1.94
15	421574	AJ000152	Hs.105924	defensin, beta 2	2.23	1.36
	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	2.22	1.37
	421948	L42583	Hs.334309	keratin 6A	2.20	2.20
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.19	1.61
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.18	2.40
20	431089	BE041395		ESTs, Weakly similar to unknown protein	2.16	2.46
	447333	BE090580	Hs.70704	hypothetical protein dJ616B8.3	2.16	2.00
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.16	1.26
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.16	1.99
	403362			NM_001615: Homo sapiens actin, gamma 2,	2.16	1.61
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.15	2.11
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.15	2.24
	402641			C1002296:gi 6677817 ref NP_033126.1 rep	2.14	2.14
	418236	AW994005	Hs.337534	ESTs	2.14	2.14
	413059	BE151498		gb:RC0-HT0295-291199-031-E11 HT0295 Homo	2.14	2.14
30	432437	W07088	Hs.293685	ESTs	2.14	2.14
	428398	AI249368	Hs.98558	ESTs	2.14	2.14
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.12	1.43
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	2.12	1.93
	436391	AJ227892	Hs.146274	ESTs	2.12	2.12
35	417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.11	2.17
	407443	AF227138		gb:Homo sapiens candidate taste receptor	2.11	2.36
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.10	1.29
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.10	2.10
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	2.10	2.00
40	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.10	1.37
	450271	AI693900	Hs.200920	ESTs	2.09	2.34
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.09	1.40
	458208	AI380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	2.08	2.00
	405600			C12001673:gi 9631264 ref NP_048045.1 or	2.07	1.97
45	434654	AI825942	Hs.139366	Homo sapiens clone L5 polyadenylated HER	2.07	2.52
	439261	AI126020	Hs.145674	basic transcription factor 3	2.05	1.45
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	2.04	2.04
	457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RDF1 Homo sapiens	2.04	2.04
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	2.02	1.33
50	412505	AA974491	Hs.21734	ESTs	2.02	2.02
	443180	R15875	Hs.258576	claudin 12	2.02	2.02
	431605	AW972407	Hs.124370	gb:EST384498 MAGE resequences, MAGL Homo	2.02	2.02
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	2.02	2.17
	452571	W31518	Hs.34665	ESTs	2.02	2.09
55	405061			Target Exon	2.01	2.52
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.01	2.41
	402327			Target Exon	2.00	2.44
	418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	2.00	2.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.00	2.00
60	438634	AW340400	Hs.126728	ESTs	1.99	2.43
	416127	N49843	Hs.79022	GTP-binding protein overexpressed in ske	1.97	1.41
	423961	D13666	Hs.136348	periostin(OSF-2os)	1.96	1.48
	430397	AI924533	Hs.105607	bicarbonate transporter related protein	1.96	1.31
	411010	AW813339		gb:MR3-ST0192-101299-013-c05 ST0192 Homo	1.96	2.73
65	439628	W81007	Hs.58628	ESTs	1.96	1.28
	444301	AK000136	Hs.10760	asporin (LRR class 1)	1.96	1.58
	431726	NM_015361	Hs.268053	KIAA0029 protein	1.95	1.72
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.95	1.87
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	1.95	1.06
70	417562	AW888754	Hs.134126	crystallin, gamma S	1.95	2.14
	424480	AA341442	Hs.205299	ESTs	1.94	1.94
	404342			C7002192:gi 7299207 gb AAF54404.1 (AE0	1.92	1.32
	443320	AI051607	Hs.16335	ESTs	1.91	2.18
	449780	AA443241		ribosomal protein L44	1.90	1.76
75	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	1.89	2.16
	434416	AA805903	Hs.59498	cell division cycle 2-like 5 (cholinese	1.89	2.04
	457505	AL044659	Hs.43791	ESTs	1.89	2.34
	425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pl	1.88	1.26
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	1.88	1.88
80	428231	U17989	Hs.183105	nuclear autoantigen	1.88	1.88
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	1.88	1.88
	404429			Target Exon	1.88	2.18
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	1.88	3.04
	406641	AJ235667		gb:Homo sapiens mRNA for immunoglobulin	1.86	2.57
	417059	AL037672	Hs.81071	extracellular matrix protein 1	1.86	1.48
	454565	BE141231		gb:MR0-HT0075-081199-003-a09 HT0075 Homo	1.86	1.21
	415115	AA214228	Hs.127751	hypothetical protein	1.85	1.23

5	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	1.85	1.45
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	1.84	1.44
	403344			NM_000341:Homo sapiens solute carrier fa	1.84	1.84
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	1.84	2.33
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.84	2.02
10	401593			Target Exon	1.83	2.34
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	1.83	2.12
	406461			hypothetical protein, clone 24751	1.83	2.01
	455557	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.83	1.26
	400609			C10001147:gi12698926[jgb]AAK01739.1[AF33	1.82	2.08
15	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	1.81	1.14
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.81	1.22
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	1.81	2.10
	426521	AF161445	Hs.170219	hypothetical protein	1.81	2.08
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.81	1.64
20	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	1.80	1.34
	439606	W79123	Hs.58561	G protein-coupled receptor 87	1.80	1.80
	459189	AI909090		gb:IL-BT198-010499-007 BT198 Homo sapien	1.80	1.80
	412429	AV650262	Hs.75765	GRO2 oncogene	1.80	2.55
	402674			Target Exon	1.80	3.41
25	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.79	1.57
	454824	AW833646		gb:QV4-TT0008-161199-033-d09 TT0008 Homo	1.78	1.94
	401677			BAI1-associated protein 3	1.78	2.28
	426291	U58913	Hs.169191	small inducible cytokine subfamily A (Cy	1.78	1.53
	430028	BE564110	Hs.227750	Target CAT	1.78	1.59
30	445988	BE007663	Hs.13503	inactivation escape 2	1.78	2.10
	452272	AW292249	Hs.252739	hypothetical protein DKFZp434P0316	1.78	2.08
	418205	L21715	Hs.83760	troponin I, skeletal, fast	1.78	2.70
	400425	AY004252	Hs.287385	PR domain containing 12	1.77	2.02
	400419	AF084545		Target	1.77	2.67
35	447169	AI989803	Hs.157289	ESTs	1.77	2.21
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	1.77	2.12
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	1.76	2.54
	432808	NM_015985	Hs.278973	angiotensin-3	1.76	1.76
	437400	AB011542	Hs.55599	EGF-like-domain, multiple 5	1.75	2.00
40	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.75	1.47
	444986	AI204197		ESTs	1.75	2.48
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	1.74	1.69
	413524	BE145837		gb:MR0-HT0208-101299-202-c07 HT0208 Homo	1.74	1.74
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	1.74	2.26
45	405579			C22000151:gi16806921[ref]NP_004165.1[so	1.74	2.12
	405797			CX001015:gi11322384[emb]CAC16687.1[(AJ	1.73	2.66
	405159			ENSP00000243337*:CDNA FLJ13984 fis, clon	1.73	2.01
	450569	AW192334	Hs.38218	ESTs	1.73	2.08
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	1.73	1.24
50	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	1.73	2.52
	454231	AW450669	Hs.45068	hypothetical protein DKFZp434I143	1.73	1.64
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	1.72	1.37
	422259	AA307584		gb:EST178498 Colon carcinoma (HCC) cell	1.72	1.72
	456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	1.72	1.34
55	451862	H09260	Hs.32333	ESTs	1.71	2.16
	403520			Target Exon	1.71	1.39
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	1.71	2.26
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	1.70	1.70
	418387	R18085	Hs.22279	gb:yg16b12.r1 Soares infant brain 1NIB H	1.70	1.70
60	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.70	1.87
	402538			C1001634:gi12621136[ref]NP_075245.1[Ba	1.69	1.57
	414844	AA296874	Hs.77494	deoxyguanosine kinase	1.69	2.06
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.69	1.63
	446553	AB021179	Hs.15299	HMBA-inducible	1.68	2.02
65	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	1.68	2.12
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	1.68	2.03
	433930	AA620338		ESTs	1.68	2.28
	404151			Target Exon	1.68	1.80
	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	1.67	2.18
70	430070	AF197927	Hs.231967	ALL1 fused gene from 5q31	1.66	2.16
	400496			ENSP00000224716*:GTP-binding protein SAR	1.66	2.13
	413464	AL121500		ESTs	1.66	2.03
	411188	BE161168		gb:PM0-HT0425-170100-002-a10 HT0425 Homo	1.66	2.12
	446281	H69416	Hs.14606	hypothetical protein FLJ20271	1.65	2.28
75	443282	T47764	Hs.132917	ESTs	1.65	2.04
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.65	1.67
	453355	AW295374	Hs.31412	myopodin	1.65	1.66
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.54
	437929	T09353	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	1.65	2.04
80	410295	AA741357		nidogen (enactin)	1.64	2.30
	437767	AA830103	Hs.293331	ESTs	1.64	1.26
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	1.64	3.38
	450795	AW173371	Hs.60435	ESTs	1.64	1.64
	421847	NM_014717	Hs.108884	KIAA0390 gene product	1.64	2.75
	403010			C21000152:gi16226483[sp]Q52118[YMO3_ERWS	1.64	2.03
	406387			Target Exon	1.64	1.78
	440423	AW293995	Hs.192277	ESTs	1.63	2.05

	444381	BE387335	Hs.283713	hypothetical protein BC014245	1.63	2.07
	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.63	1.65
	442424	AI342715	Hs.129569	ESTs, Moderately similar to B34087 hypot	1.62	2.40
5	402885			Target Exon	1.62	1.18
	408786	AA773187	Hs.294027	ESTs	1.62	1.59
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	1.62	1.63
	414684	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart,	1.62	2.10
	406838	AA827569	Hs.153	ribosomal protein L7	1.61	1.41
10	441600	AA939347	Hs.127223	Homo sapiens cysteine knot protein (ZSIG	1.61	2.32
	420693	NM_001972	Hs.99863	elastase 2, neutrophil	1.60	2.37
	412649	NM_002206	Hs.74369	integrin, alpha 7	1.60	1.23
	432331	W37862	Hs.274368	MSTP032 protein	1.60	1.23
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.60	1.69
	400279			NM_004581*:Homo sapiens Rab geranylgeran	1.60	1.56
15	437865	AI472305	Hs.19565	ESTs	1.60	2.42
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	1.60	1.29
	442993	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1	1.60	2.11
	410684	AA088500	Hs.170298	ESTs	1.59	1.46
	433149	BE257672	Hs.42949	hypothetical protein HES6	1.59	2.22
20	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	1.59	1.41
	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.59	1.26
	427654	AA410183	Hs.137475	ESTs	1.59	2.83
	411662	D60541	Hs.285519	Homo sapiens cDNA FLJ11904 fis, clone HE	1.59	2.18
25	440383	AA884208	Hs.30484	ESTs	1.58	2.19
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.58	1.58
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.58	1.47
	407857	AI928445	Hs.92254	synaptotagmin-like 2	1.58	1.51
	411573	AB029000	Hs.70823	KIAA1077 protein	1.57	1.29
30	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	1.57	1.17
	428471	X57348	Hs.184510	stratifin	1.57	1.55
	429249	X81479	Hs.2375	egf-like module containing, mucin-like,	1.57	1.19
	407966	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.57	2.12
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.57	1.05
35	430469	AW603667	Hs.288742	Homo sapiens cDNA: FLJ22712 fis, clone H	1.56	1.56
	445511	AA846512		Homo sapiens cDNA FLJ14459 fis, clone HE	1.55	2.08
	404501			nucleoside phosphorylase	1.55	2.54
	429107	AI470451	Hs.99075	ESTs	1.55	2.05
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	1.55	1.45
40	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	1.54	2.61
	458091	AF150286		gb:AF150286 Human mRNA from cd34 stem ce	1.54	1.54
	439280	AI125436	Hs.123654	ESTs	1.54	2.06
	428096	AW291771	Hs.42239	Homo sapiens, clone IMAGE:3868989, mRNA,	1.53	1.55
	414221	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCI_CGAP_Su	1.53	1.39
45	451712	AA019290	Hs.110489	ESTs	1.53	1.99
	402487			Target Exon	1.53	2.02
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.53	1.29
	452887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	1.53	1.21
	410253	T51823		ESTs	1.52	2.03
50	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	1.52	1.37
	432985	T92363	Hs.178703	ESTs	1.51	1.48
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.51	1.15
	429259	AA420450	Hs.292911	Plakophilin	1.51	1.31
	429289	AI400746	Hs.62187	phosphatidylinositol glycan, class K	1.51	1.19
55	441457	AW996651	Hs.43838	ESTs	1.51	2.08
	433365	AF026944	Hs.293797	ESTs	1.51	2.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.51	1.21
	424386	BE146577	Hs.285132	ESTs	1.50	1.53
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	1.50	1.29
60	442391	AW450544	Hs.220751	ESTs	1.50	1.65
	414341	D80004	Hs.75909	KIAA0182 protein	1.50	2.10
	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	1.50	2.16
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.50	1.50
	443878	AW292499	Hs.139709	hypothetical protein FLJ12572	1.50	1.37
65	430152	AB001325	Hs.234642	aquaporin 3	1.50	1.43
	447752	M73700	Hs.105938	lactotransferrin	1.49	0.91
	404455			opioid receptor, kappa 1	1.49	1.36
	424106	AA412442	Hs.98132	ESTs	1.49	1.30
	433095	AK001092	Hs.302480	Homo sapiens cDNA FLJ10230 fis, clone HE	1.49	2.02
70	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.48	1.50
	456256	AB000450	Hs.82771	vaccinia related kinase 2	1.48	1.42
	439310	AF086120	Hs.102793	ESTs	1.48	1.48
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	1.48	1.15
	437981	AA774445	Hs.145365	ESTs, Weakly similar to KIAA1397 protein	1.48	2.36
75	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	1.47	1.21
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	1.47	1.25
	453864	AW021407	Hs.21068	hypothetical protein	1.47	2.18
	401067			ENSP00000252105*:CDNA FLJ12240 fis, clon	1.47	1.81
80	456054	BE313241		gb:601151545F1 NIH_MGC_19 Homo sapiens c	1.47	1.99
	402324			C19001982:gil3043638[dbj]BAA25483.1[AB	1.47	2.03
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	1.47	1.29
	457734	BE394365	Hs.38750	hypothetical protein FLJ11526	1.47	2.26
	402013			Target Exon	1.46	2.42
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	1.46	2.09

5	430920	U96402	Hs.248132	goosecoid-like	1.46	2.46
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	1.46	2.02
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.46	1.43
	427719	AI393122	Hs.134726	ESTs	1.46	1.46
	433430	AI863735		ESTs	1.46	1.15
10	423790	BE152393		gb:CM2-HT0323-171199-033-a08 HT0323 Homo	1.46	2.36
	444083	AI123195		gb:oo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.45	2.29
	433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypothe	1.45	1.50
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	1.45	1.17
	456664	AW963354	Hs.334409	metallothionein 1G	1.45	2.20
15	438158	AI796556	Hs.187884	ESTs	1.45	1.18
	409883	AW452419	Hs.296098	ESTs	1.45	2.00
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.45	1.27
	413048	M93221	Hs.75182	mannose receptor, C type 1	1.45	1.36
	457462	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	1.45	2.08
20	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	1.44	1.28
	401116			Target Exon	1.44	2.19
	419618	AA528295		gb:nh26e06.s1 NCI_CGAP_Pr3 Homo sapiens	1.44	2.30
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	1.44	2.03
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.43	1.48
25	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.43	1.51
	418742	AW451197	Hs.113418	ESTs	1.43	1.24
	418335	R63267	Hs.28399	ESTs	1.43	1.14
	408404	AW192518		gb:xl45h08.x1 NCI_CGAP_Pan1 Homo sapiens	1.43	2.08
	448175	BE296174	Hs.225160	hypothetical protein FLJ13102	1.43	2.29
30	431846	BE019924	Hs.271580	uroplakin 1B	1.43	2.12
	459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	1.43	2.00
	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	1.43	1.33
	442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (1.43	1.10
	454843	AW834536	Hs.258549	gb:MR2-TT0014-241199-012-f06 TT0014 Homo	1.43	1.55
35	410281	AF076612	Hs.166186	Homo sapiens clone 23928 mRNA sequence	1.43	1.38
	402998			NM_002463*:Homo sapiens myxovirus (influ	1.42	2.16
	443709	AI082692	Hs.134662	ESTs	1.42	2.22
	435259	AA152106	Hs.4859	cyclin L ania-6a	1.42	2.01
	454407	AW578420	Hs.118843	gb:RC1-CT0249-120100-022-b04 CT0249 Homo	1.42	1.76
40	453359	AA448787	Hs.24872	ESTs	1.42	1.33
	434126	AI138589	Hs.118205	ESTs	1.41	2.06
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	1.41	1.46
	442316	Z75331	Hs.8217	stromal antigen 2	1.41	2.20
	438330	AW450572	Hs.257316	ESTs	1.41	2.20
45	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	1.41	2.02
	455885	BE153524		gb:PM0-HT0339-241199-002-C03 HT0339 Homo	1.41	1.33
	405550			C7001981*:gij565157[gib]AAB31881.1 T-cel	1.41	1.24
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	1.41	1.99
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	1.40	2.64
50	431022	AA490815	Hs.208351	ESTs	1.40	1.26
	439781	AA845538		glial cells missing (Drosophila) homolog	1.40	2.72
	429379	NM_014840	Hs.200598	KIAA0537 gene product	1.40	1.05
	435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprote	1.40	1.26
	430702	U56979	Hs.278568	H factor 1 (complement)	1.39	1.18
55	451331	AK002039		Homo sapiens cDNA FLJ11177 fis, clone PL	1.39	1.26
	459198	AI086347	Hs.151138	ESTs	1.39	1.22
	442344	AI022925	Hs.79368	epithelial membrane protein 1	1.39	1.35
	402917			ENSP00000202587*:Bicarbonate transporter	1.39	1.44
	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	1.39	2.08
60	437158	AW090198		KIAA1150 protein	1.38	2.07
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	1.38	1.24
	433911	AI923092	Hs.8899	ESTs	1.38	2.15
	402504			C1003823*:gij4826521[emb]CAB42853.1 {AL	1.38	1.38
	409465	AW393810	Hs.78054	gb:QV4-TT0008-251099-016-e11 TT0008 Homo	1.37	2.22
65	449426	T92251	Hs.198882	ESTs	1.37	2.38
	405491			Target Exon	1.37	2.74
	406685	M18728		gb:Human nonspecific crossreacting antig	1.37	1.34
	442410	AW996503	Hs.197680	ESTs	1.37	1.56
	407701	AW375009	Hs.164407	ESTs	1.36	2.02
70	400818			Target Exon	1.36	2.10
	406475			C15000508*:gij2558825[gib]AAC53387.1 {AF	1.36	2.78
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	1.36	1.41
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	1.36	2.20
	444195	AB002351	Hs.10587	KIAA0353 protein	1.35	0.94
75	447918	AI129320	Hs.115175	ESTs, Highly similar to JC5818 gamma-act	1.35	1.22
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	1.35	1.40
	412992	AI423369	Hs.75111	protease, serine, 11 (IGF binding)	1.35	1.24
	401025			NM_004055*:Homo sapiens calpain 5 (CAPN5	1.35	1.30
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	1.34	2.12
80	425308	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	1.34	1.02
	402308			Target Exon	1.34	1.21
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	1.34	1.40
	407242	M18728		gb:Human nonspecific crossreacting antig	1.34	1.22
	410741	Z11695	Hs.324473	mitogen-activated protein kinase 1	1.34	2.05
	439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobulin, fa	1.34	1.12
	431254	NM_006069	Hs.251385	murine retrovirus integration site 1 hom	1.33	1.21
	405213			Target Exon	1.33	2.03

5	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1.33	1.05
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthase	1.33	2.09
	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	1.33	1.32
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	1.33	1.18
	430385	AA113437		N-myc downstream-regulated gene 3	1.32	1.48
10	447731	AA373527	Hs.19385	CGI-58 protein	1.32	2.22
	400740			hypothetical protein FLJ14280	1.32	2.01
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	1.32	1.32
	440274	R24595	Hs.7122	scrapie responsive protein 1	1.32	1.32
	406867	AA157857	Hs.182265	keratin 19	1.32	1.42
15	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	1.32	2.30
	443144	BE246335		hypothetical protein MGC14797	1.32	2.03
	432810	AA863400		ESTs	1.32	4.01
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.31	1.24
	424075	A1807320	Hs.227630	RE1-silencing transcription factor	1.31	2.17
20	440099	AL080058	Hs.6909	DKFZP564G202 protein	1.31	1.53
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	1.31	1.31
	438874	H02780		gb:yj41a11.1 r1 Soares placenta Nb2HP Homo	1.31	2.03
	402825			Target Exon	1.31	1.24
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	1.31	1.45
25	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	1.31	1.19
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	1.31	1.12
	436027	A1864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	1.30	2.06
	447409	AF060168		gb:Homo sapiens AS10 protein mRNA, parti	1.30	2.16
	400221			NM_002082*:Homo sapiens G protein-couple	1.30	2.02
30	437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.30	2.44
	450008	H52970	Hs.36688	WAP four-disulfide core domain 1	1.30	1.19
	441591	AF055992	Hs.183	Duffy blood group	1.29	1.03
	405973			Target Exon	1.29	1.32
	424604	AW865388	Hs.151076	KIAA1243 protein	1.29	0.92
35	410899	AW809716		gb:MR4-ST0124-241199-026-h09 ST0124 Homo	1.29	2.06
	405818			CX001073:gi 4176497 emb CAA20116.1} (AL0	1.29	2.05
	402621			Target Exon	1.29	3.06
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	1.28	2.35
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.28	1.44
40	453331	AJ240665		ESTs	1.28	2.36
	439791	H77774	Hs.35755	ESTs	1.28	2.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.28	3.00
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	1.28	1.28
	446526	H89616		Homo sapiens cDNA FLJ13357 fis, clone PL	1.28	1.28
45	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	1.28	1.28
	418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	1.28	2.10
	407711	A1085846	Hs.25522	KIAA1808 protein	1.28	1.23
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	1.28	1.19
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	1.27	1.24
50	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.27	2.08
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	1.27	2.05
	444418	AL034417	Hs.11169	Gene 33/Mig-6	1.27	1.98
	427809	M26380	Hs.180878	lipoprotein lipase	1.27	1.09
	414690	BE410103	Hs.12313	hypothetical protein FLJ14566	1.27	1.36
55	439919	AA970710	Hs.128064	ESTs	1.27	2.28
	401311			Target Exon	1.27	2.05
	444235	AW207346	Hs.143202	ESTs	1.27	2.00
	430858	AF007190		Homo sapiens SIB 297 intestinal mucin (M	1.26	1.23
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	1.26	2.40
60	400161			Eos Control	1.26	1.33
	444239	R57988	Hs.10706	epithelial protein lost in neoplasm beta	1.26	1.20
	438369	T77886	Hs.83428	nuclear factor of kappa light polypeptid	1.26	1.26
	441944	AW855861	Hs.8025	Homo sapiens clone 23767 and 23782 mRNA	1.26	1.12
	431142	AA852596	Hs.250641	tropomyosin 4	1.26	1.23
65	434229	R56378	Hs.181223	hypothetical protein PRO2801	1.26	2.04
	406733	AA976565	Hs.297753	vimentin	1.26	1.29
	422292	A1815733	Hs.114360	transforming growth factor beta-stimulat	1.25	1.16
	424137	AA335769	Hs.16262	ESTs	1.25	1.27
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	1.24	1.50
70	424408	A1754813	Hs.146428	collagen, type V, alpha 1	1.24	1.29
	433750	H15448	Hs.31330	Homo sapiens clone HQ0319	1.24	1.27
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.24	1.13
	438357	A1042101	Hs.294107	ESTs	1.24	2.04
	409959	BE349470		mucin 6, gastric	1.23	2.22
75	439897	NM_015310	Hs.6763	KIAA0942 protein	1.23	2.44
	421982	AF206019	Hs.110347	REV1 (yeast homolog)- like	1.23	2.14
	407207	T03651	Hs.336780	tubulin, beta polypeptide	1.23	1.32
	416956	AA810664	Hs.101660	hypothetical protein MGC5391	1.23	2.39
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev1n)	1.23	1.06
80	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	1.23	1.51
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.23	1.01
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.22	1.41
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.22	1.17
	421341	AJ243212		deleted in malignant brain tumors 1	1.22	1.09
	406850	A1624300	Hs.172928	collagen, type I, alpha 1	1.22	1.52
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	1.22	2.55
	423189	M59371	Hs.171596	EphA2	1.22	1.15

	401899		Target Exon	1.22	1.22
	403579		Target Exon	1.22	2.34
	415954	AA171850	ESTs	1.22	2.24
5	429171	AI743173	ESTs, Weakly similar to ARL2_HUMAN ADP-R	1.21	1.14
	444071	AI627808	ESTs	1.21	2.23
	424344	AF036973	Hs.145477 HCGIV-6 protein	1.21	2.15
	434051	AF116622	gb:Homo sapiens clone FLB4217 mRNA seque	1.21	1.25
	422311	AF073515	Hs.114948 cytokine receptor-like factor 1	1.21	1.39
10	404600		Target Exon	1.21	1.29
	429751	M55210	Hs.214982 laminin, gamma 1 (formerly LAMB2)	1.21	1.03
	430392	NM_000627	Hs.241257 latent transforming growth factor beta b	1.21	1.21
	422687	AW068823	Hs.119206 insulin-like growth factor binding prote	1.21	1.23
	424855	AW204725	Hs.25560 ESTs	1.20	1.98
15	418890	AA232134	Hs.190028 ESTs	1.20	1.33
	413232	BE073258	Hs.133988 hypothetical protein FKSG28	1.20	2.18
	414154	AW205314	Hs.323060 ESTs	1.20	1.34
	416784	AA334592	Hs.79914 lumican	1.20	1.27
	410933	C15974	gb:C15974 Clontech human aorta polyA mRN	1.19	2.05
20	415388	AF018081	Hs.78409 collagen, type XVIII, alpha 1	1.19	1.11
	406731	AI559131	gb:U31g07.x1 NCL_CGAP_U11 Homo sapiens	1.19	1.19
	447563	BE536115	Hs.160983 EST	1.19	1.14
	405531		Target Exon	1.19	2.02
	400363	NM_001403	eukaryotic translation elongation factor	1.19	1.21
25	426611	BE178050	Hs.171271 catenin (cadherin-associated protein), b	1.19	1.18
	427676	AA394062	Hs.300772 tropomyosin 2 (beta)	1.18	1.16
	413929	BE501689	Hs.75617 collagen, type IV, alpha 2	1.18	1.20
	413856	D13639	Hs.75586 cyclin D2	1.18	1.20
	427111	AA351026	Hs.173594 serine (or cysteine) proteinase inhibito	1.18	1.12
30	422287	F16365	Hs.114346 cytochrome c oxidase subunit VIIa polype	1.18	1.05
	412758	Y07818	Hs.74566 dihydropyrimidinase-like 3(ULIP)	1.18	1.06
	446868	AV660737	ESTs	1.18	1.18
	417613	AV654351	Hs.82306 destrin (actin depolymerizing factor)	1.18	1.17
	405542		Target Exon	1.18	1.98
35	419908	AW971327	Hs.293315 ESTs	1.17	2.02
	434095	AA011117	Hs.3745 milk fat globule-EGF factor 8 protein	1.17	1.19
	407230	AA157857	Hs.182265 keratin 19	1.17	1.35
	448413	AI745379	Hs.42911 ESTs	1.17	2.87
	426653	AA530892	Hs.171695 dual specificity phosphatase 1	1.17	1.39
40	424572	M19650	Hs.179600 2',3'-cyclic nucleotide 3' phosphodiester	1.17	2.08
	440109	AK001138	Hs.333149 hypothetical protein FLJ10276	1.17	1.06
	405131		C1002509:gil9938010[ref]NP_064684.1[odo	1.17	2.22
	422354	U20982	Hs.1516 insulin-like growth factor-binding prote	1.17	1.19
	442124	R66412	Hs.129013 Homo sapiens cDNA FLJ14309 fis, clone PL	1.17	1.11
45	400080		Eos Control	1.16	2.53
	431924	AK000850	Hs.272203 Homo sapiens cDNA FLJ20843 fis, clone AD	1.16	2.00
	412802	U41518	Hs.74602 'aquaporin 1 (channel-forming integral pr	1.16	1.30
	429207	AA447941	Hs.123423 ESTs	1.16	1.27
	415149	X12451	Hs.78056 cathepsin L	1.16	1.12
50	400231		Eos Control	1.16	1.17
	416653	AA768553	Hs.193145 metallothionein 1E (functional)	1.16	1.16
	422813	AV656571	Hs.121068 transmembrane 4 superfamily member 6	1.16	1.10
	439318	AW837046	Hs.6527 G protein-coupled receptor 56	1.16	1.15
	422424	AI186431	Hs.296638 prostate differentiation factor	1.16	1.21
55	432745	AI821926	gb:nt78f05.x5 NCL_CGAP_Pr3 Homo sapiens	1.15	2.00
	412477	AA150864	microsomal glutathione S-transferase 1	1.15	1.23
	430361	AI033965	Hs.239926 sterol-C4-methyl oxidase-like	1.15	2.31
	424512	X53002	Hs.149846 integrin, beta 5	1.15	1.15
	449924	W30681	Hs.146233 Homo sapiens cDNA: FLJ22130 fis, clone H	1.15	1.24
60	414682	AL021154	Hs.76884 inhibitor of DNA binding 3, dominant neg	1.15	1.07
	456076	BE243877	ATPase, Na ⁺ transporting, beta 3 polypep	1.15	2.00
	403026		Target Exon	1.15	2.32
	422545	X02761	Hs.287820 fibronectin 1	1.15	1.17
	412719	AW016610	Hs.816 ESTs	1.15	1.05
65	421848	X15880	Hs.108885 collagen, type VI, alpha 1	1.15	1.14
	422087	X58968	Hs.111301 matrix metalloproteinase 2 (gelatinase A	1.15	1.16
	413936	AF113676	Hs.297681 serine (or cysteine) proteinase inhibito	1.14	1.13
	449845	AW971183	Hs.6019 DnaJ (Hsp40) homolog, subfamily C, membe	1.14	2.07
	430202	T85775	gb:yd60g02.r1 Soares fetal liver spleen	1.14	1.14
70	418806	AA486970	Hs.191718 ESTs	1.14	2.14
	424017	AA333789	gb:EST37925 Embryo, 9 week Homo sapiens	1.14	2.16
	422003	AA361760	Hs.296326 ESTs	1.14	1.17
	437272	AW975957	gb:EST388066 MAGE resequences, MAGN Homo	1.14	2.17
	438367	N79688	Hs.204354 ras homolog gene family, member B	1.14	1.23
75	453152	AK001933	Hs.31945 hypothetical protein FLJ11071	1.13	2.36
	406849	AA454809	Hs.172928 collagen, type I, alpha 1	1.13	1.33
	422110	AI376736	Hs.111779 secreted protein, acidic, cysteine-rich	1.13	1.06
	425335	BE394327	Hs.296267 follistatin-like 1	1.13	1.08
	434795	BE620794	Hs.4147 translocating chain-associating membrane	1.13	1.08
80	417426	NM_002291	Hs.82124 laminin, beta 1	1.13	1.11
	452924	AW580939	Hs.97199 complement component C1q receptor	1.13	1.01
	416379	N38857	Hs.34145 ESTs	1.12	1.12
	421464	AA291553	Hs.190086 ESTs	1.12	2.01
	442420	AI024834	Hs.131729 ESTs	1.12	1.15

	405369			NM_005569*:Homo sapiens LIM domain kinas	1.12	1.99
	421730	AW449808	Hs.334534	glucosamine (N-acetyl)-6-sulfatase (Sanf	1.12	2.08
	405932			C15000305:gi 3806122 gb AAC69198.1 (AFO	1.11	2.01
5	453542	AW836724		Homo sapiens mRNA expressed only in plac	1.11	2.00
	437585	AW976857		ESTs	1.11	2.01
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.11	1.05
	449931	AW875786	Hs.25734	ESTs, Weakly similar to BING1 [H.sapiens	1.11	1.03
	407085	Z70759		gb:H.sapiens mitochondrial 16S rRNA gene	1.10	1.12
10	447191	NM_014521	Hs.17667	SH3-domain binding protein 4	1.10	1.04
	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.10	1.07
	432675	AI791855	Hs.105884	ESTs	1.10	2.30
	432731	R31178	Hs.287820	fibronectin 1	1.09	2.12
	430763	AA485468		DNA fragmentation factor, 45 kD, alpha p	1.09	2.10
15	438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	1.09	1.04
	405156			NM_003213*:Homo sapiens TEA domain famil	1.09	2.19
	409031	AA376836		ESTs	1.09	2.22
	422608	AW160644	Hs.118695	potassium voltage-gated channel, subfam	1.09	2.26
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.09	1.28
20	410577	X91911	Hs.64639	glioma pathogenesis-related protein	1.08	2.64
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	1.07	1.02
	452219	AA024860	Hs.61224	ESTs	1.07	2.08
	430108	AA465294		ESTs	1.07	2.11
	402174			Target Exon	1.07	2.11
25	416952	AI767736	Hs.290070	gelsolin (amyloidosis, Finnish type)	1.07	1.00
	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fis, clone H	1.07	1.13
	442670	BE410050	Hs.11859	hypothetical protein FLJ13188	1.07	2.21
	442310	AF033199	Hs.8198	zinc finger protein 204	1.06	2.04
	405536			NM_005805:Homo sapiens 26S proteasome-as	1.06	2.20
30	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	1.06	1.06
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	1.06	1.06
	425371	D49441	Hs.155981	mesothelin	1.06	1.27
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	1.06	2.37
	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.06	1.05
35	409407	AW967370	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	1.05	2.00
	406109			Target Exon	1.05	2.04
	418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	1.05	2.67
	403162			C2000231*:gi 9802031 gb AAF99597.1 AF239	1.05	2.07
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	1.05	1.07
40	407225	J04617		eukaryotic translation elongation factor	1.05	1.02
	416955	AW889150	Hs.80595	NM_004552*:Homo sapiens NADH dehydrogena	1.05	1.10
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	1.04	2.12
	410276	AI554545		angiotensin-2	1.04	1.04
45	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.04	1.04
	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.03	1.05
	406773	AA812424	Hs.76067	heat shock 27kD protein 1	1.03	1.10
	452082	N51905	Hs.125133	hypothetical protein FLJ22501	1.03	2.01
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	1.03	2.24
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	1.02	1.00
50	408339	R97502	Hs.30443	sentrin/SUMO-specific protease	1.02	2.19
	400247			Eos Control	1.02	2.04
	430030	BE300094	Hs.227751	lectin, galactoside-binding, soluble, 1	1.01	1.01
	442275	AW449467	Hs.54795	ESTs	1.01	1.04
	406786	AW161678	Hs.111334	ferritin, light polypeptide	1.01	1.06
55	439403	BE265745		ESTs, Weakly similar to ALUC_HUMAN !!!!	1.01	2.11
	428043	T92248	Hs.2240	uteroglobin	1.00	1.06
	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.02
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	2.16
	450724	R55428		gb:yj79b05.r1 Soares breast 2NbHBst Homo	1.00	0.99
60	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	1.00	1.08
	432077	AL134685		gb:DKFZp547M126_r1 547 (synonym: hfrb1)	1.00	2.05
	427687	AW003867	Hs.1570	histamine receptor H1	1.00	1.00
	435256	AF193766	Hs.13872	cytokine-like protein C17	1.00	1.00
	420026	AI831190	Hs.166676	ESTs	1.00	1.00
	455128	AW861555	Hs.314372	EST	1.00	1.00
65	410685	AA497117	Hs.58893	ESTs, Moderately similar to ALU1_HUMAN A	1.00	1.00
	401404			Target Exon	1.00	1.00
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	1.00	1.00
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	1.00	1.00
70	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	1.00	1.00
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, alp	1.00	1.00
	447947	N33033	Hs.270215	ESTs	1.00	1.00
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	1.00	1.00
	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	1.00	1.00
75	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheri	1.00	1.00
	444963	AI916973	Hs.213603	ESTs	1.00	1.00
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	1.00	1.00
	442849	R10099	Hs.269805	ESTs	1.00	1.00
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	1.00	1.00
80	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	1.00	1.00
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	1.00	1.00
	459045	N69101	Hs.40730	ESTs	1.00	1.00
	455500	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	1.00	1.00
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	1.00	1.00

5	429932	AI095005	Hs.21586	ESTs	1.00	1.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	1.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	1.00	1.00
	431374	BE258532	Hs.251871	CTP synthase	1.00	1.00
	443162	T49951	Hs.9029	DKFZP434G032 protein	1.00	1.00
	432128	AA127221	Hs.296502	ESTs	0.99	2.33
	451838	AW005866	Hs.193969	ESTs	0.98	3.26
	438414	AA806794	Hs.131511	ESTs	0.97	3.61
	435872	AA701357	Hs.192759	ESTs	0.97	0.96
10	425211	M18667	Hs.1867	progastricin (pepsinogen C)	0.97	1.08
	424001	W67883	Hs.137476	paternally expressed 10	0.96	2.25
	418869	AW516565		gb:xxq01d05.x1 Soares_NHCEC_cervical_lumo	0.96	2.07
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	0.94	2.18
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	0.94	1.31
15	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	0.94	2.12
	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	0.94	2.19
	452239	AW379378		protein tyrosine phosphatase, receptor t	0.94	0.79
	403167			Target Exon	0.94	2.06
	402209			Target Exon	0.92	2.04
20	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	0.92	0.74
	424090	X99699	Hs.139262	XIAP associated factor-1	0.91	2.11
	432816	N38913	Hs.221575	ESTs	0.91	2.15
	451779	AW968616	Hs.296234	ESTs, Weakly similar to T31613 hypotheti	0.91	2.14
	406851	AA609784		major histocompatibility complex, class	0.89	1.04
25	427698	AW972594	Hs.335499	ESTs	0.89	0.90
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-II	0.88	2.42
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.87	1.14
	426024	Z43405	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	0.87	2.04
	400986			NM_024085*.Homo sapiens hypothetical pro	0.87	2.10
30	430353	AW952337		citrate synthase	0.86	2.28
	404975			uncharacterized hypothalamus protein HT0	0.86	2.50
	406673	M34996	Hs.198253	major histocompatibility complex, class	0.86	1.94
	431323	AW970623		gb:EST382705 MAGE resequences, MAGK Homo	0.80	2.08
	404926			Target Exon	0.79	2.01
35	432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	0.77	0.86
	437601	AA761546	Hs.248844	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	2.10
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	0.76	2.66
	406646	M33600	Hs.308026	major histocompatibility complex, class	0.76	1.09
	442195	NM_001430		endothelial PAS domain protein 1	0.76	2.00
40	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.76	0.78
	413916	N49813	Hs.75615	apolipoprotein C-II	0.73	2.06
	453716	AA037675	Hs.152675	ESTs	0.73	2.10
	437802	AI475995	Hs.122910	ESTs	0.70	2.08
	422282	AF019225	Hs.114309	apolipoprotein L	0.68	2.95
45	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	0.54	2.11
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	0.53	0.53

TABLE 34B:

50	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
55	Pkey	CAT Number	Accession
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	420195	28714_1	AK002039 AL117524 AV714494 AW954901 AL045243 BF955185 AU137860 AW880615 AW880496 AA256290 BE767078 N44348 AI886676 AA455877 N66571 AA999864 AU157344 AI817146 R54821 BE223107 AA455880 AI355752 BF589210 N63487 AI924033 AI923020 AI306145 AI919421 AI584169 AI250173 AI440227 AA669696 AW244040 AI358104 AI570333 AI418315 N94787 R72348 N94780 BF944396 BF754698 AW005707 N98831 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N63481 BE838574 BF909132 BI084973 BG257295 BG818471 BE348449 AI420623 AW271213 BE048764 W44682 AI887849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 BI045196 AW880645
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BG290073 BI667399 BM451469 BI667173 BI602139 BG532171 BI669216 BI544727 BG721852 AV716503 AV701327 BM090738 BI492000
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 AV647719 BG501392 BG428433 BE895629 BM313117 AW021050 BG435032 BM152910 AA313503 AA872377 BG574714 AV712054 AV732696
 AA252476 AV712759 AL599643 BE790872 BG654930 W73337 AW675377 AV760376 AV725139 AV716379 AA887165 BE830003 AW023796
 AL599291 AI902948 BG944042 F00781 AA352483 BG217897 N33888 AW581924 BG654730 D31410 AA353088 D31288 AA295029 H95170
 BE935104 AU139980 BG772963 BG776470 BG532512 BG105449 BI545421 AV715456 AW386083 BG699714 AL535832 AL514940 BG190861
 BG210593 AW999254 H95138 AA353863 BE764809 N50375 BE091363 BG701255 BI860846 BI832485 BG168150 BG028647 BE546301
 BG900321 BI909737 BG702363 BG614141 BG611137 BG700121 BF031492 N85802 AV715940 N51590 BG993478 BE172016 AW893622
 AK056692 AF086220 AI375066 AA284293 W32566 AW797961 AA960897 AA504145
 BF060834 BI019048 AW862002 AK056737 AA429538 AW063311 AW440655 AW231970 AA428584 AA995028 AW854593 AA984131 AA552874
 AA564758 AA528743 BG927275 BE045117 AW975234 AA664937 BF749390 BG928948 AA984546 BE009153 AV732487 BE078167 AW872716
 AW063245 AA578441 AI820704 AI732283 R55428 BF999154 BF880485
 AL134685 AW972760 AA525319 AA526644 AA525342 AA526632 AA525296 AV739423 AW972755
 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526
 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
 AW852530 AW852526 AW852527 AL597969
 AW811114 AW811095 AW811094 AW811124 AW811157 AW811054 AW811087
 AW810001 BF374633 AW809694 AW809672 BF374748 BF374562 AW810209 AW810092 AW809786 AW810428 AW810429 AW809884 BF374650
 BF374641 BF374764 BF374744 AW810552 BF374678 BF374653 BF374579 AW810168 AW810170 BF374611 BF374676 BF374667 AW810353
 BF374682 AW810154 BF374688 BF374565 BF374757 BF374637 BF374743 BF374719 AW809664 BF374643 BF374680 BF374714 BF374708
 BF374716 AW810432 BF374691 BF358066 AW810006 AW810345 AW809960
 AW963582 BE064192 BE064169 BE152580 AW963587
 AV704306 BF368780 AW867826 AW859896
 AA229762 AA230035
 AW972670 AA525808 H28359 H28383
 BG034853 AW173315 AW303375 BG190225 BG939153 BF057308 AA600736 AI751258 AI090486 BE939504 AW631492 AI768270 AI862133
 AA417652 BE378218 AA599207 AW794702 AA024968 AA446024 AI148235 AI191710 BI493797 AI272646 BI493796 AA634323 AI754332
 AA258414 C05155 AI218226 AI039656 AI350380 AI084698 AI754989 AI673545 AI432010 AI751035 AA375571 AA446297 BG216743
 AA609784 R97304
 BC010106 AL560552 AU133296 AU133086 BE268567 BE268523 BI544879 BE398161 BG473088 BI544445 BE258021 BE296339 BE255040
 BE263020 BG706790 AL598627 AW952337 BG758113 AW512753 BE267666 BE253415 BI225718 BE268350 BE258245 BI224965 AW772605
 BG723903 BE397282 BI196341 BG702880 AI878949 AL600437 AA416759 BE259917 AI031582 BF512142 AI088248 BE560328 AI802623
 AI288613 AL597585 AW768553 AI816352 BF732831 BI225687 AA833686 AA722593 AA807750 AW068064 AA405187 AI923236 N51593 AL527710
 BG282576 AL525927 AL525971 BI869547 AI064725 R91856 H46814 H20112 W01682 AW848870 AW848585 AW376662 AW848985 AW848937
 AW848862 AW848581 AW848512 AW848176 AW752623 AW752618 AW376822 AW376821 AW376684 AW376623 AW376622 BE706047
 AW752602 AW752691 AW752674 AW752652 AA379167 AW752610 AW752684 AW752613 AW752660 AW848709 AW848576 AW848915
 AW848981 AW848980 AW848979 AW848978 AW848973 AW848916 AW848713 AW848708 AW848642 AW848641 AW848639 AW848573
 AW848493 AW848492 AW848489 AW848488 AW848487 AW848353 AW848352 AW848220 AW752698 AW752697 AW752682 AW752681
 AW752680 AW752679 AW752664 AW752651 AW752638 AW752637 AW752636 AW752628 AW752626 AW752624 AW752619 AW752596
 AW752608 AL582019 BE875587 AL529175 AW965868 BG686208 AA259073 BE696973 AA459543 AA358314 W40564 BF926427 AW849000
 AW848718 AW848515 AW848507 AW848444 AW848440 AW848232 AW848222 AW752657 AW376786 AW376781 AW376615 AW376614
 BI752581 AA534520 AI748906 AA047799 AI014753 AL514460 AL581982 BG743146 W24171 H20102 H11227 AW752607 AW006596 AW130378
 BE716519 AW752661 AW848289 BF349557 AW752612 AW752632 AW848910 NM_004077 AF047042 AL560606 BI765896 BI196831 BI855656
 BE906674 BG749937 BE535486 BE019810 AA313713 AA992542 AA332541 AA682985 AA356125 BE140478 BG750945 BI457548 BG025661
 BF326302 AA325019 BG980676 AA337465 AA321974 BG949285 BG427585 R23979 BG611485 BE560678 W16977 N50379 BG824101 BG471750
 BI463171 W04691 AU099360 BG471590 BM011999 BE262945 BE559801 BF756438 BE881957 BE314546 BG911831 BG150811 BG112017
 AA157518 T92368 AW752620
 AW970623 AA502839 AA502819
 U81984 NM_001430 BE907085 BI333232 AI021986 AU138476 C18601 U51626 AU100517 BI054387 AU076970 BE786454 BG010080 AW377189
 BF998789 AA368139 R11395 T83613 BG006324 BI012404 BG001643 BF757957 AL549361 AL544018 BE002870 BE929314 BE090199 AL046650
 BI053717 BE929315 BI054967 BF960055 BF925432 R05421 BF922073 T70331 BI004403

TABLE 34C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405443	7408143	Plus	90716-90887,101420-101577
401645	7657839	Minus	34986-35133
401673	7689903	Minus	122587-122705,122765-123047
405120	8099940	Plus	140176-140340
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
402333	8844110	Minus	165693-165856
404942	7382153	Plus	92095-92252
403362	8571772	Plus	64099-64260
402641	9958129	Minus	122596-125136
405600	5923640	Plus	26662-27225
405061	7656744	Minus	132492-132932
402327	7656695	Minus	108675-108770,109801-109910
404342	9838093	Plus	115854-116033
404429	7407979	Plus	31352-31498
403344	8569726	Plus	70823-70990
401593	7230957	Plus	10368-10572,11293-12356
406461	9756020	Minus	158842-159136
400609	9887671	Minus	92037-92247
402674	8077108	Minus	39290-39502
401677	9965537	Minus	62856-63086,63603-63884
405579	6456174	Plus	100996-101542
405797	1934909	Minus	5599-5681,5821-6104

5	405159	9966252	Plus	79659-79804
	403520	7684483	Minus	97621-98084
	402538	9801137	Minus	96314-96539
	404151	7534014	Minus	69038-69399
	400496	9743564	Plus	41515-41695
	403010	3132346	Plus	78385-79052
	406387	9256180	Plus	116229-116371,117512-117651
	402885	9926751	Plus	71919-72049
10	404501	7229859	Minus	37270-37526
	402487	9797538	Plus	75677-75843
	404455	7677926	Minus	26927-27611
	401067	5764724	Minus	153366-153509
	402324	7630361	Plus	26052-26803
15	402013	7407997	Plus	174540-174634,175449-175568
	401116	9966559	Plus	123579-124447
	402998	2996643	Minus	17175-17373
	405550	1552494	Plus	91720-92115
	402917	7406502	Minus	1034-1177,3143-3266
20	402504	9797871	Plus	12366-12614
	405491	5801645	Plus	81857-82045
	400818	8569994	Plus	172644-172765,173085-173200
	406475	9797684	Plus	125417-125563,128052-128180
	401025	8117518	Minus	179287-179483,181044-181166,181844-18203
25	402308	7340295	Minus	92080-93638
	405213	6692345	Minus	50267-51151
	400740	7329267	Minus	79920-80510,80576-80746
	402825	6165330	Minus	78572-78807
	405973	8247789	Plus	103859-104254
30	405818	4071056	Plus	29055-29196
	402621	9930950	Plus	130806-131036
	401311	9212516	Minus	180124-180754
	401899	7230209	Minus	155620-155815
	403579	8101179	Minus	36167-36365
35	404600	8705107	Plus	118354-118444,118649-118792
	405531	9665194	Plus	35602-35803
	405542	9857564	Plus	71331-72183
	405131	8516051	Minus	136764-137594
	403026	7670575	Plus	56521-56840
40	405369	2078469	Minus	34183-34357,35686-35751
	405932	7767812	Minus	123525-123713
	405156	9966228	Plus	146733-146860,147899-147961,153127-15325
	402174	8575912	Plus	253499-253674
	405536	9795661	Plus	164091-164162,164397-164516,166720-16679
45	406109	9127147	Minus	58328-58485
	403162	9838085	Plus	82652-83613
	401404	7710968	Plus	136474-136646
	403167	9838127	Plus	162599-162935
	402209	8576119	Minus	53315-53472
50	400986	8085497	Minus	63140-63319
	404975	3419864	Minus	86096-86605
	404926	7341919	Minus	150411-151484

55

TABLE 35A: About 323 genes upregulated in hypersensitivity pneumonitis relative to idiopathic pulmonary fibrosis or non-specific interstitial pneumonitis

60	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigenelD:	Unigene number				
	Unigene Title:	Unigene gene title				
	R1:	90th percentile of HP AIs divided by 90th percentile of IPF AIs, where 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.				
65	R2:	90th percentile of HP AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.				
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
70	402550			Target Exon	4.03	4.70
	421563	NM_006433	Hs.105806	granulysin	3.37	2.70
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	3.31	2.42
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	3.09	1.51
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	2.99	1.28
	416350	AF188625	Hs.189507	phospholipase A2, group IID	2.71	1.43
75	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	2.70	1.53
	459705	BE082764	Hs.270252	ESTs, Weakly similar to androgen recepto	2.70	1.14
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.69	2.99
	452194	AI694413		olfactory receptor, family 2, subfamily	2.63	2.67
	447709	U97145	Hs.19317	GDNF family receptor alpha 2	2.63	1.52
80	410910	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.59	1.00
	454671	AW812929	Hs.336908	ESTs	2.50	2.34
	441859	AW194364	Hs.94814	interleukin-4 induced gene-1 protein (FI	2.45	1.90
	422398	AI476149	Hs.334489	hypothetical protein FLJ21992	2.45	1.36
	403244			C2002870*:g[82698]pir[JQ0985 hydroxypr	2.40	1.53

5	415462	R52692	Hs.12698	ESTs	2.40	1.00
	447028	AI973128	Hs.167257	brain link protein-1	2.33	1.64
	412394	AW984150		gb:PM2-HN0008-170300-001-h09 HN0008 Homo	2.32	1.00
	450165	AA007235	Hs.63931	ESTs	2.32	1.32
	431093	AB031038	Hs.301704	eomesodermin (Xenopus laevis) homolog	2.30	1.81
10	444090	S69115	Hs.10306	natural killer cell group 7 sequence	2.28	1.69
	413682	BE156991		gb:RC3-HT0371-290100-013-e02 HT0371 Homo	2.27	1.59
	441320	AI768724		fibulin 1	2.27	1.87
	456766	R87310	Hs.7740	oxysterol binding protein-like 1	2.27	1.36
	420340	NM_000734	Hs.97087	CD3Z antigen, zeta polypeptide (TIT3 com	2.26	1.98
15	459721	AI299050	Hs.143835	gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	2.25	1.82
	405452			Target Exon	2.25	1.29
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.25	5.80
	401447			Target Exon	2.25	1.55
	423066	Y18264	Hs.123094	sal (Drosophila)-like 1	2.24	1.51
20	441704	AI458766	Hs.192125	ESTs	2.24	1.00
	405097			ENSP00000175238*:A disintegrin and metal	2.24	1.00
	408544	AW293825		ESTs	2.22	1.95
	413454	BE141162		gb:MR0-HT0076-021299-001-d03 HT0076 Homo	2.20	2.26
	444404	M31525		major histocompatibility complex, class	2.20	1.37
25	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.19	2.88
	436063	AK000028		ribosomal protein S24	2.19	1.42
	429212	NM_001504	Hs.198252	G protein-coupled receptor 9	2.18	1.22
	400712			Target Exon	2.18	1.00
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	2.17	1.79
30	403478			NM_022342:Homo sapiens kinesin protein 9	2.17	1.80
	418747	AJ249977	Hs.88049	protein kinase, AMP-activated, gamma 3 n	2.17	1.76
	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquinone oxidore	2.16	1.44
	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.16	2.12
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	2.15	2.88
35	456057	AA947457	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.15	2.50
	444346	AI142274		ESTs	2.15	2.38
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.14	1.93
	451318	AA029888	Hs.95071	ESTs	2.14	1.16
	458935	Y16521	Hs.24812	CDP-diacylglycerol synthase (phosphatida	2.13	1.52
40	417105	X60992	Hs.81226	CD6 antigen	2.13	2.61
	408219	BE061111	Hs.254211	gb:QV0-BT0041-011199-039-f02 BT0041 Homo	2.13	1.94
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.11	2.66
	443711	N67861	Hs.49390	ESTs	2.10	1.00
	423234	AA323534	Hs.296162	AD037 protein	2.10	1.52
45	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.09	3.74
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	2.08	1.84
	405827			Target Exon	2.08	1.00
	406909	L20777	Hs.73885	gb:Human MHC class I HLA-G gene (HLA-A33	2.08	2.29
	437295	AW779318	Hs.88417	ESTs	2.07	1.72
50	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	2.07	1.00
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.07	2.16
	423901	AA333006		gb:EST37064 Embryo, 8 week I Homo sapien	2.07	1.50
	405075			Target Exon	2.07	1.15
	457423	AK000642	Hs.265018	hypothetical protein FLJ20635	2.07	2.67
55	406267			Target Exon	2.07	1.30
	423365	AA324992	Hs.257168	ESTs	2.06	1.70
	449970	AI678058	Hs.201227	ESTs	2.06	2.48
	430733	AW975920	Hs.121036	ESTs	2.06	1.00
	446323	AI288274	Hs.345792	ESTs	2.06	1.00
60	402240			Target Exon	2.05	1.94
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.05	1.44
	424463	AW195353	Hs.119903	ESTs	2.04	1.32
	400107			Eos Control	2.04	2.42
	404811			NM_021096:Homo sapiens calcium channel,	2.03	2.18
65	403589			Target Exon	2.03	1.57
	404088			Target Exon	2.03	1.00
	414991	C17898		gb:C17898 Human placenta cDNA (TFujiwara	2.03	2.04
	429073	AA446167	Hs.47385	ESTs	2.03	3.10
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfami	2.02	1.92
70	401897			C17001987:gi 7303380 gb AAF58438.1 (AE0	2.02	1.55
	431094	AW972276	Hs.116195	ESTs	2.02	1.00
	424899	AL119387	Hs.119062	ESTs	2.01	2.41
	419711	C02621	Hs.159282	ESTs	2.01	1.92
	459019	AA017156	Hs.40719	hypothetical protein KIAA1164	2.01	1.76
75	405453			NM_005748*:Homo sapiens YY1-associated f	2.01	1.24
	402516			Target Exon	2.01	1.00
	457365	AA577297	Hs.303249	EST	2.01	2.36
	407928	NM_002262	Hs.41682	killer cell lectin-like receptor subfami	2.01	2.62
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	2.00	1.64
80	406266			Target Exon	2.00	2.46
	419409	AW297831	Hs.143792	hypothetical protein MGC2656	2.00	1.60
	435028	AW193035	Hs.187370	ESTs	2.00	1.55
	404696			NM_013443:Homo sapiens CMP-NeuAC;(beta)-	2.00	1.21
	403533			Target Exon	2.00	1.17
	411673	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	2.00	1.00
	424148	BE242274	Hs.1741	integrin, beta 7	1.99	3.66
	419833	AA251131	Hs.220697	ESTs	1.99	1.69

5	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	1.99	1.84
	426416	AW612744	Hs.169824	killer cell lectin-like receptor subfam	1.98	2.56
	449317	AW293413	Hs.132906	19A24 protein	1.98	2.44
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	1.97	2.51
	422109	S73265	Hs.1473	gastrin-releasing peptide	1.97	3.32
10	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.96	1.86
	406303			C16000922:g 7499103 pir T20903 hypothe	1.96	2.16
	438676	AA813745	Hs.123446	ESTs	1.95	3.62
	404240			NM_018950:Homo sapiens major histocompat	1.95	2.06
	404056			Target Exon	1.94	2.60
15	425508	AA991551	Hs.97013	Homo sapiens, Similar to RIKEN cDNA 2310	1.93	3.24
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	1.93	2.35
	416941	BE000150	Hs.48778	niban protein	1.92	2.24
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.92	5.44
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	1.92	6.08
20	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	1.90	5.52
	446608	N75217	Hs.257846	ESTs	1.90	4.63
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.89	1.50
	414812	X72755	Hs.77367	monokine induced by gamma interferon	1.89	4.93
	422994	AW891802	Hs.296276	ESTs	1.88	3.30
25	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.88	2.17
	433671	AW138797	Hs.132906	19A24 protein	1.88	1.83
	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	1.86	3.12
	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of	1.86	1.88
	432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TIT3	1.84	1.65
30	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheli	1.83	2.46
	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	1.82	2.07
	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	1.82	2.63
	436485	X59135	Hs.156110	immunoglobulin kappa constant	1.82	2.75
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.81	4.56
35	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.80	5.10
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.79	1.89
	429670	L01087	Hs.211593	protein kinase C, theta	1.78	3.34
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.78	3.55
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.78	1.97
40	406672	M26041	Hs.198253	major histocompatibility complex, class	1.76	2.12
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.75	1.55
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	1.73	2.04
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	1.73	1.56
	414512	AL044336	Hs.6831	golgi phosphoprotein 1	1.73	2.00
45	426752	X69490	Hs.172004	titin	1.73	2.62
	444793	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	1.72	2.30
	452334	D60471	Hs.13390	gb:HUM111D09B Clontech human fetal brain	1.72	2.12
	446227	AI281459	Hs.270114	ESTs	1.72	2.48
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.72	2.72
50	423799	AW026300	Hs.132906	19A24 protein	1.71	2.40
	458332	AI000341		ESTs	1.70	3.71
	408380	AF123050	Hs.44532	diubiquitin	1.70	2.71
	437644	AA748575	Hs.136748	lectin-like NK cell receptor	1.70	2.58
	402736			NM_024852:Homo sapiens hypothetical prot	1.69	2.10
55	438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2	1.69	1.39
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	1.68	2.02
	426202	BE266484	Hs.82916	chaperonin containing TCP1, subunit 6A (1.68	2.14
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	1.68	3.30
	420440	NM_002407	Hs.97644	mammaglobin 2	1.67	2.42
60	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.67	1.49
	415823	R81864	Hs.205103	ESTs	1.65	2.16
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	1.65	1.58
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	1.63	1.94
	444929	AI685841	Hs.161354	ESTs	1.63	2.16
65	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.63	1.74
	418196	AI745649	Hs.26549	KIAA1708 protein	1.62	2.76
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.62	4.42
	438568	R98865	Hs.11135	major histocompatibility complex, class	1.62	1.74
	430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	1.62	1.85
70	433934	AW273261	Hs.216292	ESTs	1.62	2.00
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	1.61	2.00
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	1.61	1.46
	415349	AI766697	Hs.13231	ESTs	1.60	2.00
	406656	M16714	Hs.89643	major histocompatibility complex, class	1.60	1.47
75	456974	M15259	Hs.169401	apolipoprotein E	1.60	1.63
	416401	N80139	Hs.268916	ESTs	1.59	1.68
	439372	AF088033	Hs.159225	ESTs	1.59	2.04
	434666	AF151103	Hs.112259	T cell receptor gamma locus	1.59	4.08
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	1.58	3.06
80	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	1.58	2.37
	431903	AB029488	Hs.272100	SMS3 protein	1.57	2.14
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	1.57	2.28
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	1.56	1.46
	412472	AW975398	Hs.293836	ESTs	1.56	2.26
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	1.56	2.38
	412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.55	1.67
	449835	AW979300	Hs.293813	ESTs	1.55	2.16

	405545		Target Exon	1.55	2.64	
	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypothe	1.55	3.81
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.54	2.14
5	424243	AI949359	Hs.143600	ESTs, Highly similar to cis Golgi-locali	1.53	2.62
	457500	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	1.53	2.04
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	1.53	2.00
	439039	AI656707	Hs.48713	ESTs	1.53	2.38
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	1.52	2.65
10	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.52	2.06
	415198	AW009480	Hs.943	natural killer cell transcript 4	1.52	1.40
	431594	AI823999		ESTs	1.52	2.12
	432656	NM_000246	Hs.3076	MHC class II transactivator	1.52	2.20
	422426	W79117	Hs.58559	ESTs	1.52	2.22
15	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	1.51	2.80
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	1.50	1.67
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.49	3.12
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.49	1.78
	419166	AA234638	Hs.293584	ESTs	1.49	2.10
20	418323	NM_002118	Hs.1162	major histocompatibility complex, class	1.49	1.47
	435304	H10709	Hs.269524	ESTs	1.48	2.96
	452834	AI638627	Hs.105685	KIAA1688 protein	1.48	2.14
	446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.48	1.38
	429272	W25140	Hs.110667	ESTs	1.48	3.19
25	428379	X06026	Hs.2259	CD3G antigen, gamma polypeptide (Tit3 co	1.48	1.66
	433231	AB040926	Hs.143552	KIAA1493 protein	1.47	2.16
	408847	AW290997	Hs.30348	ESTs	1.46	2.08
	405441			Target Exon	1.46	2.99
30	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	1.45	1.56
	459644	AW197203		gb:xm38b01.x1 NCL_CGAP_GC6 Homo sapiens	1.45	2.44
	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	1.45	1.70
	422934	BE244189	Hs.122492	hypothetical protein	1.44	1.27
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	1.44	3.46
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.44	1.71
35	421407	T82331	Hs.182278	ESTs, Weakly similar to CGHU6C collagen	1.43	1.56
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	1.43	1.25
	400269			Eos Control	1.43	2.02
	420973	AA743415	Hs.291368	ESTs	1.42	2.06
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	1.42	2.20
40	430015	AW768399		ESTs	1.41	2.06
	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	1.41	1.31
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.40	1.72
	437479	R61866	Hs.101277	ESTs	1.40	2.52
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	1.40	2.17
45	416030	H15261	Hs.21948	ESTs	1.40	2.62
	419886	AA251562	Hs.146168	ESTs, Weakly similar to AF118023 1 SH3 d	1.40	1.68
	443951	F13272		ferritin, light polypeptide	1.40	1.64
	414875	H42679	Hs.77522	major histocompatibility complex, class	1.40	1.42
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platel	1.40	1.34
50	428782	X12830	Hs.193400	interleukin 6 receptor	1.40	2.30
	400680			NM_014207:Homo sapiens CD5 antigen (p56-	1.39	1.93
	428289	M26301	Hs.2253	complement component 2	1.39	1.39
	441410	AA932689	Hs.233304	ESTs, Weakly similar to I38022 hypothe	1.39	1.42
	406645	M57466	Hs.814	major histocompatibility complex, class	1.39	1.45
55	441379	AW175787	Hs.334841	selenium binding protein 1	1.38	1.32
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	1.38	2.04
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.38	1.35
	423526	AB011086	Hs.129739	KIAA0514 gene product	1.37	1.41
	424168	L29277	Hs.321677	signal transducer and activator of trans	1.37	1.33
60	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.37	1.74
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.35	1.38
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.35	1.54
	452353	C18825	Hs.29191	epithelial membrane protein 2	1.34	1.47
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	1.31	1.77
65	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	1.31	1.53
	444633	AF111713	Hs.286218	junctional adhesion molecule 1	1.30	1.37
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	1.29	1.49
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.28	1.36
	451864	N20370	Hs.69547	ESTs	1.28	1.42
70	421140	AA298741	Hs.102135	signal sequence receptor, delta (translo	1.28	1.31
	412790	NM_014767	Hs.74583	KIAA0275 gene product	1.28	1.63
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	1.28	1.38
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	1.28	1.36
	435822	T95594	Hs.187435	ESTs	1.27	1.82
75	455863	AA907305	Hs.36475	ESTs	1.27	1.36
	404277			NM_019111*:Homo sapiens major histocompa	1.27	1.52
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	1.27	1.54
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	1.27	1.53
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.26	1.27
80	434747	AA837085		ESTs	1.26	1.60
	425320	U29344	Hs.83190	fatty acid synthase	1.25	1.35
	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	1.25	1.41
	434644	H98071	Hs.4055	chromosome 21 open reading frame 50	1.25	1.30
	404854			Target Exon	1.25	1.57

5	406973	M34996	Hs.198253	major histocompatibility complex, class	1.25	1.57
	421071	AI311238	Hs.104476	ESTs, Weakly similar to CGHU1E collagen	1.24	1.26
	431779	AW971178	Hs.268571	apolipoprotein C-I	1.24	1.39
	416047	BE439894	Hs.78991	DNA segment, numerous copies, expressed	1.23	2.08
	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	1.23	1.20
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1.22	1.24
	415661	AF057307	Hs.78575	prosaposin (variant Gaucher disease and	1.22	1.16
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	1.22	1.17
10	420679	X57152	Hs.99853	fibrillarin	1.22	1.30
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	1.22	1.58
	418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfami	1.21	1.33
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	1.21	1.60
	406825	AI982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.20	1.20
15	436906	H95990	Hs.181244	major histocompatibility complex, class	1.19	1.27
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.19	1.62
	408279	AF216965	Hs.44095	Homo sapiens, clone MGC:12617, mRNA, com	1.18	1.25
	411372	AI147861	Hs.213289	low density lipoprotein receptor (famili	1.17	1.33
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.16	1.49
20	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.16	1.15
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	1.16	1.38
	432805	X94630	Hs.3107	CD97 antigen	1.16	1.22
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	1.16	1.41
	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group 1, m	1.16	1.36
25	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	1.15	1.27
	429832	AW293301	Hs.288472	ESTs, Weakly similar to UBPF_HUMAN UBIQU	1.15	1.72
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	1.15	1.21
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	1.14	1.21
	406782	AA430373		gb:zw20f11.s1 Soares ovary tumor NbHOT H	1.14	1.41
30	414662	AL036058	Hs.76807	major histocompatibility complex, class	1.12	1.25
	452547	AA335295	Hs.74120	adipose specific 2	1.11	1.39
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	1.11	1.22
	430280	AA361258	Hs.237868	interleukin 7 receptor	1.10	1.73
	441384	AA447849	Hs.288660	retinoic acid induced 3	1.09	1.22
35	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	1.09	1.14
	419200	AW966405		EST	1.08	1.64
	416511	NM_006762	Hs.79356	Lysosomal-associated multispinning membr	1.08	1.18
	409428	M33680	Hs.54457	CD81 antigen (target of antiproliferativ	1.07	1.12
	447023	AA356764	Hs.17109	integral membrane protein 2A	1.07	1.71
40	421481	AW391972	Hs.104696	KIAA1324 protein	1.07	1.58
	406868	AA505445	Hs.300697	Immunoglobulin heavy constant gamma 3 (G	1.07	1.23
	412819	T25829	Hs.24048	FK506 binding protein precursor	1.06	1.45
	418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	1.06	1.24
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.05	1.17
45	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.04	1.21
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.04	9.14
	418156	W17056	Hs.83623	nuclear receptor subfamily 1, group 1, m	1.03	6.65
	438089	W05391		nuclear receptor subfamily 1, group 1, m	1.03	8.00
	429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1	1.01	1.25
50	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.18
	438091	AW373062		nuclear receptor subfamily 1, group 1, m	0.99	12.84
	407018	U49869		NM_018955:Homo sapiens ubiquitin B (UBB)	0.99	1.07
	412896	AW804157	Hs.308026	major histocompatibility complex, class	0.98	1.57
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	0.97	1.40
55	426530	U24578	Hs.278625	complement component 4A	0.96	1.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	0.95	1.29
	407241	M34516		gb:Human omega light chain protein 14.1	0.94	1.11
	425371	D49441	Hs.155981	mesothelin	0.92	1.45
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (0.91	1.28

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TABLE 35B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

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Pkey CAT Number Accession

70

411089 5597_6 BI009308 BI009893 BF922203 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291
AW905577 AW975593 AA713730 AW836781 AA666384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555 AA586369
AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389
AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680
452194 90339_1 AI694413 AW994700 AI912946 N73548 AI082035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043
AI709339
410910 1063929_1 AW810196 AW810555 AW810507 AW810204 AW810619 AW810534
412394 1174616_1 AW947794 AW947793 AW947802 AW947798 AW947792 AW984150 AW984166 AW984167 AW984168 AW984179 AW984134 AW984160
AW984180 AW984194 AW984202 AW984190
413682 1527038_1 BE156943 BE157375 BE156965 BE156949 BE156956
441320 58978_5 AI346734 AI377971 BG193341 BG548376 AA928353 AI768724 BG215700 AA449370 BI462157 BI060283 BG677508 AA318802 BG719160
408544 683260_1 AW293825 AW235391
80 413454 1515217_1 BE141291 BE141306 BE141288 BE141283 BE141162 BE141168 BE141290 BE141161 BE141165
444404 16136_1 BC013183 AW408658 NM_002119 M31525 M26039 BM456399 BF732381 BM152457 AW407685 BM193161 AW407778 BI819141 AA702254
BF855074 BI761232

436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593 AI147991 AI142274 AI198553 AA338252 AA338213 AW962691 AA333006 AA332289 D78831 C17898 D78863 BF330730 BF350539 BE153665 BE065062 BE064650 BE064863 BF330763 BE153820 BE064737 BE155079 BE064651 AW856751 AW856622 BE064691 BE153674 BE153698 BE064730 BE153536 BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 W79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586 AI000341 AI766341 AW873274 AI823999 AA970060 AA508176 AW972585 AI873427 AW972389 BI093452 AW970865 BG118285 AA569075 AA492132 AW753140 AA213770 AA143654 W03900 AW197203 AW753300 X65018 BC022318 NM_003019 BE465060 AI732255 BF446634 AI820677 AI002217 AI924488 BI821373 BI770406 BI823937 BI820265 BI489632 BG482911 AA617783 AI807697 AW205576 T94427 AA487101 T94513 BI819407 BI822450 BI820618 BI824619 BG542824 BG537862 BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375827 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H06534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W58690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612085 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 AI334106 R63583 AI028079 AI140098 AI911625 AI890637 F34815 T65959 N40935 W52768 AA854747 AA861945 AA878472 AA778270 W32249 AA026061 W52662 W15352 W79670 W95384 T94283 AA002155 R82052 BE825493 BE825520 BE177661 H06215 BE144709 BE144829 AW976537 AI033582 AA837085 AA745261 AA648395 AA430373 AA968771 BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258 AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798 BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 BI496876 AI264159 BM128481 AI624657 AI689301 AI969467 AA861685 AA251595 AA625761 AA872090 AI826790 AA328366 BE827416 T75951 D56918 R68122 BE827384 AL118797 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302 BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701 AK054860 AV652198 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 BI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
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TABLE 35C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402550	7652009	Minus	80413-80673
403244	7637828	Plus	175792-176144
405452	7656638	Minus	93876-94275

5	401447	8574299	Minus	65053-65283
	405097	8072599	Plus	171191-171360
	400712	8118874	Plus	36087-36268
	403478	9958258	Plus	116458-116564
	405827	7109593	Plus	10279-10972
	405075	7770506	Minus	124680-125321
	406267	7528342	Minus	2570-2731
10	402240	7690131	Plus	104382-104527,106136-106372
	404811	3702428	Plus	26424-26596,28854-28987
	403589	8101229	Plus	5-330
	404088	9958257	Plus	184131-184295
	401897	8569218	Plus	604-767
	405453	7656675	Minus	83710-83980
15	402516	9798099	Minus	195342-195511
	406266	7528342	Minus	2365-2518
	404696	9800109	Minus	60037-60144,62675-63081
	403533	8076874	Plus	162922-163658
	406303	8575868	Plus	173622-173786
20	404240	5002624	Minus	116132-116407,116653-116922
	404056	3548785	Plus	75843-76980,77146-78263
	402736	9212044	Minus	66876-67010
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405441	7408124	Plus	100952-101283
25	400680	8118752	Plus	118343-118684,120720-121013
	404277	1834458	Minus	91665-91946
	404854	7143420	Plus	14260-14537

30 TABLE 36A: About 52 genes upregulated in non-specific interstitial pneumonitis relative to hypersensitivity pneumonitis or idiopathic pulmonary fibrosis

35 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of NSIP AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50.
 R2: 90th percentile of NSIP AIs divided by 90th percentile of IPF AIs, where the minimum value for the numerator and denominator was set to 50.

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
40	435140	AA668123	Hs.134170	ESTs	2.76	2.76
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57	1.00
	435375	AI733610		ESTs	2.55	2.55
45	420813	X51501	Hs.99949	prolactin-induced protein	2.55	1.35
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.52	0.73
	421296	NM_002666	Hs.103253	perilipin	2.50	2.45
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	2.43	1.79
	408882	H12084	Hs.31110	ESTs, Weakly similar to MAGE-B4 [H.sapie	2.42	1.77
50	437318	AW362939	Hs.120721	ESTs	2.36	1.61
	421823	N40850	Hs.28625	ESTs	2.29	0.56
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.28	0.89
	430536	AI809163	Hs.9908	nitrogen fixation cluster-like	2.25	2.80
	414009	R67516		ESTs	2.19	1.86
55	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.19	0.33
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	2.18	1.24
	413722	BE247354	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.14	1.95
	433874	AW204429	Hs.155033	ESTs	2.13	1.72
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.12	0.91
60	414290	AI568801	Hs.71721	ESTs	2.11	0.81
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.11	1.01
	406785	AA588061		gb:nk10d03.s1 NCI_CGAP_Co2 Homo sapiens	2.10	1.61
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.08	0.85
	444179	W35132	Hs.267442	ESTs	2.08	1.13
65	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.05	0.80
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.04	0.79
	439134	AA830599		ESTs	2.04	1.89
	418512	AW498974		diacylglycerol kinase, zeta (104kD)	2.02	2.02
	457311	AI497811	Hs.172753	Homo sapiens chromosome 19, BAC 41195 (C	2.00	1.45
70	402274			C{9000498*:gil4567179 gb AAD23607.1 AC00	1.88	2.24
	453222	AA033929	Hs.19156	ESTs	1.77	2.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	1.73	2.02
	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	1.69	1.69
	406714	AI219304	Hs.266959	hemoglobin, gamma G	1.62	2.47
75	418333	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	1.59	2.04
	404090			Target Exon	1.48	2.03
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	1.39	2.06
	414386	X00442	Hs.75990	haptoglobin	1.09	1.44
	439372	AF088033	Hs.159225	ESTs	1.05	2.13
80	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.01	2.08
	412472	AW975398	Hs.293836	ESTs	1.00	2.26
	432894	AW167668	Hs.279772	brain specific protein	0.97	1.19
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.96	2.06
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	0.95	1.08

424310	AA338648	Hs.50334	testes development-related NYD-SP22	0.93	1.47
422109	S73265	Hs.1473	gastrin-releasing peptide	0.92	3.05
420440	NM_002407	Hs.97644	mammaglobin 2	0.91	2.11
418196	AI745649	Hs.26549	KIAA1708 protein	0.90	2.25
418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	0.89	1.11
419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	0.85	1.74
446608	N75217	Hs.257846	ESTs	0.82	2.10
418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	0.73	1.32
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	0.70	1.76

TABLE 36B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
435375	130020_1	AI733610 AI049989 AA678769
414009	438978_1	BE221268 R67515 AV730582 R67516
406785	0_0	AA588061
439134	2581476_1	AA830599 AA970659 AA883802
418512	12225_6	BM046773 AA224297 T33786 T08951 T09274 T08592 T30936 AA350905
418333	73080_1	AF264624 AW668618 AV731446 R93353 AA584550 AV732728 BF802614 BF434359 AA077092 BI027317 AA199812 AW629027 AA831618 AI124782 AA765804 AA055698 AA677404 AA055366 AA889402 AA765530 BE503126 BE467367 AW139964 W81697 AI887846 W81696 AA447817 AA447667 F13631 BF055573 AW268271 AW088477 BF677839 AL601859 AW502118 AW502624 AA574189 BI020104

TABLE 36C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402274	2935596	Plus	5604-6527
404090	9967460	Minus	100815-100966

TABLE 37A: About 206 genes downregulated in lung fibrosis relative to normal lung

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of normal lung AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.

Pkey	ExAccn	UnigenelD	Unigene Title	R1
454229	AW957744	Hs.278469	lacrimal proline rich protein	11.67
432128	AA127221	Hs.296502	ESTs	9.86
421218	NM_000499	Hs.72912	cytochrome P450, subfamily 1 (aromatic c	7.69
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	7.32
420958	AA309431	Hs.66	interleukin 1 receptor-like 1	7.13
402608			Homo sapiens defensin, alpha 1, myeloid-	6.67
406714	AI219304	Hs.266959	hemoglobin, gamma G	5.40
406673	M34996	Hs.198253	major histocompatibility complex, class	5.22
416539	Y07909	Hs.79368	epithelial membrane protein 1	5.04
418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horsfall gly	4.77
409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	4.74
450847	NM_003155	Hs.25590	stanniocalcin 1	4.46
404518			CD83 antigen (activated B lymphocytes, i	4.36
413951	AW051200	Hs.75640	natriuretic peptide precursor A	4.32
407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	4.25
456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.23
429509	AW614420	Hs.204354	ras homolog gene family, member B	4.14
445769	AI741471	Hs.23666	ESTs	4.10
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.06
425571	AJ007292	Hs.158306	ephrin-A2	3.92
423168	R34385	Hs.124940	GTP-binding protein	3.80
401234			mitogen-activated protein kinase 8 inter	3.78
402181			Target Exon	3.77
403479			NM_007064:Homo sapiens serine/threonine	3.68
435424	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL	3.68
402911			NM_021158*:Homo sapiens protein kinase d	3.66
442195	NM_001430		endothelial PAS domain protein 1	3.65
400089			Eos Control	3.60

	413948	C05145	Hs.75636	myosin light chain 2a	3.56
	438564	AA381553	Hs.198253	major histocompatibility complex, class	3.54
	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.54
	431319	AA873350	Hs.302232	ESTs	3.52
5	434292	AF124368	Hs.306551	Homo sapiens IMAGE Consortium ID 839832,	3.48
	401540			NM_002675:Homo sapiens promyelocytic leu	3.46
	426477	AA379464	Hs.154073	gb:EST92386 Skin tumor l Homo sapiens cD	3.43
	402328			Target Exon	3.42
10	401590			Target Exon	3.42
	403645			NM_024513*:Homo sapiens FYVE and coiled-	3.37
	403376			Target Exon	3.36
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.35
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.28
15	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.27
	401126			NM_006856*:Homo sapiens activating trans	3.27
	408243	Y00787	Hs.624	interleukin 8	3.23
	412429	AV650262	Hs.75765	GRO2 oncogene	3.22
	426420	BE383808	Hs.322430	NDRG family, member 4	3.21
20	449338	H73444	Hs.394	adrenomedullin	3.19
	401904			Target Exon	3.16
	401919			NM_012448*:Homo sapiens signal transduce	3.14
	406443			ENSP00000236574*:Hypothetical 21.8 kDa p	3.14
	458232	BE217872	Hs.279537	ESTs	3.12
25	406016			Target Exon	3.12
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	3.11
	451831	NM_001674	Hs.460	activating transcription factor 3	3.08
	450562	AW136468	Hs.202199	ESTs	3.07
	405838			Target Exon	3.04
30	451029	AA852097	Hs.25829	ras-related protein	3.02
	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	2.98
	439839	AA889354		ESTs	2.98
	439891	AL389940	Hs.109968	ESTs	2.96
	418935	T28499	Hs.89485	carbonic anhydrase IV	2.95
35	418853	NM_005236	Hs.89296	excision repair cross-complementing rode	2.95
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.94
	410326	AI368909	Hs.47650	ESTs	2.88
	407244	M10014		fibrinogen, gamma polypeptide	2.85
40	459721	AI299050	Hs.143835	gb:gn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	2.84
	416212	R40290	Hs.124685	ESTs	2.84
	428686	AA431801	Hs.98764	ESTs, Weakly similar to A29861 actin gam	2.83
	437508	AI204354	Hs.121347	ESTs	2.82
	437990	AI686579	Hs.121784	ESTs	2.82
	443709	AI082692	Hs.134662	ESTs	2.81
45	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	2.80
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	2.79
	404231			Target Exon	2.78
	434305	AI018280	Hs.130189	ESTs	2.77
	445493	AI915771		metallothionein 1E (functional)	2.76
50	418056	AA524886		gb:nh34f02.s1 NCI_CGAP_Pr3 Homo sapiens	2.76
	404102			Target Exon	2.75
	440206	AI762232	Hs.46794	ESTs	2.75
	403031			cathepsin D (lysosomal aspartyl protease	2.75
	413164	BE068494		gb:MR1-BT0371-050500-009-a12 BT0371 Homo	2.74
55	459330	C16931		gb:C16931 Clontech human aorta polyA mRNA	2.74
	456967	AW004056	Hs.168357	T-box 2	2.74
	427602	AI375258	Hs.98005	ESTs	2.74
	431367	Z20964	Hs.323817	DKFZP547E1010 protein	2.72
	406059			Target Exon	2.71
60	420575	BE263301	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	2.71
	457275	AA463422	Hs.209431	ESTs	2.71
	432559	AW452948	Hs.257631	ESTs	2.71
	402483			NM_020389:Homo sapiens putative capacita	2.70
	416069	R37101	Hs.20982	ESTs	2.70
65	445445	AF238870	Hs.275706	Homo sapiens clone GLSH-3 similar to gli	2.69
	436232	AA707006	Hs.187863	ESTs	2.68
	418773	T39748	Hs.325474	Target CAT	2.67
	434038	AA622104		ESTs	2.67
	405448			Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.66
70	404439			ENSP00000067222*:Mitochondrial 28S ribos	2.65
	435724	N39308	Hs.117898	ESTs	2.65
	404026			Target Exon	2.65
	400881			NM_025080:Homo sapiens hypothetical prot	2.64
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	2.62
75	405429			Target Exon	2.62
	402642			C1002296:gij6677817[ref NP_033126.1] rep	2.61
	438575	BE304709	Hs.146550	myosin, heavy polypeptide 9, non-muscle	2.61
	449293	AA001088	Hs.29739	ESTs, Weakly similar to C34323 GTP-bindi	2.61
	416157	NM_003243	Hs.342874	transforming growth factor, beta recepto	2.60
80	446122	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.59
	433291	AF007191		gb:Homo sapiens SIB 276 intestinal mucin	2.59
	426795	AI810474	Hs.196945	ESTs	2.58
	423503	M92843	Hs.343586	zinc finger protein homologous to Zfp-36	2.58
	430768	AB030207	Hs.247888	guanine nucleotide binding protein 13, g	2.58

	423387	AJ012074		vasoactive intestinal peptide receptor 1	2.57
	442681	AI809182	Hs.130907	ESTs	2.57
	408652	R43409	Hs.6829	Homo sapiens mRNA for KIAA1644 protein,	2.56
5	402217			C19001662*:gil6753872[ref]NP_034345.1 i	2.56
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.56
	455674	BE065941		gb:RC3-BT0319-100100-012-d12 BT0319 Homo	2.56
	457831	AA706937	Hs.120802	ESTs, Moderately similar to A26641 Na?ex	2.56
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.55
10	458648	AW444551	Hs.35380	x 001 protein	2.55
	456663	BE251104	Hs.113052	RNA cyclase homolog	2.54
	440178	AW502463	Hs.196521	ESTs	2.53
	457139	AI557280	Hs.184270	capping protein (actin filament) muscle	2.52
	405857			Target Exon	2.51
15	410204	AJ243425	Hs.326035	early growth response 1	2.50
	412851	AI826502	Hs.97269	ESTs	2.49
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	2.49
	409209	AA460160	Hs.73217	ESTs	2.49
	447173	AW449385	Hs.157294	ESTs	2.48
20	440034	AI908639	Hs.246781	ESTs	2.44
	418168	R85350	Hs.101368	ESTs	2.43
	417295	AW993524	Hs.43148	epithelial membrane protein 1	2.43
	405305			transcriptional adaptor 3 (ADA3, yeast h	2.42
	427886	AA417083	Hs.104789	ESTs	2.42
25	436409	AJ238982	Hs.183656	VNN3 protein	2.42
	413861	BE175424		gb:RC4-HT0578-170300-012-d01 HT0578 Homo	2.40
	403605			C3000142*:gil4503015[ref]NP_003900.1 co	2.37
	402594			C1002603*:gil9887091[gb]AAG01738.1 AF248	2.37
	402803			NM_001397:Homo sapiens endothelin conver	2.37
30	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.36
	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	2.36
	442630	AW572938	Hs.130580	ESTs	2.35
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	2.33
	405156			NM_003213*:Homo sapiens TEA domain famil	2.31
35	448162	AL039531	Hs.323363	hypothetical protein FLJ22169	2.31
	403591			Target Exon	2.31
	406193			Target Exon	2.30
	420813	X51501	Hs.99949	prolactin-induced protein	2.30
	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	2.28
40	400703			C11001794*:gil10946612[ref]NP_067286.1	2.27
	415026	AA159356	Hs.72308	ESTs	2.25
	400334	Y13187		Homo sapiens dmd gene, intron 11	2.18
	445878	AI262974	Hs.145587	ESTs	2.18
	404975			uncharacterized hypothalamus protein HT0	2.18
45	436370	R01220	Hs.185679	ESTs	2.17
	400513			Target Exon	2.16
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.15
	415405	R59141		gb:yg96d11.r1 Soares infant brain 1NIB H	2.15
	407612	U26403	Hs.37142	ephrin-A5	2.12
50	409837	AW501504		gb:UI-HF-BP0p-ajd-h-04-0-UI.r1 NIH_MGC_5	2.08
	458637	AV657446		gb:AV657446 GLC Homo sapiens cDNA clone	2.07
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	2.00
	418922	AW956580	Hs.42699	ESTs	1.98
	402404			NM_024967*:Homo sapiens hypothetical pro	1.98
55	421993	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	1.98
	413731	BE243845	Hs.75511	connective tissue growth factor	1.96
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	1.96
	428193	NM_004235		Kruppel-like factor 4 (gut)	1.93
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.92
60	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	1.92
	433883	AI925688	Hs.222312	ESTs	1.91
	406564			msh (Drosophila) homeo box homolog 2	1.91
	403581			Target Exon	1.90
	403716			Target Exon	1.90
	404758			Target Exon	1.90
65	439500	W73158	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	1.89
	448793	AI864581		ESTs	1.84
	435857	AF253468	Hs.3736	delta-like 4 homolog (Drosophila)	1.83
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.82
70	402051			Target Exon	1.81
	409859	AW501926		gb:UI-HF-BR0p-ajp-f-08-0-UI.r1 NIH_MGC_5	1.78
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	1.78
	405063			Target Exon	1.78
	405163			C5000561*:gil7513700[pir]T14151 Inv pro	1.75
75	402386			Target Exon	1.73
	406755	N80129	Hs.199263	metallothionein 1L	1.73
	409811	AW500896		gb:UI-HF-BP0p-air-a-03-0-UI.r1 NIH_MGC_5	1.70
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.70
	400489			Target Exon	1.70
80	428704	AA432007	Hs.192090	ESTs	1.69
	429307	AU076592	Hs.198951	jun B proto-oncogene	1.67
	400116			Eos Control	1.65
	404795			Target Exon	1.65
	408053	AW139474	Hs.246862	ESTs	1.65

414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	1.63
428800	M57627	Hs.193717	interleukin 10	1.63
451676	R84770	Hs.33538	ESTs, Weakly similar to oxygen-regulated	1.62
402394			Target Exon	1.61
404818			Target Exon	1.60
436364	X06096		gb:Human macrophage alpha1-antitrypsin c	1.55
420369	U96769	Hs.97220	chondroadherin	1.54
405590			CX001497*:gi 4557543 ref NP_001384.1 ex	1.54
402448			Target Exon	1.53
433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	1.51
409020	AA062549	Hs.21162	retbindin	1.51
405443			Target Exon	1.12

TABLE 37B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409385	110758_1	T65940 T64515 AA071267 AA071334
442195	15007_1	U81984 NM_001430 BE907085 BI333232 AI021986 AU138476 C18601 U51626 AU100517 BI054387 AU076970 BE786454 BG010080 AW377189 BF998789 AA368139 R11396 T83613 BG006324 BI012404 BG001643 BF757957 AL549361 AL544018 BE002870 BE929314 BE090199 AL046650 BI053717 BE929315 BI054967 BF960055 BF925432 R05421 BF922073 T70331 BI004403
439839	2594580_1	AI023587 AA889354 AA846791
445493	423456_1	AV711317 AI809938 AI808768 AI240593 AI915771
418056	286199_1	AW971347 AA524886 AA211537 BF903005 BF357120
413164	1492512_1	BE068758 BE068745 BE068689 BE068778 BE068529 BE068683 BE068445 BE068392 BE068719 BE068473 BE068521 BE068628 BE068422 BE068618 BE068354 BE068390 BE068414 BE068433 BE068369 BE068384 BE068661 BE068324 BE068301 BE068436 BE068754 BE068329 BE068672 BE068494 BE068596 BE068332 BE068347 BE068588 BE068328 BE068493 BE068740 BE068685 BE068759 BE068307 BE068429 BE068303 BE068693 BE068374 BE068295 BE068625 BE068302 BE068663 BE068675 BE068579 BE068311 BE068674 BE068547 BE068602 BE068605 BE068352 BE068306 BE068401 BE068537 BE068552 BE068450 BE068723 BE068393 BE068671 BE068748 BE068317 BE068447 BE068568 BE068632 BE068357 BE068330 BE068498 BE068631 BE068540 BE068410 BE068626 BE068591 BE068522 BE068676 BE068499 BE068361 BE068598 BE068350 BE068299 BE068580 BE068567 BE068692 BE068321 BE068327 BE068739 BE068526 BE068538 BE068765 BE068340 BE068733 BE068293 BE068565 BE068480 BE068476 BE068761 BE068712 BE068706 BE068549 BE068419 BE068383 BE068434 BE068418 BE068525 BE068543 BE068752 BE068550 BE068623 BE068470
459330	105725_1	BG563152 BF846777 BF849354 BF849359 BF846636 BF849201 BF849356 C16931 AA056717 AW864542 AW882724 AA056567
434038	630986_1	AI910738 AW139227 AA932891 AA622104
433291	73706_1	AF007191 AW820706 BG978594 BF872238
432387	2612_2	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138
455674	1490762_1	BE065941 BE065997 BE066003 BE066070 BE066098
413861	1561647_1	BF352282 BE175424 BE175418 BE175383
409368	110612_1	AA071059 AA085201 AA085020
415405	1872126_1	W18191 R59141 R54142 R12130 F11362 Z42794 F08242 F07925 H21084 R54090 R59142
409837	915621_1	AW501504 AW501656 AW503048 AW502449 AW502098
458637	395206_1	AV657752 AV657446
428193	430_1	AF105036 U70663 NM_004235 AF022184 AU141767 AU141110 AL040569 D44830 BI011351 AL575805 AI290876 AI014784 AI393429 AI266211 AW074303 AA620711 BF197792 AW008766 D25944 AI687397 AA621680 AV714408 BF446905 BM314505 BF514079 BM314197 AA845201 AW874084 BE720622 AI127241 AA236239 AI679709 AI679135 AI572470 AA573434 AI568487 BE049325 AA687950 BG925989 AI338031 AI365073 AI024576 AA298805 H04001 H45668 BG682146 AL552388 BI462361 BG547513 BG896863 BI256661
448793	3006936_1	A936948 AI864581 AI570641
409859	916430_1	AW501926 AW502566 AW501927
409811	58948_2	AK057581 AW500962 AW500896 AW501105
400116	5269_1	D42041 NM_014610 AJ000332 BI758702 BG720650 AU141129 AU130711 AU141380 AU132402 BM048556 AU127520 BE259984 AU128952 BE614151 AL601516 BM146777 AU128103 BM194094 BE937951 BE696396 AK026997 AK026567 BF969293 BE798100 BI086881 BI166248 BE877845 BG385414 AW886747 BF093789 AW390159 BF820311 AA421676 AW880845 AW04827 BF726465 BE161190 BE254102 AW406002 BE161223 AI912055 BF930228 AW374357 AW794531 BE720524 BE933982 BE933658 BE933694 BE933978 BE933654 BE933583 BE166557 BE933874 BE933641 BE933859 BE933626 BE933866 BE933633 BE933864 BE933631 BE933867 BE933634 BE933857 BE933624 BE933883 BE933650 BE720491 AA420426 BE720410 BE720458 BE720444 BE720411 AW368748 BF874616 BE933498 BE835979 BF926667 AW849921 AW850026 AW850022 AW849977 AW849900 BG250251 W87689 AI192825 AI692824 AA426263 AI090315 AI309537 AA877437 AA478438 AI538868 AW276162 AI279916 AA600318 AI188836 AW662284 AI262619 AA293457 BF347442 AA421677 AA658063 AA565510 AA937060 AI142684 AA788940 AA827426 AU152614 AI342784 AU148738 AA219664 AA047835 H99450 AA018563 AI073634 BM475120 BG875251 BG248778 U46372 AA383858 AU140356 BG821891 BF935049 BI760656 BI054103 BF982309 BE872215 BI257291 AU158469 AU160599 AU152469 AU152375 AU152059 AU148575 N32267 AU149554 AI627459 AI719840 AW779017 AI291493 AW304181 AW470055 AI086491 AI311387 AI634232 AI151241 AI288848 AW050588 AW589580 AI241353 AI880219 AA039309 AA026517 AA016238 AA013444 H86822 R87530 AA058462 N27082 Z39679 BE544309 W52619 AA018076 AI813668 AW189907 AI418104 AU159878 AU150087 R21754 AA015932 H67274 AU153097 AI961344 AA018208 W32429 R45344 R77453 BM470129 AU130415 BI227374 BE298179 AW844963 AW844983 AI904066 AA379006 BF850571 AA355641 BG747156 AL547262 AW357941 BE560004 BI116061 BG899031 BE560318 BF174177 BI051456 BE001967 BE386446 BF969326 BF808765 BF684480 BG421617 AI940607 AW875483 BE789632 BF808711 BI192691 AW904249 BI911430 BE265407 BE730343 BE397808 BI226516
414580	623093_1	BG333973 BE385437 BE408833 BE387650
436364	1414_37	X05826 X06096 BG468890 AW951851 W23562 T28392 H56742 H58030 T69205

TABLE 37C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	402608	9910096	Plus	37495-37669
	404518	8151988	Plus	84494-84603
	401234	9929642	Plus	120173-120337
	402181	8575912	Plus	449746-450040
10	403479	7329292	Minus	148369-148533,150678-150809
	402911	7263904	Plus	142689-142979
	401540	8072433	Plus	106838-107310
	402328	4464283	Minus	13758-13922,14558-14752
	401590	9966320	Minus	33547-33649
15	403645	8699714	Minus	4433-4582
	403376	9369545	Minus	108698-108830
	401126	8699701	Minus	68290-68487
	401904	8671966	Plus	60959-61603,62670-62890,63778-63838
	401919	9502466	Plus	67536-67666
20	406443	9280765	Plus	85951-87327
	406016	8272661	Plus	41341-41940
	405938	6758795	Minus	166671-167411
	404231	8218035	Minus	61077-61322
	404102	7229900	Plus	97685-98018
25	403031	7768597	Minus	1308-1416
	406059	9103984	Minus	13856-14004
	402483	7574980	Minus	65578-66119
	405448	7582529	Plus	136347-136532
	404439	7139680	Plus	55316-55585
30	404026	7582549	Minus	79674-79968
	400881	2842777	Minus	91446-91603,92123-92265
	405429	7321905	Minus	51577-51723
	402642	9958129	Minus	125599-125756
	402217	9795981	Minus	21521-21757
35	405857	6758728	Plus	26564-26819
	406305	8575869	Plus	108239-108386,112216-112378,115388-11557
	403605	6862654	Plus	91614-91718
	402594	7705170	Plus	103082-103414
	402803	3287156	Minus	55923-56033
40	405156	9966228	Plus	146733-146860,147899-147961,153127-15325
	403591	8101229	Plus	4201-4833
	406193	7289992	Plus	30183-30662
	400703	8118859	Plus	63657-63857,64802-64905
	404975	3419864	Minus	86096-86605
45	400513	9796593	Plus	74613-74823
	402404	3970932	Plus	53154-53280
	406564	7711604	Minus	52788-53013
	403581	8101182	Plus	6794-7396
	403716	7239669	Plus	86899-87122
50	404758	7706327	Minus	130204-130806
	402051	8082020	Minus	19346-19480,20041-20119
	405063	7658414	Minus	111047-111666
	405163	9966267	Minus	161171-161299
	402386	9799769	Plus	22069-22303
55	400489	8954013	Plus	131475-131652
	404795	4826439	Plus	147501-147780
	402394	9929680	Plus	33308-33482
	404818	2769655	Plus	33671-33839
	405590	6960456	Plus	90492-90818
60	402448	9796640	Plus	112942-113069,114303-114521
	405443	7408143	Plus	90716-90887,101420-101577

65 TABLE 38A: About 207 genes upregulated in lung fibrosis relative to normal tissues

65 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 70 Unigene Title: Unigene gene title
 R1: 90th percentile of lung fibrosis AIs divided by 70th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
75	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.28
	407891	AA486620	Hs.41135	endomucin-2	4.14
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.07
	410219	T98226	Hs.171952	occludin	3.96
80	434666	AF151103	Hs.112259	T cell receptor gamma locus	3.88
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	3.87
	406617			Target Exon	3.76
	420568	F09247	Hs.247735	protocadherin alpha 10	3.70
	425873	NM_013390	Hs.160417	transmembrane protein 2	3.69

	438797	C16161	Hs.283040	hypothetical protein PRO2543	3.68
	410315	AI638871	Hs.152519	Homo sapiens cDNA: FLJ22524 fis, clone H	3.65
	446714	W73818	Hs.110028	ESTs	3.64
5	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.61
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	3.58
	412790	NM_014767	Hs.74583	KIAA0275 gene product	3.56
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	3.56
	412654	AI093480		hypothetical protein FLJ11896	3.56
10	414386	X00442	Hs.75990	haptoglobin	3.54
	451035	AU076785	Hs.430	plastin 1 (I isoform)	3.52
	436473	AI193122	Hs.132275	ESTs	3.51
	406714	AI219304	Hs.266959	hemoglobin, gamma G	3.46
	414586	AA306160	Hs.16488	lymphocyte cytosolic protein 1 (L-plasti	3.45
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	3.45
15	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	3.39
	452813	U54727	Hs.191445	ESTs	3.36
	442831	AI798959	Hs.131686	ESTs	3.35
	427774	AA278583	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA	3.34
	445330	R52656	Hs.21691	ESTs	3.31
20	436001	AW903849	Hs.173840	HUEL (C4orf1)-interacting protein	3.31
	431681	AK000378	Hs.267566	hypothetical protein FLJ20371	3.29
	432314	AA533447	Hs.312989	ESTs	3.28
	435129	AI381659	Hs.267086	ESTs	3.28
25	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.24
	422607	Z45471	Hs.118684	stromal cell-derived factor 2	3.21
	421205	AL137540	Hs.102541	netrin 4	3.20
	428582	BE336699	Hs.185055	BENE protein	3.20
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.19
30	424880	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	3.17
	421233	AA209534	Hs.284243	tetraspan NET-6 protein	3.17
	429350	AI754634	Hs.131987	ESTs	3.16
	428727	AF078847	Hs.191356	general transcription factor IIH, polype	3.16
	434850	Z43161	Hs.283714	30 kDa protein	3.13
35	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	3.12
	446506	AI123118	Hs.15159	chemokine-like factor, alternatively spl	3.11
	416114	AI695549	Hs.183868	glucuronidase, beta	3.10
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	3.09
	444212	AW503976	Hs.10649	basement membrane-induced gene	3.08
40	422442	AA324998	Hs.147066	signal transducer and activator of trans	3.08
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	3.08
	424456	AA341017	Hs.25549	hypothetical protein FLJ20898	3.07
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.07
	445107	AI208121	Hs.147313	ESTs, Weakly similar to I38022 hypothe	3.06
45	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	3.04
	428106	BE620016	Hs.182470	PTD010 protein	3.04
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	3.04
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.03
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.02
50	423067	AA321355	Hs.285401	colony stimulating factor 2 receptor, be	3.01
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	2.96
	415000	AW025529	Hs.239812	Homo sapiens serologically defined breas	2.96
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	2.96
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	2.96
55	419660	BE280337	Hs.194693	solute carrier family 7 (cationic amino	2.96
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.95
	414493	AL133921	Hs.76272	retinoblastoma-binding protein 2	2.94
	416883	AW140128	Hs.184902	ESTs	2.92
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	2.92
60	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	2.92
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	2.92
	429640	U83508	Hs.2463	angiopoietin 1	2.91
	449843	R85337	Hs.24030	solute carrier family 31 (copper transpo	2.91
	401958			Target Exon	2.90
65	416926	H03109	Hs.263395	HT018 protein	2.90
	433691	AA605012		ESTs	2.88
	441892	AB028981	Hs.8021	KIAA1058 protein	2.87
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.87
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	2.87
70	414291	AI289619	Hs.13040	G protein-coupled receptor 86	2.87
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	2.87
	435913	W95006	Hs.269559	ESTs, Weakly similar to S65657 alpha-1C-	2.86
	422050	AA302741	Hs.25786	ESTs, Moderately similar to JC5238 galac	2.85
	451356	AA748418	Hs.164577	ESTs	2.85
75	442085	AA975688	Hs.159955	ESTs	2.84
	427704	AW971063	Hs.292882	ESTs	2.83
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	2.83
	441965	AA972712	Hs.269737	ESTs	2.82
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	2.82
80	450056	BE047394	Hs.8208	ESTs, Weakly similar to S71512 hypothe	2.80
	407245	X90568	Hs.172004	titin	2.80
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.80
	446601	AI312783	Hs.155772	Homo sapiens thymic stromal co-transport	2.80
	432195	AJ243669	Hs.8127	KIAA0144 gene product	2.80

	449088	AI654048	Hs.196556	ESTs	2.80
	416511	NM_006762	Hs.79356	Lysosomal-associated multispinning membr	2.80
	406648	AA563730	Hs.277477	major histocompatibility complex, class	2.79
	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	2.78
5	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	2.78
	440255	AI932285	Hs.160569	ESTs	2.78
	410057	R66634	Hs.268107	multimerin	2.77
	417497	AW402482	Hs.82212	CD53 antigen	2.77
10	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.76
	431884	AA521246	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.75
	409969	AW514668	Hs.194258	ESTs, Moderately similar to ALU5_HUMAN A	2.75
	436729	BE621807		transmembrane 4 superfamily member 1	2.75
	431451	AA761378	Hs.192013	ESTs	2.74
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.74
15	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	2.74
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	2.74
	424673	AA345051	Hs.294092	ESTs, Weakly similar to I38022 hypotheti	2.74
	443194	AI954968		matrix Gla protein	2.71
20	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.71
	452870	AW502761	Hs.30909	KIAA0430 gene product	2.70
	430334	AI824719	Hs.143251	ESTs	2.70
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	2.70
	432279	N95104	Hs.274260	ATP-binding cassette, sub-family C (CFTR	2.70
25	413950	AA249096	Hs.32793	ESTs	2.70
	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus rec	2.70
	431710	AI735482		ESTs	2.70
	448749	AW859679	Hs.21902	Homo sapiens clone 25237 mRNA sequence	2.69
	451154	AA015879	Hs.33536	ESTs	2.69
30	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	2.69
	446899	NM_005397	Hs.16426	podocalyxin-like	2.68
	418031	AA648744	Hs.269493	ESTs	2.68
	453902	BE502341	Hs.3402	ESTs	2.68
	405121			mitogen-activated protein kinase 8 inter	2.68
35	410163	AF151977	Hs.59260	NTT5 protein	2.67
	429632	AW195336	Hs.148910	ESTs	2.67
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	2.67
	455004	AW850303		gb:IL3-CT0219-191199-030-F09 CT0219 Homo	2.67
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	2.67
40	401113			solute carrier family 22 (organic cation	2.66
	419462	AF071076	Hs.112255	nucleoporin 98kD	2.66
	407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-lin	2.66
	419175	AW270037		KIAA0779 protein	2.66
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	2.66
45	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	2.66
	430592	AJ224864	Hs.9688	leukocyte membrane antigen (IRC1)	2.65
	446830	BE179030		Human DNA sequence from clone RP5-1174N9	2.64
	433327	AI674779	Hs.126744	ESTs	2.64
	424868	AI568170	Hs.96886	ESTs	2.64
50	429854	R55508	Hs.99472	ESTs	2.63
	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.63
	456711	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	2.63
	419777	D60134	Hs.270975	ESTs	2.63
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	2.62
55	427596	AA449506	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.62
	452445	AB002438	Hs.29596	Homo sapiens mRNA from chromosome 5q21-2	2.62
	447482	AB033059	Hs.18705	KIAA1233 protein	2.62
	419110	AA234171	Hs.187626	ESTs	2.62
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	2.62
60	419828	T81422	Hs.14922	ESTs	2.62
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	2.62
	412491	W31589	Hs.73957	RAB5A, member RAS oncogene family	2.61
	436496	AA281959	Hs.5210	glia maturation factor, gamma	2.61
	435053	AW629386		ESTs	2.61
65	435029	AF167706	Hs.19280	cysteine-rich motor neuron 1	2.61
	425976	C75094	Hs.334514	NG22 protein	2.60
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	2.60
	430539	AK001489		ADP-ribosylation factor-like 1	2.60
	419825	AI754011	Hs.7326	ESTs	2.59
70	412577	Z22968	Hs.74076	CD163 antigen	2.58
	425894	AW954011	Hs.180711	ESTs	2.58
	410883	D43767	Hs.66742	CCL17 chemokine (TARC) (SCYA17)	2.58
	441028	AI333660	Hs.17558	Homo sapiens cDNA FLJ14446 fls, clone HE	2.58
	413949	AA316077	Hs.75639	Human TB1 gene mRNA, 3' end	2.58
75	434943	AI929819	Hs.92909	chromosome 21 open reading frame 50	2.58
	443605	H06865	Hs.134131	ESTs	2.57
	425017	AL119305	Hs.26409	ESTs	2.57
	440334	BE276112	Hs.7165	zinc finger protein 259	2.56
80	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.56
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.56
	407174	T79938	Hs.77062	leukocyte immunoglobulin-like receptor,	2.56
	443834	AI741510	Hs.173548	ESTs	2.55
	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	2.55
	420539	AA282735	Hs.44004	AD031 protein	2.55

421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	2.54
437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.54
422994	AW891802	Hs.296276	ESTs	2.54
411992	AW816214	Hs.143055	ESTs	2.54
451180	H61899	Hs.171937	steroid dehydrogenase-like	2.54
415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypothei	2.53
429752	H52348	Hs.36636	ESTs	2.53
414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.53
453329	T97205	Hs.193400	ESTs, Weakly similar to 2109260A B cell	2.53
436503	AJ277750	Hs.183924	ubiquitin associated and SH3 domain cont	2.52
445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	2.52
433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.52
435943	R60194	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.52
452253	AA928891	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H	2.52
442506	BE566411	Hs.41726	ESTs	2.52
419972	AL041465	Hs.182982	golgin-67	2.52
431074	BE072772	Hs.8997	ESTs, Moderately similar to A46010 X-lin	2.52
449129	AI631602	Hs.258949	ESTs	2.52
440524	R71264	Hs.16798	ESTs	2.51
419203	AA488719	Hs.190151	ESTs	2.51
404370			Target Exon	2.51
432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	2.51
439219	N33883	Hs.41322	ESTs	2.51
428044	AA093322	Hs.301404	RNA binding motif protein 3	2.50
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.50
437644	AA748575	Hs.136748	lectin-like NK cell receptor	2.50
442566	R37337	Hs.12111	ESTs	2.50
409317	U20165	Hs.53250	bone morphogenetic protein receptor, typ	2.50
450506	NM_004460	Hs.418	fibroblast activation protein, alpha	2.50
447484	AA464839	Hs.292566	hypothetical protein FLJ14697	2.50
415165	AW887604	Hs.78065	complement component 7	2.50
435284	AA879470	Hs.96849	Homo sapiens cDNA FLJ11492 fis, clone HE	2.50

TABLE 38B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
412654	1350_1	BG743181 AI830050 BE695688 AA126591 AI903503 R26045 N62894 N63950 AA131619 AI681480 N79626 AA461603 R78979 AW608865 N66622 BF448838 AA779000 AA460314 AI092721 AI870182 AI436284 AI494151 AI127704 AI127702 BE349350 AI093480 AA115264 AA131567 R26840 R78885
433691	2203511_1	AI223854 AI129852 AA605012
436729	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI242384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820730 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AI565586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI707221 BE910282 BG538748 AW960564 AV732879 DI16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 BI754027 BF696071 AI351939 BG151298 AI919334 AI401620 BI770165 W72057 T96158 T29478 AA181252 BG927793 AA714431 AA600749 AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832406 AA102441 BG928081 AA993445 AA916041 AA987847 AA983329 AA737219 AA916443 AW128994 AI492560 AI761847 BC005272 NM_000900 X53331 M58549 BI758966 AL598829 BI754530 BG699770 BE439699 BE440148 AV704365 AV733652 BG212015 BG184149 BG200180 BG212690 BI761222 BG182079 AW338822 AI925631 AI423041 AW071181 AI889836 AW129112 BG925339 AI017633 AA568864 BF725590 AI004210 AI809799 BE083097 BG896220 AW997681 BF668788 BE083134 AW631281 BG193052 BG183095 BE440088 BG185728 AI499579 AA188162 AA864282 BI493352 AA155854 AA836749 AA836844 AA985478 AW082299 AI816747 AA450221 AA971294 BE327509 AI719662 BG576669 AI479382 BF824747 AI741800 BG982962 AI088473 AA916151 AW473324 BG901177 BE439998 AW023269 BE813871 AW999947 BE839108 AV707983 AA369722 AW796627 AW890608 AI341771 AA302459 BI493353 AA366332 AA371104 AA367277 AL547972 BG928011 AI678903 AI699886 AI956165 AA484893 AA643953 AW591063 BG203275 BG211093 AI334791 AA916589 AW058266 AI362370 AI143352 AA508721 AI928079 D57214 BE045265 AA541785

BG219510 BG201686 BG195572 AW019904 AW089242 AA953322 AI686698 F27562 AA614749 D56645 F20774 F30660 F25646 AW023542
 AA827300 AA582214 AI701289 AA228293 AI906950 AA230156 AA384572 AW438988 AA742516 BI490938 AA731082 BF665869 BG190518
 AV704158 BE439643 AA910666 AA155913 AA923097 AA975721 AA985555 BG927032 AA948389 AA451625 AA916141 AL572719 AV707258
 AW083733 AA128053 AI953789 AI911993 AA421798 BG429150 AI915306 Z30130 AA126929 BG926630 AA081013 AA553696 AA916094
 BG924321 AI039722 AI954968 AI372839 AI401406 AI538215
 AI422419 AA514370 AI741678 AI735482 AI735081 AI371436
 AW850587 AW850589 AW850318 AW850303
 AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331
 AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA365626
 Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618
 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634
 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572
 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403
 F02090 AI187299 AI609644 Z40516 AW952314
 BC020595 BI488430 BG168023 BE179030 AW294203 BF849776 AA459064 AI917452 AW403072 W27419 BF914568 BF798468 AW370558
 T35055 AW370623 AA399232 AA214221 AW802987 BF902228 AW370622 BF819597 AW370567 BF914313 AW954040 BF060706 AA194237
 T25074 C01285 BI489433
 AI332638 AA663215 AW629386
 AK001489 AU129447 BF959274 BG565452 AI245327 AU116848 BF358559 BF358554 BF358570 BG678119 AL515852 AU154607 AI357567
 AW874359 AI122554 AA406478 AI091013 AI866679 AI686163 AA662158 AA911580 D31095 AI302576 BF588761 AU151560 AU143828 AI291610
 AW169600 D31161 AA905362 C21179 BE327258 D31474 AW439053 D31309 BF756901 BI838626 BF979839 AU149562 BM142116 AU156455
 AA452028 AW473972 AW468490 AA410271 AI475944 BF821859 AA658188 AI360390 AA226320 F37355 F27660 F36093 AA152126 BF930021
 BF375775 AW821784 AW975085 W16475 D31031 BG696392 AW860676 AW752864 BI013705 BF965715 BF326604 AW821786

TABLE 38C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406617	8439858	Plus	36430-36552
401958	3258613	Plus	108411-108629
405121	8102330	Minus	35816-36004,36587-36684
401113	9966541	Minus	19419-19959
404370	7631003	Plus	127868-128244

TABLE 40A: 656 genes upregulated in fibrosis relative to normal body tissues

Table 40A lists about 656 genes upregulated in fibrosis relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1 95th percentile of fibrosis AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prot.Domains; R1

442275; AW449467; Hs.54795; Homo sapiens secretoglobulin, family 3A, m; Uteroglobulin; TM=M; SS=Y; 39.47
 428434; AW363590; Hs.65551; Homo sapiens, Similar to DNA segment, Ch; LBP_BPL_CETP_C; TM=M; SS=Y; 32.35
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretoglobulin, fa; none; 28.49
 406964; M21305; ; FGENES predicted novel secreted protein; none, none; 27.90
 425211; M18667; Hs.1867; progastricsin (pepsinogen C); asp; TM=M; SS=M; 27.90
 441835; AB036432; Hs.184; advanced glycosylation end product-spec; homeobox, Acyltransferase, notch, EGF, ank, Acyltransferase; 27.23
 446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL8; 24.97
 428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase_M10; 24.38
 431723; AW058350; Hs.278966; Homo sapiens mRNA; cDNA DKFZp564B2062 (f; PMP22_Claudin, none; 23.35
 409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibrinogen_C; 23.29
 431089; BE041395; Hs.374629; ESTs, Weakly similar to unknown protein ; none, none; 18.23
 425371; D49441; Hs.155981; mesothelin; none; TM=M; SS=M; 18.17
 448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec, MIP; TM=M; SS=M; 17.64
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phospho; Ribosomal_L20, Na_Pi_cotrans; TM=Y; SS=N; 17.33
 421798; N74880; Hs.355462; N-acylsphingosine amidohydrolase (acid c; SAPA, Surfactant_B, none; 16.81
 419556; U29615; Hs.91093; chitinase 1 (chitotriosidase); Glyco_hydro_18, CBM_14; TM=M; SS=Y; 16.24
 419092; J05581; Hs.89603; mucin 1, transmembrane; SEA; TM=Y; SS=M; 16.06
 426174; AA547959; Hs.115838; Homo sapiens similar to Echinoidin (LOC1; none, none; 15.84
 406672; M26041; Hs.198253; major histocompatibility complex, class ; ig, MHC_II_alpha; TM=M; SS=M; 15.42
 421110; AJ250717; Hs.1355; cathepsin E; asp; 15.08
 444342; NM_014398; Hs.10887; similar to lysosome-associated membrane ; Lamp; TM=Y; SS=M; 14.94

- 406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 14.36
 443709; AI082692; Hs.134662; ESTs; SNF,fn3,none; 14.05
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3;TM=Y;SS=M; 13.88
 457200; U33749; Hs.197764; thyroid transcription factor 1; homeobox;TM=M;SS=N; 13.86
 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUA S-100 pro; none,none; 13.82
 422355; AW403724; Hs.300697; coagulation factor VII (serum prothrombi; none,ig; 13.62
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 13.47
 415457; AW081710; Hs.7369; Homo sapiens testes specific A2 homolog ; MORN,sugar_lr;TM=Y;SS=M; 13.35
 431164; AA493650; Hs.94367; thyroid transcription factor 1; none,homeobox; 13.32
 414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 12.83
 400269; ; Hs.253495; Eos Control; lectin_c,Collagen,Xlink;; 12.30
 424310; AA338648; Hs.50334; testes development-related NYD-SP22; none;TM=M;SS=N; 11.81
 451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1; ABC_tran,SRP54;TM=Y;SS=M; 11.79
 452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine ; none,none; 11.68
 445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM;; 11.56
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 11.41
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 11.31
 430832; AI073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior ; none,none; 11.25
 407910; AA650274; Hs.41296; fibronectin leucine rich transmembrane p; fn3,LRR,LRRCT,LRRNT;TM=Y;SS=M; 11.15
 451497; H83294; Hs.284122; Wnt inhibitory factor-1; EGF,WIF;; 11.07
 430250; NM_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;SS=N; 11.07
 411020; NM_006770; Hs.67726; macrophage receptor with collagenous str; SRCR,Collagen;TM=Y;SS=M; 11.05
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin; ; Osteopontin;; 11.01
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 10.97
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin_c,Ricin_B_lectin,Xlink;TM=Y;SS=M; 10.93
 432231; AA339977; Hs.274127; CLST 11240 protein; none;TM=M;SS=M; 10.81
 416402; NM_000715; Hs.1012; complement component 4-binding protein, ; sushi;TM=M;SS=M; 10.77
 418156; W17056; Hs.83623; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 10.63
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 10.58
 421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen ; none;TM=Y;SS=M; 10.57
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (interstitial; hemopexin,Peptidase_M10,Astacin,PG_binding_1;; 10.33
 419086; NM_000216; Hs.89591; Kallmann syndrome 1 sequence; fn3,wap;; 10.30
 407786; AA687538; Hs.38972; telraspan 1; transmembrane4;TM=Y;SS=M; 10.28
 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 10.26
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBPase;TM=M;SS=N; 10.22
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 10.09
 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alph; vwa,Cache;TM=M;SS=N; 10.03
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 10.02
 408562; AI436323; Hs.31141; roundabout (axon guidance receptor, Dros; ig,fn3;TM=M;SS=N; 10.02
 448782; AL050295; Hs.362806; KIAA0758 protein; 7tm_2,ig,GPS,SEA;TM=Y;SS=N; 9.86
 419235; AW470411; Hs.288433; neurotrophin; none,none; 9.79
 415992; C05837; Hs.145807; hypothetical protein FLJ13593; none;TM=Y;SS=M; 9.74
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 9.70
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.69
 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; none;TM=M;SS=N; 9.68
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 9.64
 408380; AF123050; Hs.44532; diubiquitin; ubiquitin;TM=M;SS=N; 9.54
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 9.52
 449494; AW237014; Hs.315369; aquaporin 4; MIP,none; 9.51
 456062; AI866286; Hs.71962; ESTs, Weakly similar to B36298 proline-r; none,none; 9.42
 446428; AW082270; Hs.12496; ESTs, Weakly similar to ALU4_HUMAN ALU S; none,none; 9.41
 421952; AA300900; Hs.98849; dynein light chain 2B (DNLC2B); none,none; 9.19
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell ; Ribosomal_S14,ank,pkinase,death,none; 9.16
 456034; AW450979; ; gb:U1-H-BI3-ala-a-12-O-UI.s1 NCL_CGAP_Su; none,none; 9.15
 407788; BE514982; Hs.38991; S100 calcium-binding protein A2; ehand,S_100,S_100,ehand; 9.15
 416965; N26223; Hs.160436; MDAC1; none;NA;NA; 9.03
 443324; R44013; Hs.164225; ESTs; none,none; 9.03
 435575; AF213457; Hs.44234; triggering receptor expressed on myeloid; ig;TM=Y;SS=M; 9.00
 440273; AI805392; Hs.325335; Homo sapiens cDNA: FLJ23523 fis, clone L; none,none; 8.99
 424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374 gene NF2 ; Zn_carbOpept,none; 8.80
 409203; AA780473; Hs.687; cytochrome P450, subfamily IVB, polypept; p450;TM=M;SS=Y; 8.76
 423387; AJ012074; Hs.348500; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 8.74
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 8.73
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 8.68
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; ig;TM=Y;SS=M; 8.56
 421563; NM_006433; Hs.105806; granulysin; none;; 8.55
 450726; AW204600; Hs.355462; HUMPSBPA Human pulmonary surfactant-asso; SAPA,Surfactant_B,none; 8.51
 419693; AA133749; Hs.301350; FXVD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 8.51
 424450; AL137526; Hs.374425; dynein intermediate chain 2; WD40;; 8.42
 402474; ; NM_004079;Homo sapiens cathepsin S (CTSS; Peptidase_C1;; 8.41
 458079; AI796870; Hs.54277; Homo sapiens similar to RIKEN cDNA 28100; none;TM=M;SS=N; 8.40
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 8.36
 453310; X70697; Hs.553; solute carrier family 6 (neurotransmitte; SNF,5HT_transporter;TM=Y;SS=N; 8.34
 448140; AF146761; Hs.20450; BCM-like membrane protein precursor; ig;TM=Y;SS=N; 8.33
 404240; ; NM_018950;Homo sapiens major histocompat; ig,MHC_L;TM=Y;SS=M; 8.28
 459702; AI204995; ; gb:an03c03.x1 Stratagene schizo brain S1; none,none; 8.17
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.17
 442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 8.12
 446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFZp564B2062 (f; PMP22_Claudin,none; 8.07
 420137; AA305478; Hs.95327; CD3D antigen, delta polypeptide (TIT3 co; ITAM;TM=Y;SS=M; 8.01
 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; ig;TM=M;SS=M; 7.99
 432441; AW292425; Hs.163484; intron of hepatocyte nuclear factor-3 al; Fork_head,none; 7.99
 409208; Y00093; Hs.172631; integrin, alpha X (antigen CD11C (p150)); vwa,FG-GAP,integrin_A,vwa,integrin_A,FG-GAP; 7.94

- 432606; NM_002104; Hs.3066; granzyme K (serine protease, granzyme 3; trypsin; TM=Y; SS=M; 7.92
 442832; AW206560; Hs.253569; ESTs; none, none; 7.90
 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN cDNA 2210; none; TM=M; SS=N; 7.89
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 7.86
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22, Claudin, none; 7.84
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin_B, EGF, PSI; TM=Y; SS=M; 7.79
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazaro; none; TM=Y; SS=N; 7.78
 423961; D13666; Hs.136348; periostin (OSF-2os); Fasciclin; TM=M; SS=M; 7.73
 424917; AI636208; Hs.96901; hypothetical protein FLJ23049; none; TM=M; SS=N; 7.72
 438564; AA381553; Hs.198253; major histocompatibility complex, class ; ig, MHC_II_alpha, none; 7.65
 456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, com; none, PK, PK_C, myosin_head, RhoGAP; 7.64
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily; SRP14, TNFR_c6; 7.63
 436954; AA740151; Hs.130425; ESTs; none, none; 7.58
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain; SH2; 7.56
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC; TM=Y; SS=M; 7.55
 417105; X60992; Hs.81226; CD6 antigen; SRCR; TM=Y; SS=M; 7.51
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 7.46
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 7.40
 432222; AI204995; ; gb:an03c03.x1 Stratagene schizo brain S1; none, none; 7.38
 422667; H25642; Hs.132821; ESTs; FMO-like, FMO-like; 7.37
 444527; NM_005408; Hs.11383; small inducible cytokine subfamily A (Cy; IL8; 7.36
 457411; AW085961; Hs.130093; Iroquois-class homeobox protein IRX2; none, none; 7.32
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP, none; 7.32
 419231; AL046294; Hs.136245; ESTs, Weakly similar to T17227 hypotheti; none, none; 7.30
 438873; AI302471; Hs.124292; Homo sapiens cDNA: FLJ23123 fis, clone L; none, none; 7.27
 424027; AW337575; Hs.201591; ESTs; 7tm_2, HRM, none; 7.26
 428927; AA441837; Hs.90250; Homo sapiens hypothetical protein FLJ231; none, none; 7.24
 432435; BE218886; Hs.282070; ESTs; none, none; 7.22
 428467; AK002121; Hs.184465; hypothetical protein FLJ11259; none; TM=Y; SS=M; 7.21
 416030; H15261; Hs.21948; ESTs; none, none; 7.20
 433293; AF007835; Hs.32417; hypothetical protein MGC2742; none; TM=M; SS=N; 7.18
 418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosom; pkinase, Activin_rec, pkinase, Activin_rec; 7.16
 420656; AA279098; Hs.187636; ESTs; none, none; 7.14
 427698; AW972594; Hs.335499; ESTs; none, none; 7.11
 432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase, ATP-sulfurylase; TM=M; SS=N; 7.06
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT, none; 7.04
 430413; AW842182; Hs.241392; small inducible cytokine A5 (RANTES); IL8; TM=M; SS=Y; 7.04
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement comp; C1q, Collagen; 7.03
 421481; AW391972; Hs.104696; KIAA1324 protein; none; TM=M; SS=M; 7.01
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase, PLAT; TM=M; SS=N; 6.97
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide, TGF-beta, none; 6.96
 458124; AW005548; Hs.124590; ESTs; none, none; 6.94
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3, PX; TM=M; SS=N; 6.93
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, ; inositol_p, ig; TM=M; SS=N; 6.92
 428820; AA436187; Hs.172631; integrin, alpha M (complement component ; vwa, integrin_A, FG-GAP; TM=Y; SS=M; 6.90
 423575; C18863; Hs.163443; intron of periostin (OSF-2os); Fasciclin, none; 6.89
 419490; NM_006144; Hs.90708; granzyme A (granzyme 1, cytotoxic T-lymp; trypsin; TM=M; SS=M; 6.89
 450954; AI904740; Hs.25691; receptor (calcitonin) activity modifying; none; TM=Y; SS=M; 6.87
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC; TM=Y; SS=M; 6.84
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 fis, clone L; LRR; TM=M; SS=N; 6.81
 414991; C17898; ; Homo sapiens up-regulated by BCG-CWS (LO; Zip, none; 6.80
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM; TM=Y; SS=M; 6.80
 422163; AF027208; Hs.112360; prominin (mouse)-like 1; none; TM=Y; SS=M; 6.79
 445885; AI734009; Hs.127699; KIAA1603 protein; none, none; 6.77
 436576; AI458213; Hs.77542; ESTs; 7tm_1, DnaJ; 6.77
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; 6.76
 424711; NM_005795; Hs.152175; calcitonin receptor-like; 7tm_2, HRM; TM=Y; SS=M; 6.75
 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3; TM=M; SS=N; 6.73
 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54); ig, ICAM_N; TM=M; SS=M; 6.71
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; ig, abhydrolase; 6.70
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none, lectin_c; 6.70
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 6.68
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans, K_tetra, asp; 6.65
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C, IMPDH_N, CBS, integrin_B, Ricin_B_lectin; 6.62
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 6.60
 453142; AA033648; Hs.7473; Homo sapiens gap junction protein, alpha; connexin; TM=Y; SS=M; 6.60
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis, clone PL; none, none; 6.56
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT_bind, STAT_prot; TM=M; SS=N; 6.54
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2, SH3, pkinase; TM=M; SS=N; 6.51
 446932; AA961459; Hs.125644; ESTs; none, LRR, LRRNT; 6.50
 427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180)); vwa, integrin_A, FG-GAP; TM=Y; SS=M; 6.48
 425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; ig, pkinase; TM=M; SS=M; 6.47
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none; TM=M; SS=M; 6.46
 431745; AW972448; Hs.163425; Novel FGENESH predicted cadherin repeat ; none, none; 6.43
 417370; T28651; Hs.374466; tryptophanyl-tRNA synthetase; WHEP-TRS, tRNA-syntL1b; 6.41
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, fn3, Y_phosphatase; TM=M; SS=N; 6.40
 429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate lung and nas; none; 6.39
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_P14_kinase, FAT, FATC, BOLA, RUN; TM=M; SS=N; 6.37
 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxygenase; IDO; TM=M; SS=N; 6.36
 451820; AW058357; Hs.199248; ESTs; 7tm_1; TM=Y; SS=M; 6.34
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/pep; PTR2; TM=Y; SS=N; 6.32
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, ig, FAD_Synth, ldh, ldh_C, pkinase; 6.32

- 444090; S69115; Hs.10306; natural killer cell group 7 sequence; PMP22_Claudin; TM=Y; SS=M; 6.31
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase;; 6.30
 421659; NM_014459; Hs.106511; protocadherin 17; cadherin; TM=M; SS=M; 6.27
 415199; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M; SS=N; 6.26
 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip; TM=M; SS=Y; 6.24
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; SS=N; 6.23
 452194; A1694413; Hs.373599; olfactory receptor, family 2, subfamily ; none, none; 6.22
 424144; AA454033; Hs.41644; AKAP-associated sperm protein; Rila; 6.21
 414142; AW368397; Hs.334485; hemiscitin (fibulin 6); EGF, ig, lsp_1, hormone4, squash, TIL, Adeno_E3_CR1; TM=M; SS=M; 6.21
 442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482 hypotheti; none, none; 6.20
 420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin (vascula; cadherin, Cadherin_C_term; TM=Y; SS=M; 6.19
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 6.17
 440452; A1925136; Hs.55150; ESTs, Weakly similar to CAYP_HUMAN CALCY; none; NA; NA; 6.17
 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 6.16
 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor t; Y_phosphatase, none; 6.15
 410361; BE391804; Hs.62661; guanylate binding protein 1, interferon-; GBP, GBP_C; TM=Y; SS=M; 6.13
 415765; NM_005424; Hs.78824; tyrosine kinase with immunoglobulin and ; EGF, fn3, ig, pkinase, laminin_EGF; TM=M; SS=Y; 6.12
 430478; NM_014349; Hs.241535; apolipoprotein L, 3; MotA_ExbB; TM=Y; SS=M; 6.12
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none; TM=Y; SS=M; 6.09
 446608; N75217; Hs.175622; ESTs; Armadillo_seg, HEAT_PBS; TM=M; SS=M; 6.08
 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfam; IL2;; 6.08
 426116; AA868729; Hs.144694; ESTs; none, none; 6.06
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank;; 6.05
 426721; AA383588; Hs.288545; ESTs, Weakly similar to T29012 hypotheti; zf-C2H2; TM=M; SS=N; 6.05
 429228; A1553633; Hs.356828; ESTs; none, none; 6.05
 421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase;; 6.04
 437669; A1358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA; none, pkinase, pkinase_C; 6.03
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran, ABC_membrane; TM=Y; SS=M; 6.02
 428667; A1375550; Hs.346868; nucleolar protein p40; homolog of yeast ; none, none; 6.01
 432731; R31178; Hs.287820; fibronectin 1; fn1, fn2, fn3, none; 5.95
 446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.95
 450656; AA010539; Hs.18912; unnamed protein product; zf-C2H2;; 5.94
 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide (p32); ig; TM=Y; SS=M; 5.94
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.94
 408048; NM_007203; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemmin; TM=M; SS=N; 5.94
 438670; A1275803; Hs.123428; ESTs; none; NA; NA; 5.91
 424238; AA337401; Hs.137635; ESTs; none; TM=M; SS=M; 5.90
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2, none; 5.89
 423690; AA329648; Hs.23804; ESTs, Weakly similar to PN0099 son3 prot; ion_trans, IQ, none; 5.88
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; SS=N; 5.81
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, ; ig; TM=Y; SS=M; 5.81
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none; TM=Y; SS=M; 5.80
 420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TIT3 com; ITAM; TM=M; SS=M; 5.79
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr; TM=Y; SS=N; 5.79
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2, SH3; TM=M; SS=N; 5.79
 443257; A1334040; Hs.11614; HSPC065 protein; trypsin; TM=M; SS=N; 5.76
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; ig; TM=Y; SS=N; 5.70
 435299; A1745458; Hs.343026; ESTs, Weakly similar to T20593 hypotheti; none; NA; NA; 5.69
 415995; NM_004573; Hs.355888; phospholipase C, beta 2; C2, PI-PLC-Y, PI-PLC-X; TM=M; SS=N; 5.67
 436772; AW975688; Hs.348918; metallothionein 1E (functional); 7tm_2, HRM, none; 5.67
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A; none, none; 5.66
 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA synthetas; WHEP-TRS, tRNA-synt_1b, none; 5.66
 421859; AA356620; Hs.108947; KIAA0050 gene product; ank, PH, ArfGap; 5.64
 407756; AA116021; Hs.38260; ubiquitin specific protease 18; UCH-1, UCH-2;; 5.63
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1; TM=Y; SS=M; 5.63
 423533; NM_014339; Hs.129751; interleukin 17 receptor; none; TM=Y; SS=M; 5.63
 419577; L36531; Hs.91296; integrin, alpha 8; integrin_A, FG-GAP; TM=Y; SS=N; 5.61
 452561; A1692181; Hs.49169; KIAA1634 protein; TPR, PDZ, WW, Guanylate_kin; TM=M; SS=N; 5.61
 428677; A1657119; Hs.351582; troponin I, cardiac; none; TM=M; SS=N; 5.60
 425509; AF079363; Hs.158213; sperm associated antigen 6; Armadillo_seg, HEAT_PBS; TM=M; SS=N; 5.58
 453852; AW961818; Hs.211592; MUM2 protein; pkinase, DAG_PE-bind, C2, pkinase_C, none; 5.57
 421924; BE514514; Hs.109606; coronin, actin-binding protein, 1A; WD40, Idh_C; TM=M; SS=N; 5.57
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.55
 431630; NM_002204; Hs.265829; Integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP, Rhabd_glycop, integrin_A; TM=Y; SS=M; 5.53
 410257; BE244044; Hs.61469; hypothetical protein; none, none; 5.53
 441965; AA92712; Hs.269737; ESTs; pkinase, Activin_rec, TSPN, Collagen; 5.52
 413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; integrin_B, Glyco_hydro_56;; 5.52
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2, STAT, STAT_bind, STAT_prot, none; 5.50
 447357; A1375922; Hs.132821; ESTs; FMO-like, FMO-like; 5.46
 422109; S73265; Hs.1473; gastrin-releasing peptide; Bombesin, Defensin_propep; TM=M; SS=M; 5.46
 447033; A1357412; Hs.157601; Predicted gene: Eos cloned; secreted w/V; none, none; 5.45
 417412; X16896; Hs.82112; interleukin 1 receptor, type I; ig, TIR; TM=M; SS=M; 5.45
 436057; AJ004832; Hs.5038; neuropathy target esterase; cNMP_binding, ion_trans, Patatin; TM=Y; SS=M; 5.41
 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4; TM=Y; SS=M; 5.41
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; ig, pkinase, LRR, LRRNT, LRRCT, none; 5.40
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1; TM=Y; SS=M; 5.40
 443623; AA345519; Hs.9641; complement component 1, q subcomponent ; C1q, Collagen;; 5.40
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3, HS1_rep; TM=M; SS=N; 5.38
 437275; AW976035; Hs.292396; ESTs, Weakly similar to A47582 B-cell gr; none, Frizzled, Fz; 5.37
 419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino ; aa_permeases; TM=Y; SS=M; 5.37
 449853; AF006823; Hs.24040; potassium channel, subfamily K, member 3; ion_trans; TM=Y; SS=M; 5.36
 442434; AA995787; Hs.129583; ESTs; IRK, none; 5.36
 428065; A1634046; Hs.157313; ESTs; ICE_p20, DED, ICE_p10, ICE_p20, DED; 5.36

- 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras,arf,Tk; 5.33
 425638; NM_012337; Hs.158450; nasopharyngeal epithelium specific prote; none;TM=M;SS=N; 5.32
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M;SS=N; 5.32
 452416; AA026115; Hs.114777; ESTs; none,Porphobil_deam; 5.29
 425205; NM_005854; Hs.155106; receptor (calcitonin) activity modifying; none;TM=Y;SS=N; 5.29
 440475; AI807671; Hs.24040; potassium channel, subfamily K, member 3; ion_trans,none; 5.28
 417355; D13168; Hs.82002; endothelin receptor type B; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 5.28
 436120; AI248193; Hs.119860; ESTs; heme_1,none; 5.27
 418307; U70867; Hs.83974; solute carrier family 21 (prostaglandin ; OATP_N,OATP_C;TM=Y;SS=M; 5.27
 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 5.26
 421554; AW137676; Hs.97775; ESTs; none,none; 5.23
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none,none; 5.22
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 5.21
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2 ; 7tm_1;TM=Y;SS=M; 5.19
 400261; ; Hs.1802; Eos Control; ig,MHC_II_beta;TM=Y;SS=M; 5.19
 436856; AI469355; Hs.127310; ESTs; pkinase,rm;TM=M;SS=N; 5.18
 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not ava; 7tm_1,none; 5.17
 425023; AW956889; Hs.154210; EDG-1 (endothelial differentiation, sph; 7tm_1;TM=Y;SS=M; 5.16
 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 5.16
 451220; AF124251; Hs.26054; novel SH2-containing protein 3; SH2;TM=M;SS=N; 5.15
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 5.14
 424925; NM_002432; Hs.153837; myeloid cell nuclear differentiation ant; PAAD_DAPIN,HIN;; 5.14
 451099; R52795; Hs.25954; interleukin 13 receptor, alpha 2; fn3;TM=Y;SS=M; 5.13
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm_1;TM=Y;SS=M; 5.12
 423196; AK001866; Hs.125139; hypothetical protein FLJ11004; none;TM=M;SS=N; 5.12
 433671; AW138797; Hs.132906; 19A24 protein; ig;TM=M;SS=M; 5.11
 426457; AW894667; Hs.380138; chimerin (chimaerin) 1; DAG_PE-bind,RhoGAP,SH2;TM=M;SS=N; 5.06
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 5.05
 418185; AW958272; Hs.347326; intercellular adhesion molecule 2 (ICAM; none;TM=Y;SS=M; 5.05
 437352; AL353957; Hs.284181; hypothetical protein DKFZp434P0531; DJF221;TM=Y;SS=M; 5.03
 457918; AL359590; Hs.162604; hypothetical protein DKFZp762M186; PLDC;TM=M;SS=N; 5.02
 452924; AW580939; Hs.97199; complement component C1q receptor; EGF,lectin_c,Tissue_fac,Xlink,TIL;TM=Y;SS=M; 5.02
 426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR m; Kunitz_BPTI,Kunitz_BPTI,7tm_2,HRM; 4.99
 432805; X94630; Hs.3107; CD97 antigen; 7tm_2,EGF,GPS,FecCD;TM=Y;SS=M; 4.95
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,VVV,RhoGAP;; 4.95
 414291; AI289619; Hs.13040; G protein-coupled receptor 86; 7tm_1;TM=Y;SS=M; 4.94
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_HUMAN ALU S; none,rm; 4.92
 451154; AA015879; Hs.33536; ESTs; TIMP,none; 4.92
 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase,TikA-N,2-Hacid_DH_C;TM=M;SS=N; 4.90
 413011; AW068115; Hs.821; biglycan; LRR,LRRNT;; 4.90
 422732; AA577455; Hs.24937; transformer-2 alpha (htra-2 alpha); rm,ig; 4.89
 417015; M83772; Hs.80876; flavin containing monooxygenase 3; FMO-like,pyr_redox;TM=Y;SS=M; 4.88
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L OR; PLDC;TM=M;SS=N; 4.88
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7tm_1,LRR;TM=Y;SS=N; 4.87
 405102; ; C15001220; jg14469558[gb]AAD21311.1) (AF; DAG_PE-bind,PH,RhoGEF,DC1;; 4.86
 422795; AB033109; Hs.375610; KIAA1283 protein; 7tm_1,kazal,A2M,A2M_N;TM=Y;SS=M; 4.84
 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 4.83
 414936; C14774; ; gb:C14774 Clontech human aorta polyA mRNA; ank,pkinase,death,none; 4.82
 430152; AB001325; Hs.234642; aquaporin 3; MiP;TM=Y;SS=M; 4.82
 444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP,none; 4.81
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-recept; SH2,Y_phosphatase,DSPC;TM=M;SS=N; 4.81
 453107; NM_016113; Hs.279746; vanilloid receptor-like protein 1; ank,ion_trans;TM=Y;SS=N; 4.80
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;; 4.80
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar_tr; 4.78
 419542; AA366037; Hs.90911; solute carrier family 16 (monocarboxylic; none,none; 4.76
 438899; AF085833; Hs.135624; ESTs; none,PI3_P14_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B; 4.75
 427418; AA402587; Hs.356667; LAT1-3TM protein; none,none; 4.75
 431924; AK000850; Hs.272203; Homo sapiens cDNA FLJ20843 fis, clone AD; SH3,none; 4.73
 424218; AF031824; Hs.143212; cystatin F (leukocystatin); cystatin;; 4.72
 414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14_17,none; 4.72
 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none;TM=M;SS=N; 4.71
 430037; BE409649; Hs.227789; mitogen-activated protein kinase-activat; pkinase;TM=M;SS=N; 4.71
 451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none,none; 4.71
 453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 fis, clone L; FG-GAP,integrin_A,NIF; 4.71
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3,none; 4.70
 438543; AA810141; Hs.192182; ESTs; SH2,pkinase,none; 4.70
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M;SS=N; 4.70
 438113; AI467908; Hs.8882; ESTs; 7tm_1,none; 4.70
 422164; NM_014312; Hs.112377; cortic al thymocyte receptor (X. laevis ; ig,Gemini_mov;TM=Y;SS=M; 4.69
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 4.69
 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-; aldo_ket_red,none; 4.67
 432314; AA533447; Hs.285173; ESTs; Xlink,none; 4.66
 453518; AW503205; Hs.27268; gb:U1-HF-BN0-akt-g-03-0-Ul.r1 NIH_MGC_50; SH3,PH,RhoGEF;TM=M;SS=N; 4.66
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase ; pkinase,CNH;TM=M;SS=N; 4.66
 446063; AI720140; Hs.151079; ESTs; ISK_Channel,none; 4.65
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh;; 4.65
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 4.65
 443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, ; none,PDZ,LIM,pkinase; 4.65
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=N; 4.64
 427535; R29543; Hs.2164; pro-platelet basic protein (includes pla; IL8;TM=M;SS=M; 4.64
 437119; AI379921; Hs.177043; XP_171387 similar to rhotekin; none,none; 4.63
 411779; AA292811; Hs.72050; non-metastatic cells 5, protein expresse; NDK;; 4.63
 429784; M89796; Hs.30; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=N; 4.62

- 415934; NM_000928; Hs.992; phospholipase A2, group IB (pancreas); phoslip; 4.61
 408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delta; none, none; 4.61
 426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase; TM=M; SS=N; 4.59
 444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligase; WW, HECT, RNA_pol_A, none; 4.59
 408000; L11690; Hs.198689; bulous pemphigoid antigen 1 (230/240kD); efhand, spectrin, GAS2, SH3, Plectin, RA, Xylose_isom, FliD, bZIP, Tropomyosin, Myc-LZ, M, Idh, C, CH, AIP3; TM=M; SS=N; 4.59
 431087; H12723; Hs.290791; ESTs; ion_trans, none; 4.58
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase, DAG_PE-bind, pkinase_C, OPR; TM=M; SS=N; 4.58
 422427; AA310514; Hs.96692; ESTs; PH, Ets, CH, spectrin, Ca_channel_B, none; 4.57
 441527; W19504; Hs.7884; solute carrier family 21 (organic anion ; OATP_N, OATP_C; TM=Y; SS=N; 4.56
 416464; NM_000132; Hs.79345; coagulation factor VIII, procoagulant co; Cu-oxidase, F5_F8_type_C; 4.56
 421233; AA209534; Hs.284243; tetraspan NET-6 protein; transmembrane4; TM=Y; SS=M; 4.56
 422311; AF073515; Hs.114948; cytokine receptor-like factor 1; fn3; TM=M; SS=N; 4.55
 444895; A1674383; Hs.22891; solute carrier family 7 (cationic amino ; ASC, death, TNFR_c6; 4.55
 428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled; Nramp; TM=Y; SS=N; 4.55
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema, PSI, TIC, integrin_B; TM=Y; SS=M; 4.54
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg, UQ_con, none; 4.54
 450086; AW016343; Hs.233301; ESTs; ank, death, ZU5, NMU, none; 4.54
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear trans; HLH, PAS, IL8; TM=M; SS=N; 4.54
 414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase; TM=M; SS=N; 4.53
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3, OPR, PX; TM=M; SS=N; 4.53
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6, ET, PLA2_inh; 4.53
 411213; AA676939; Hs.69285; neuropilin 1; MAM, F5_F8_type_C, CUB, CUB, MAM, F5_F8_type_C; 4.53
 434158; T86534; Hs.14372; ESTs; adenylatekinase, none; 4.52
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase, Furin-like, Recep_L_domain, none; 4.52
 447341; AF106941; Hs.18142; arrestin, beta 2; arrestin, arrestin_C, PX, PH, PLDc; 4.52
 447656; NM_003726; Hs.19126; src kinase-associated phosphoprotein of ; SH3, PH; TM=M; SS=N; 4.51
 417018; M16038; Hs.80887; y-yes-1 Yamaguchi sarcoma viral related ; SH2, SH3, pkinase; TM=M; SS=N; 4.51
 422893; X98411; Hs.380077; myosin IF; SH3, myosin_head, IQ; TM=M; SS=N; 4.51
 407202; N58172; Hs.109370; ESTs; F5_F8_type_C, pkinase, Ets, none; 4.51
 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.s.]; zf-C2H2, zf-C3HC4, UIM; TM=M; SS=N; 4.51
 450747; A1064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm, zf-RanBP, GAS2; 4.50
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig, pkinase; TM=Y; SS=M; 4.50
 453856; AA804789; Hs.379109; PDZ-LIM protein mystique; LIM, PDZ; TM=M; SS=N; 4.49
 432744; AA988835; Hs.38664; ESTs; none, none; 4.49
 419032; W81330; Hs.99877; ESTs, Highly similar to JAK3B [H.sapiens; pkinase, SH2, Insulin, pkinase, SH2; 4.48
 444009; A1380792; Hs.135104; ESTs; TNFR_c6, TIL, none; 4.48
 426416; AW512744; Hs.169824; killer cell lectin-like receptor subfami; lectin_c; TM=Y; SS=M; 4.48
 412802; U41518; Hs.74602; aquaporin 1 (channel-forming integral pr; MIP; TM=Y; SS=M; 4.48
 447217; BE465754; Hs.17778; neuropilin 2; CUB, MAM, F5_F8_type_C; TM=M; SS=M; 4.47
 408771; AW732573; Hs.47584; potassium voltage-gated channel, delayed; efhand, ion_trans, K_tetra, none; 4.47
 435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none; TM=M; SS=N; 4.46
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 4.45
 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF, zf-C3HC4, IBR, zf-RanBP; TM=M; SS=N; 4.45
 434308; N51517; Hs.47282; ESTs; pkinase, pkinase_C, none; 4.45
 434448; W26667; Hs.184581; Homo sapiens cDNA FLJ14821 fis, clone OV; pkinase, pkinase_C; 4.45
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Nterm, integrin_B; 4.44
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN, MK; TM=M; SS=Y; 4.44
 430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse homolog; fn3, RA, RasGEF; TM=M; SS=M; 4.44
 436001; AW903849; Hs.173840; HUEL (C4orf1)-interacting protein; ig; TM=M; SS=M; 4.44
 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1, OATP_C; TM=Y; SS=N; 4.43
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory su; SH2, none; 4.43
 410068; A1633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3; TM=M; SS=N; 4.43
 449961; AW265634; Hs.133100; ESTs; pkinase, Furin-like, Recep_L_domain, none; 4.42
 451734; NM_006176; Hs.26944; neurogranin (protein kinase C substrate, 1; IQ, 7tm_1; TM=M; SS=N; 4.42
 410598; A1817130; Hs.9195; Homo sapiens cDNA FLJ13698 fis, clone PL; RasGEF, PRK; 4.42
 439411; AA044876; Hs.58043; ESTs, Weakly similar to CYA2_HUMAN ADENY; guanylate_cyc; TM=Y; SS=M; 4.42
 433179; AW362945; Hs.162459; ESTs; Armadillo_seg, none; 4.42
 414849; AW372721; Hs.291623; ESTs, Weakly similar to unnamed protein ; pkinase, none; 4.42
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M; SS=N; 4.41
 445903; A1347487; Hs.132761; class I cytokine receptor; fn3; TM=Y; SS=N; 4.41
 438507; AA809052; Hs.356627; ESTs; none, none; 4.41
 409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfam; TNF; TM=Y; SS=M; 4.40
 453037; AA045175; Hs.17914; ESTs; none; TM=Y; SS=M; 4.40
 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vi; sushi; TM=Y; SS=M; 4.40
 451035; AU076785; Hs.430; plastin 1 (I isoform); efhand, CH, Adaptin_N; 4.40
 415149; X12451; Hs.78056; cathepsin L; Peptidase_C1; 4.39
 408105; AW152207; Hs.270977; ESTs, Weakly similar to I38022 hypothe; Y_phosphatase, carb_anhydrase, DSPc, none; 4.39
 423099; NM_002837; Hs.123641; protein tyrosine phosphatase, receptor t; fn3, Y_phosphatase, DSPc, COX6C; TM=M; SS=M; 4.39
 438330; AW450572; Hs.257316; ESTs; pkinase, zf-C4, ERM, CNH, none; 4.39
 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10, ICE_p20; 4.39
 429747; M87507; Hs.2490; caspase 1, apoptosis-related cysteine pr; CARD, ICE_p10, ICE_p20; 4.39
 426410; BE298446; Hs.305890; BCL2-like 1; Bcl-2, BH4, none; 4.38
 434511; R29882; Hs.18106; ESTs; pkinase, Glyco_hydro_39; 4.38
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; SS=N; 4.37
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; fn3, ig, Y_phosphatase, MAM; TM=Y; SS=M; 4.36
 432583; AW023624; Hs.162282; potassium channel TASK-4; potassium chan; ion_trans, X; TM=Y; SS=M; 4.36
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF; TM=Y; SS=M; 4.36
 426828; NM_000020; Hs.172670; activin A receptor type II-like 1; pkinase, Activin_rec; TM=M; SS=M; 4.36
 449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none; TM=Y; SS=M; 4.36
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbon; HCO3_cotransp; TM=Y; SS=N; 4.36
 429670; L01087; Hs.211593; protein kinase C, theta; DAG_PE-bind, pkinase, pkinase_C, DNA_pol_viral_N, PHD, DC1; TM=M; SS=N; 4.35
 421195; BE464560; Hs.133017; ESTs; none, none; 4.35

- 415758; BE270465; Hs.78793; protein kinase C, zeta; pkinase,DAG_PE-bind,pkinase_C,OPR;; 4.35
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;SS=N; 4.34
 419150; T29618; Hs.89640; TEK tyrosine kinase, endothelial (venous; EGF,fn3,pkinase,lg,laminin_EGF,DSL;TM=Y;SS=M; 4.34
 440675; AW005054; Hs.279788; ESTs, Weakly similar to KCC1_HUMAN CALCI; pkinase,none; 4.34
 429657; D13626; Hs.2465; KIAA0001 gene product; putative G-protein; 7tm_1;TM=Y;SS=M; 4.34
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4;TM=Y;SS=M; 4.34
 425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinase; SH2,SH3,pkinase,PH,BTK;TM=M;SS=N; 4.34
 452124; AA454220; Hs.61170; ESTs; pkinase,none; 4.33
 407775; NM_004914; Hs.38772; RAB36, member RAS oncogene family; ras,arf;TM=M;SS=N; 4.33
 452688; AA721140; Hs.49930; ESTs, Weakly similar to putative p150 [H; SH3,none; 4.33
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;SS=N; 4.32
 445330; R52656; Hs.21691; ESTs; 7tm_1,none; 4.32
 437527; AL241019; Hs.145644; ESTs; PIP5K,none; 4.32
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 ; TIMP,pkinase,DAG_PE-bind,RBD; 4.31
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated; lg,ITAM,Zn_clus;TM=Y;SS=M; 4.31
 416269; AA177138; Hs.161671; ESTs; pkinase,DAG_PE-bind,RBD,none; 4.30
 425458; H89317; Hs.182889; ESTs; ion_trans,none; 4.30
 424206; NM_003734; Hs.198241; amine oxidase, copper containing 3 (vasc; Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3;TM=M;SS=M; 4.29
 451876; T63141; ; gb;yb99a12.s1 Stratagene lung (937210) H; SH3,none; 4.29
 417801; AA417383; Hs.82582; integrin, beta-like 1 (with EGF-like rep; EGF;; 4.29
 435240; AI025435; Hs.117532; ESTs; GHMP_kinases,none; 4.27
 444051; N48373; Hs.10247; activated leucocyte cell adhesion molecu; none,none; 4.26
 423523; AW299828; Hs.193580; ESTs; none,none; 4.26
 426274; D38122; Hs.2007; tumor necrosis factor (ligand) superfami; TNF;TM=Y;SS=N; 4.26
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2;TM=M;SS=N; 4.26
 448386; AB037750; Hs.21061; KIAA1329 protein; PKD,BNR;TM=Y;SS=M; 4.26
 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 4.26
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, fo; ig,pkinase;TM=Y;SS=M; 4.26
 416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF,vwc,TSPN;; 4.25
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.25
 436494; AA720997; Hs.128295; ESTs; none,CAP_GLY,HCO3_cotransp,Glyco_hydro_63,PH; 4.24
 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 4.24
 418255; AW135405; Hs.37251; ESTs; pkinase,none; 4.24
 400328; X87344; ; transporter 2, ATP-binding cassette, sub; none;TM=Y;SS=N; 4.24
 405121; ; ; mitogen-activated protein kinase 8 inter; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;; 4.24
 425795; AJ000479; Hs.159543; EDG-6 (endothelial differentiation, G-p; 7tm_1;TM=Y;SS=M; 4.23
 406786; AW161678; Hs.111334; ferritin, light polypeptide; ferritin;TM=M;SS=N; 4.23
 449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none;TM=Y;SS=M; 4.23
 445657; AW612141; Hs.279575; Homo sapiens G-protein coupled receptor ; 7tm_1;TM=Y;SS=M; 4.23
 413795; AL040178; Hs.142003; ESTs; none,pkinase,LRR,LRRCT; 4.22
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 4.22
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;SS=N; 4.22
 417318; AW953937; Hs.240845; ESTs; SH3,PH,RhoGEF;; 4.21
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 4.21
 408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, com; none,none; 4.20
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 4.20
 424618; L29472; Hs.1802; major histocompatibility complex, class ; ig,MHC_IL_beta;TM=Y;SS=M; 4.19
 445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK,none; 4.19
 432882; NM_013257; Hs.279696; serum/glucocorticoid regulated kinase-II; pkinase,PX,pkinase_C;; 4.19
 425481; AW978162; Hs.372811; ESTs; none,Oxysterol_BP; 4.19
 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M;SS=N; 4.18
 401083; ; ; NM_016582;Homo sapiens peptide transpor; PTR2;TM=Y;SS=M; 4.18
 420676; AI434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind,none; 4.18
 424377; AF081675; Hs.146322; killer cell lectin-like receptor subfami; lectin_c;TM=Y;SS=M; 4.17
 424148; BE242274; Hs.1741; integrin, beta 7; integrin_B,EGF,metalthio,PSI;TM=Y;SS=M; 4.17
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor tran; ig,none; 4.17
 452100; AI668668; Hs.379032; inositol polyphosphate-5-phosphatase, 75; Exo_endo_phos,RhoGAP,none; 4.17
 413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidylin; SH2,SH3,C2,PH,PI-PLC-Y,PI-PLC-X,PDGF;; 4.17
 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none,pkinase,fn3,ig; 4.17
 444034; AL161957; Hs.10177; pleckstrin homology domain interacting p; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,Ribosomal_S15,bromodomain,WD40;TM=M;SS=N; 4.16
 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheti; ABC_tran,ABC_membrane,ig,MHC_IL_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.16
 407245; X90568; Hs.172004; titin; fn3,ig,SGXXSG,pkinase;TM=M;SS=N; 4.16
 418962; AA714835; Hs.271863; ESTs; RhoGAP,SH2,pkinase,POLO_box,none; 4.15
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 4.15
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.15
 446967; AI699629; Hs.156781; ESTs; none,none; 4.14
 432176; AW090386; Hs.112278; arrestin, beta 1; arrestin,arrestin_C,none; 4.14
 452571; W31518; Hs.34665; ESTs; none;TM=M;SS=N; 4.14
 425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar_tr;TM=Y;SS=M; 4.14
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_Oxidase;; 4.14
 417871; AA521368; Hs.24252; ESTs; IBB,Armaddillo_seg,none; 4.13
 429819; AL133011; Hs.253920; Homo sapiens mRNA; cDNA DKFZp434P201 (fr; none,none; 4.12
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;; 4.12
 429623; NM_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase,RGS;TM=M;SS=N; 4.12
 413019; BE281604; Hs.75140; low density lipoprotein-related protein-; none;TM=M;SS=Y; 4.12
 434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M;SS=N; 4.11
 434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK;TM=Y;SS=N; 4.11
 449656; AA002008; Hs.188633; ESTs; PIP5K,none; 4.11
 406403; ; ; NM_002162;Homo sapiens intercellular ad; ig;TM=Y;SS=M; 4.10
 427732; NM_002980; Hs.2199; secretin receptor; 7tm_2,HRM;TM=M;SS=M; 4.10
 437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,RIO1,none; 4.10
 432885; AA595607; Hs.368129; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,pkinase_C,none; 4.10

- 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase, pkinase_C, HR1; TM=M; SS=N; 4.10
 418342; BE002723; Hs.334330; leptin receptor; ICE_p20, DED, ICE_p10, ICE_p20, DED; 4.10
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese;; 4.10
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3, RhoGAP, FCH; TM=M; SS=N; 4.10
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz, Frizzled, 7tm_2; TM=Y; SS=M; 4.10
 437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none; TM=Y; SS=M; 4.10
 432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH, RhoGAP, SH3; TM=M; SS=N; 4.09
 435140; AA668123; Hs.134170; ESTs; none, none; 4.09
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 4.08
 428483; AI908539; Hs.184592; KIAA0344 gene product; none, none; 4.08
 446232; AI281848; Hs.194691; retinoic acid induced 3; 7tm_3, none; 4.07
 431674; AA098901; Hs.301642; G-protein coupled receptor; none, GCV_H; 4.07
 409686; AK000002; Hs.55879; Homo sapiens mRNA; cDNA DKFZp434L0827 (f; ABC_tran, ABC_membrane; TM=M; SS=M; 4.07
 441518; AW161697; Hs.294150; ESTs; Y_phosphatase, DSPc, none; 4.07
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3, ank; TM=M; SS=N; 4.06
 436982; AB018305; Hs.5378; spondin 1, (f-spondin) extracellular mat; tsp_1, Reeler;; 4.05
 420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP, 7tm_1; 4.05
 439549; AW937885; Hs.137314; ESTs; SH2, none; 4.04
 419981; AA897581; Hs.128773; ESTs; pkinase, DAG_PE-bind, pkinase_C, OPR, none; 4.04
 418836; AI655499; Hs.161712; ESTs; pkinase, Activin_rec, PDZ, ZU5, death; 4.04
 408806; AW847814; Hs.75608; Homo sapiens cDNA: FLJ21532 fis, clone C; SH3, PDZ, Guanylate_kin, none; 4.04
 432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3, PDZ, Guanylate_kin, none; 4.03
 426086; T94907; Hs.188572; ESTs; PH, Ets, CH, spectrin, Ca_channel_B, none; 4.03
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 4.03
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha, arf; TM=M; SS=N; 4.03
 416350; AF188625; Hs.189507; phospholipase A2, group IID; phospholip; TM=M; SS=Y; 4.02
 434457; AF141332; Hs.200333; apolipoprotein B48 receptor; none; TM=M; SS=N; 4.02
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain, PHD, PWWP, zf-MYND; TM=M; SS=N; 4.02
 425694; U51333; Hs.159237; hexokinase 3 (white cell); hexokinase, hexokinase2; TM=M; SS=N; 4.02
 449943; AF104266; Hs.24212; latrophilin; 7tm_2, GPS, Gal_Lectin, OLF, Latrophilin, HRM; TM=Y; SS=M; 4.01
 408938; AA059013; Hs.22607; ESTs; fn3, Y_phosphatase, carb_anhydase, none; 4.01
 426839; M74782; Hs.172689; interleukin 3 receptor, alpha (low affin; none; TM=M; SS=M; 4.00
 422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExcB; TM=Y; SS=M; 4.00
 410726; AI623859; Hs.15936; ESTs; pkinase, pro_isomerase, none; 4.00
 428318; BE300110; Hs.183842; ubiquitin B; lipocalin, aldedh, ubiquitin, IRK;; 4.00
 440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK; TM=M; SS=N; 3.99
 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase, ubiquitin, Enterotoxin_A, PHO4, pkinase, ubiquitin; 3.99
 414700; H63202; Hs.38163; ESTs; 7tm_1; TM=Y; SS=M; 3.99
 432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase, Sema, PSI, TIG, A4_EXTRA; TM=M; SS=M; 3.99
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M; SS=N; 3.98
 427541; AI798983; Hs.375835; solute carrier family 35 (CMP-sialic act; none, none; 3.98
 440248; AA876138; Hs.369458; ESTs; SH2, none; 3.98
 437400; AB011542; Hs.5599; EGF-like-domain, multiple 5; TNFR_c6, laminin_EGF; TM=Y; SS=N; 3.98
 425262; D87119; Hs.155418; GS3955 protein; pkinase;; 3.98
 420166; AW732276; Hs.95583; transmembrane 4 superfamily member (tetra; transmembrane4; TM=Y; SS=M; 3.98
 437151; AA745618; Hs.380121; BANP homolog, SMAR1 homolog; none, none; 3.98
 443574; U83993; Hs.321709; purinergic receptor P2X, ligand-gated io; P2X_receptor; TM=Y; SS=M; 3.97
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49, EGF, ig, Neuregulin; TM=M; SS=N; 3.97
 411574; BE242842; Hs.6780; protein tyrosine kinase 9-like (A6-relat; LRR, LRRCT, TIR, cofilin_ADF; TM=M; SS=N; 3.97
 432639; AW973785; ; gb:EST385886 MAGE resequences, MAGM Homo; none, IRK; 3.97
 457675; AF119917; Hs.306574; Homo sapiens PRO3098 mRNA, complete cds; none;; 3.97
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2, PH; TM=M; SS=N; 3.96
 437157; BE048860; Hs.17287; ESTs; IRK, none; 3.96
 453641; AA444140; Hs.90960; ESTs; Cbl_N, Cbl_N2, Cbl_N3, UBA, zf-C3HC4, none; 3.96
 446714; W73818; Hs.110028; ESTs; 7tm_1, 7tm_1; 3.96
 427648; AI376722; Hs.180062; proteasome (prosome, macropain) subunit; proteasome;; 3.96
 453686; AL110326; Hs.304679; ESTs, Moderately similar to Z195_HUMAN Z; none, lectin_c, lig_chan; 3.96
 457718; F18572; Hs.22978; ESTs, Weakly similar to ALU4_HUMAN ALU S; pkinase, pkinase; 3.95
 428727; AF078847; Hs.78452; general transcription factor IIH, polype; PHO4, LIM; TM=M; SS=N; 3.95
 435411; AW444619; Hs.138211; ESTs; none, pkinase; 3.94
 440209; H05049; Hs.247837; neurexin 3; laminin_G, EGF, none; 3.94
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none, none; 3.94
 435272; AA906415; Hs.110041; ESTs; none, pkinase; 3.93
 402550; ; ; Target Exon; none, none; 3.93
 425233; Z17861; Hs.155218; E1B-55kDa-associated protein 5; SPRY, SAP, pkinase, fn3, ig; 3.93
 410073; AW408163; Hs.58488; catenin (cadherin-associated protein), alpha; Statmin, Vinculin;; 3.92
 453548; AL079983; Hs.116774; integrin, alpha 1; none, vva, FG-GAP, integrin_A; 3.92
 417226; AW505054; Hs.4283; ESTs; pkinase, RGS, PH, myosin_head, Myosin_tail; 3.92
 446755; AW451473; Hs.16134; serine/threonine kinase 10; pkinase, TYA; TM=M; SS=N; 3.92
 452344; AI264357; Hs.55405; hypothetical protein MGC16212; Sulfate_transp, STAS;; 3.92
 418516; NM_006218; Hs.85701; phosphoinositide-3-kinase, catalytic, alpha; PI3_P14_kinase, PI3Ka, PI3K_C2, PI3K_rbd, PI3K_p85B, none; 3.91
 423069; W15613; Hs.1613; adenosine A2a receptor; 7tm_1; TM=Y; SS=M; 3.91
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor;; ig, pkinase; TM=Y; SS=N; 3.91
 434392; AW983709; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone H; pkinase, none; 3.91
 429615; AF258627; Hs.211562; ATP-binding cassette, sub-family A (ABC1; ABC_tran; TM=Y; SS=M; 3.91
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle, trypsin, plant_thionins;; 3.91
 442831; AI798959; Hs.131686; ESTs; ABC_tran, PRK, ABC_tran; 3.91
 441657; BE314696; Hs.7936; BAI1-associated protein 2; SH3; TM=M; SS=N; 3.91
 438698; AW297855; Hs.361171; ESTs, Weakly similar to I38022 hypotheti; lipoxigenase, PLAT, none; 3.90
 447560; AF065214; Hs.18858; phospholipase A2, group IVC (cytosolic; PLA2_B; TM=M; SS=N; 3.90
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC, none; 3.89
 429379; NM_014840; Hs.200598; KIAA0537 gene product; pkinase, RIO1; TM=M; SS=N; 3.89
 410179; W27723; Hs.59499; cell division cycle 2-like 5 (cholineste; pkinase;; 3.89

428713; AA432067; Hs.268551; ESTs, Moderately similar to CYA4 RAT ADE; pkinase;; 3.89
 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD:none; 3.89
 425190; AW028302; Hs.155079; protein phosphatase 2, regulatory subunit; B56;TM=M;SS=N; 3.89
 426752; X69490; Hs.172004; titin; fn3,ig,pkinase,SGXXSG;TM=M;SS=N; 3.89
 417767; BE242241; Hs.82542; acylglycerol hydrolase (neutrophil); Lipase_GDSL;TM=M;SS=M; 3.88
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dep; Man-6-P_recep;TM=M;SS=M; 3.88
 416140; AI918035; Hs.301198; roundabout (axon guidance receptor, Dros; none:none; 3.88
 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe co; fn3;TM=Y;SS=M; 3.88
 410011; AB020641; Hs.57856; PFTAIRES protein kinase 1; pkinase;TM=M;SS=N; 3.87
 406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gen; none:none; 3.87
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;; 3.87
 441859; AW194364; Hs.9877; interleukin-4 induced gene-1 protein (FI; Amino_oxidase,FAD_binding_3,TBC;TM=M;SS=N; 3.87
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p_like;TM=M;SS=N; 3.87
 415392; Z44067; Hs.10957; ESTs; PIP5K:none; 3.86
 416033; NM_012201; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR;TM=Y;SS=M; 3.86
 414649; AI672727; Hs.76753; endoglin (CD105 antigen) (ENG); none;TM=Y;SS=M; 3.85
 425729; L22647; Hs.159360; prostaglandin E receptor 1 (subtype EP1); 7tm_1;TM=Y;SS=M; 3.85
 414496; W73853; Hs.355424; ESTs; pkinase,F5_F8_type_C,adh_short:none; 3.84
 412204; AI125507; Hs.24937; ESTs; ig,rrm:none; 3.84
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase,PRK,Thymidylate_kin;; 3.84
 444981; AW855398; Hs.12210; hypothetical protein FLJ13732 similar to; SH2;TM=M;SS=N; 3.84
 412309; M23892; Hs.73809; arachidonate 15-lipoxygenase; lipoxygenase,PLAT;; 3.84
 405545; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.84
 407143; C14076; Hs.332329; EST; none;TM=Y;SS=M; 3.84
 420593; AA280356; Hs.187634; ESTs; B56:none; 3.84
 413420; AW410235; Hs.75348; proteasome (prosome, macropain) activator; PA28_alpha,PA28_beta,bioplerin_H;; 3.83
 448253; H25899; Hs.201591; ESTs; 7tm_2,HRM:none; 3.83
 444042; NM_004915; Hs.10237; ATP-binding cassette, sub-family G (WHIT; ABC_tran,PRK,GBP;TM=Y;SS=N; 3.83
 430397; AI924533; Hs.105607; bicarbonate transporter related protein 1; HCO3_cotransp;TM=Y;SS=N; 3.83
 423067; AA321355; Hs.285401; colony stimulating factor 2 receptor, be; fn3;TM=Y;SS=M; 3.83
 458188; AW297226; Hs.137840; ESTs, Moderately similar to SIX4_HUMAN H; pkinase,WD40; 3.82
 426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFZp586B0220 (f; pkinase:none; 3.82
 428791; AA435661; Hs.264750; ESTs; zf-C3HC4:none; 3.82
 438068; AI927209; Hs.306210; Homo sapiens cDNA: FLJ23133 fis, clone L; NusG;; 3.82
 453370; AI470523; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=N; 3.82
 419250; AW770185; Hs.356066; U5 snRNP-specific protein, 116 kD; 7tm_1,BAH,zf-CXXC,DNA_methylase; 3.82
 410017; AW952426; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none:none; 3.82
 420679; X57152; Hs.165843; fibrillarin; CK_IL_beta,Fibrillarin,WD40;TM=M;SS=N; 3.82
 417916; NM_006416; Hs.82921; solute carrier family 35 (CMP-sialic aci; DUF6;TM=Y;SS=M; 3.81
 425923; NM_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, de; none:none; 3.81
 417365; D50583; Hs.82028; transforming growth factor, beta recepto; pkinase,WD40;TM=Y;SS=N; 3.64
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 3.52
 422398; AI476149; Hs.334489; hypothetical protein FLJ21992; SH2,SH3;; 3.51
 418432; M14156; Hs.85112; insulin-like growth factor 1 (somatomedi; Insulin;; 3.50
 459705; BE082764; Hs.270252; ESTs, Weakly similar to androgen recepto; none,C2,WW,HECT; 3.48
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t; fn3,ig,Y_phosphatase,MAM;TM=Y;SS=M; 3.38
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor t; fn3,Y_phosphatase,carb_anhydase;TM=Y;SS=M; 3.37
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz,NTR;; 3.24
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolo; EGF,cadherin,laminin_G;TM=Y;SS=M; 3.11
 419721; NM_001650; Hs.315369; aquaporin 4; MIP:none; 2.99
 433147; AF091434; Hs.43080; platelet derived growth factor C; PDGF,CUB;; 2.91
 417976; BE565892; Hs.83077; interleukin 18 (interferon-gamma-inducin; none;TM=M;SS=N; 2.89
 439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.59
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.23
 411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none:none; 2.07
 428800; M57627; Hs.193717; interleukin 10; IL10;; 1.10

TABLE 40B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

456034 685586_1 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
 459702 539529_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
 432222 539529_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
 414991 1785136_1 D78831 C17898 D78863
 409745 MH1944_5 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625
 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377
 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
 414936 1782849_1 C14774 C17911 D79033
 451876 2328579_1 T63141 AI821021 BF370092 BF370127 BF370060 T62998
 432639 1237887_1 AW973785 H60163 AA557608

TABLE 40C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	404240	5002624	Minus	116132-116407,116653-116922
	405102	8076881	Minus	120922-121296
	405121	8102330	Minus	35816-36004,36587-36684
10	401083	3242744	Plus	33192-33360
	406403	9256305	Minus	151426-151680
	402550	7652009	Minus	80413-80673
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182

15

TABLE 41A: 556 GENES UP-REGULATED IN PANCREATIC TUMORS OR PANCREATITIS RELATIVE TO NORMAL TISSUES

20 Table 41A lists about 556 genes up-regulated in pancreatic tumors or pancreatitis relative to normal tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

25	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	90th percentile of pancreatic cancer/median of normal pancreas			
	Pkey	ExAccn	UnigenelD	Unigene Title	R1
30	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	7.25
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.64
	444995	AJ272265	Hs.12230	secreted phosphoprotein 2, 24kD	3.58
	453863	X02544	Hs.572	orosomucoid 1	114.18
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	922.40
35	421344	AW631030	Hs.103665	villin-like	2.19
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	61.10
	438091	AW373062	Hs.83623	nuclear receptor subfamily 1, group 1, m	607.40
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	228.20
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	4.97
40	443162	T49951	Hs.9029	DKFZP434G032 protein	38.01
	423096	AA732684	Hs.278428	progesterone induced protein	189.60
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	11.06
	448243	AW369771	Hs.52620	integrin, beta 8	116.90
	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	21.52
45	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	8.74
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (COM	3.11
	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	307.70
	457059	BE561665	Hs.177677	exosome component Rrp40	33.60
	451945	BE504055	Hs.211420	ESTs	7.31
50	453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE	133.70
	443247	BE614387	Hs.333893	c-Myc target JPO1	349.10
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	330.00
	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	3.78
	413835	AI272727	Hs.249163	fatty acid hydroxylase	3.53
55	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	73.90
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.39
	410639	BE269047	Hs.65234	hypothetical protein FLJ20596	1.72
	410541	AA065003	Hs.64179	syntenin-2 protein	10.29
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	6.79
60	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	4.62
	407604	AW191962	Hs.249239	collagen, type VIII, alpha 2	366.30
	431193	AW749505	Hs.296770	KIAA1719 protein	6.99
	442080	AW444761	Hs.44565	ESTs	118.00
	427670	BE612888	Hs.180224	myosin regulatory light chain	2.73
65	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	647.30
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	738.90
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	68.43
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.03
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	7.73
70	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	227.30
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	115.60
	452355	N54926	Hs.29202	G protein-coupled receptor 34	192.20
	419481	AI879195	Hs.90606	15 kDa selenoprotein	119.90
	407230	AA157857	Hs.182265	keratin 19	12.11
75	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	6.63
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	592.10
	411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	120.40
	445517	AF208855	Hs.12830	hypothetical protein	117.40
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.25
80	428385	AF112213	Hs.184062	putative Rab5-interacting protein	3.12
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	135.20
	406867	AA157857	Hs.182265	keratin 19	11.32
	417426	NM_002291	Hs.82124	laminin, beta 1	406.20

	406366	AF026692	Hs.105700	secreted frizzled-related protein 4	0.62
	401201	#(NOCAT)		Target Exon	0.75
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	0.63
5	405556	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.75
	442776	AW959498	Hs.8709	chymotrypsin C (caldecrin)	0.67
	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.83
	403207	#(NOCAT)		C2000960:gi 131432 sp P23132 LITH_BOVIN	0.80
	427858	NM_001971	Hs.21	elastase 1, pancreatic	0.98
10	426004	AW600300	Hs.124123	ESTs, Moderately similar to SYNLRAT SYN	0.88
	401541	NA		Target Exon	0.91
	429793	AI417638	Hs.114648	estrogen regulated gene 1	0.85
	423068	M25629	Hs.123107	kallikrein 1, renal/pancreas/salivary	0.81
	433110	D56494	Hs.3191	rat regenerating islet-derived-like, hum	0.72
15	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	0.95
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	0.87
	412470	M93283	Hs.73923	pancreatic lipase-related protein 1	0.89
	431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	0.97
	419219	AW583139	Hs.89717	carboxypeptidase A2 (pancreatic)	0.95
20	412688	AW583062	Hs.74502	chymotrypsinogen B1	0.95
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.07
	420937	AW966719	Hs.1340	colipase, pancreatic	0.99
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	1.02
	410839	NM_006849	Hs.66581	protein disulfide isomerase	1.00
25	437986	AA774575	Hs.121776	lestin expressed sequence 11	1.02
	415934	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)	1.06
	427965	D00306	Hs.181289	elastase 3, pancreatic (protease E)	1.22
	406399	#(NOCAT)		NM_003122*:Homo sapiens serine protease	1.08
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.11
30	414061	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	1.22
	421243	AW873803	Hs.102876	pancreatic lipase	1.13
	419263	AW583874	Hs.89832	insulin	1.12
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.13
	408983	NM_000492	Hs.663	cystic fibrosis transmembrane conductanc	1.32
35	436217	T53925	Hs.107	fibrinogen-like 1	1.72
	435975	AL118990	Hs.41997	alpha-1-B glycoprotein	1.60
	431330	X69532	Hs.2777	inter-alpha (globulin) inhibitor, H1 pol	2.02
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	1.82
	415003	M11437	Hs.77741	kininogen	3.83
40	422281	M36803	Hs.1504	hemopexin	2.14
	414910	X12662	Hs.289057	arginase, liver	97.90
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	236.70
	400836	#(NOCAT)		Target Exon	2.47
	452983	L32140	Hs.531	afamin	117.10
45	419768	T72104	Hs.93194	apolipoprotein A-I	4.87
	413841	M34276	Hs.75576	plasminogen	374.00
	400560	#(NOCAT)		NM_030878*:Homo sapiens cytochrome P450,	144.50
	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	266.50
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	77.80
50	426205	D63521	Hs.167877	leukocyte cell-derived chemotaxin 2	169.80
	414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	3.60
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	400.40
	429023	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	4.72
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	5.26
55	425260	L47726	Hs.1870	phenylalanine hydroxylase	73.78
	443316	AI478463	Hs.18443	aldehyde dehydrogenase 8 family, member	182.20
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	335.00
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	173.40
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	565.30
60	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	86.20
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	477.20
	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	201.50
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	426.10
	425573	AB006423	Hs.158308	serine (or cysteine) proteinase inhibito	1.10
65	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H	0.62
	406672	M26041	Hs.198253	major histocompatibility complex, class	4.02
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (5.34
	421712	AK000140	Hs.107139	hypothetical protein	5.62
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	8.85
70	442896	R37725	Hs.261108	ESTs	157.70
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	137.70
	428486	AW583497	Hs.184604	pancreatic polypeptide	2.59
	457489	AI693815	Hs.127179	cryptic gene	3.23
	404866	NA		ENSP00000251112*:Sodium/potassium-transp	2.84
75	432874	W94322	Hs.279651	melanoma inhibitory activity	2.48
	445891	AW391342	Hs.199460	ESTs	70.38
	404682	NA		C9001188*:gi 12738842 ref NP_073725.1 p	1.38
	429547	AW009166	Hs.99376	ESTs	6.85
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	5.21
80	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	1.74
	446868	AV660737	Hs.135100	ESTs	102.10
	404287	NA		C6001909:gi 704441 dbj BAA18909.1 (D298	242.70
	443267	AW450630	Hs.133851	ESTs	98.90
	451635	AA018899	Hs.127179	cryptic gene	2.16

5	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	131.70
	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	128.70
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	92.90
	410309	BE043077	Hs.278153	ESTs	108.80
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	170.10
10	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	75.70
	449592	AI655494	Hs.195718	ESTs	4.58
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	188.50
	406685	M18728		gb:Human nonspecific crossreacting antig	1123.60
	411573	AB029000	Hs.70823	KIAA1077 protein	995.60
15	429201	X03178	Hs.198246	group-specific component (vitamin D bind	11.32
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	8.38
	428698	AA852773	Hs.334838	KIAA1866 protein	662.00
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	4.00
	432596	AJ224741	Hs.278461	matriin 3	283.50
20	428824	W23624	Hs.173059	ESTs	4.55
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.01
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.21
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	4.80
	448844	AI581519	Hs.177164	ESTs	362.80
25	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	133.90
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	128.20
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	13.83
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	316.00
	452571	W31518	Hs.34665	ESTs	245.50
30	443646	AI085198	Hs.164226	ESTs	189.40
	436032	AA150797	Hs.109276	latexin protein	291.10
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	252.20
	422109	S73265	Hs.1473	gastrin-releasing peptide	278.20
	430407	H23551	Hs.30974	ESTs	6.20
35	419235	AW470411	Hs.288433	neurotrimin	423.50
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.01
	444301	AK000136	Hs.10760	asporin (LRR class 1)	499.90
	427333	AF067797	Hs.176658	aquaporin 8	1.05
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	4.33
40	407777	AA161071	Hs.71465	squalene epoxidase	3.64
	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	1.47
	421341	AJ243212	Hs.279611	deleted in malignant brain tumors 1	3.98
	453935	AI633770	Hs.42572	ESTs	2.08
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	3.84
45	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	14.21
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	315.70
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.53
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	3.13
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	9.33
50	440484	BE328156	Hs.150356	ESTs	1.03
	447395	AI418412	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	1.09
	440099	AL080058	Hs.6909	DKFZP564G202 protein	14.74
	434665	AA642125		gb:nr60c01.s1 NCL_CGAP_Lym3 Hmo sapiens	0.98
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	2.23
55	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	329.40
	424411	NM_005209	Hs.146549	crystallin, beta A2	1.71
	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	2.69
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	1.70
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	3.19
60	429010	Y18198	Hs.194725	one cut domain, family member 2	1.96
	414420	AA043424	Hs.76095	immediate early response 3	2.54
	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	3.30
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	312.80
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	177.80
65	406173	\$(NOCAT)		ENSP00000250148*:Growth hormone variant	1.46
	403776	\$(NOCAT)		ENSP00000226542*:Small inducible cytokin	121.80
	403574	NA		Target Exon	16.12
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.94
	458449	H04482	Hs.29019	ESTs	71.60
70	409958	NM_001523	Hs.57697	hyaluronan synthase 1	1.77
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	3.13
	451181	AI796330	Hs.207461	ESTs	68.00
	440508	BE267911	Hs.196970	ESTs	38.00
	429636	AA455692	Hs.163232	ESTs	30.70
75	419570	W68738		gb:zd37g06.s1 Soares_fetal_heart_NbHH19W	1.02
	431779	AW971178	Hs.268571	apolipoprotein C-I	3.36
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.20
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (MMP7; uterin	3.94
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	1171.10
80	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	809.50
	440482	AA886658	Hs.50873	ESTs	9.95
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	30.70
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	82.90
	452239	AW379378	Hs.170121	protein tyrosine phosphatase, receptor t	26.01
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	5.38
	409335	NM_001502	Hs.53985	glycoprotein 2 (zymogen granule membrane	0.54
	420876	AA918425	Hs.177744	ESTs	0.89

	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	0.94
	401732	\$(NOCAT)		NM_001176*:Homo sapiens Rho GDP dissocia	1.13
	404142	NA		Target Exon	1.33
5	424165	AW582904	Hs.142255	islet amyloid polypeptide	2.95
	413880	AI660842	Hs.110915	interleukin 22 receptor	1.34
	407007	U22961		gb:Human mRNA clone with similarity to L	1.57
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.48
	432855	AF017988	Hs.279565	secreted frizzled-related protein 5	1.28
10	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.31
	445730	AI624342	Hs.170042	ESTs	2.14
	406666	V00495	Hs.184411	albumin	2.95
	435849	BE305242	Hs.16098	claudin 2	1.96
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	2.49
	430272	X04898	Hs.237658	apolipoprotein A-II	3.29
15	412374	X01388	Hs.73849	apolipoprotein C-III	2.42
	419276	BE165909	Hs.306881	MSTP043 protein	83.40
	415448	T68645	Hs.952	solute carrier family 10 (sodium/bile ac	3.52
	423541	AA296922	Hs.129778	gastrointestinal peptide	3.16
20	428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	6.24
	425551	AA359252	Hs.126485	hypothetical protein FLJ12604; KIAA1692	14.67
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	4.30
	428786	Y16577	Hs.2314	mannose-binding lectin (protein C) 2, so	92.10
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	203.30
25	451253	H48299	Hs.26126	claudin 10	1.37
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	3.38
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibito	7.04
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.84
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.65
30	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	9.28
	422237	M13149	Hs.1498	histidine-rich glycoprotein	34.26
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	1.92
	414386	X00442	Hs.75990	haploglobin	8.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stro	1.74
35	452689	F33868	Hs.284176	transferrin	6.51
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	35.08
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	170.30
	428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis t	2.34
	405849	\$(NOCAT)		Target Exon	103.10
40	405281	\$(NOCAT)		NM_002864:Homo sapiens pregnancy-zone pr	31.20
	419078	M93119	Hs.89584	insulinoma-associated 1	6.28
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.89
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.80
45	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.82
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	13.15
	450400	AI694722	Hs.279744	ESTs	5.22
	413916	N49813	Hs.75615	apolipoprotein C-II	8.60
	444632	AI184027	Hs.146986	ESTs, Weakly similar to FATH_HUMAN CADHE	71.30
	415906	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.70
50	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.65
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	3.01
	436961	AW375974	Hs.156704	ESTs	164.60
	446319	AW207590	Hs.160711	ESTs	1.88
	427899	AA829286	Hs.332053	serum amyloid A1	6.98
55	419092	J05581	Hs.89603	mucin 1, transmembrane	2.12
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	132.20
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.23
	406319	NA		CX000780:gi 6679197 ref NP_032800.1 pol	51.50
	404286	NA		C6001909:gi 704441 dbj BAA18909.1 (D298	1.75
60	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	52.90
	406293	NA		Target Exon	68.30
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	102.43
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	206.30
	425200	BE255203	Hs.155101	ATP synthase, H transporting, mitochondr	5.76
65	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	200.10
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	97.70
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.96
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	30.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.66
70	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	193.80
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.05
	420001	J05064	Hs.1282	complement component 6	159.00
	449038	AL133084	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f	39.10
	423184	NM_004428	Hs.1624	ephrin-A1	2.39
75	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	327.90
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	90.50
	445593	AW203963	Hs.150896	ESTs	49.20
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	3.12
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.93
80	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	39.90
	417940	R28205	Hs.24230	ESTs	57.20
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	2.51
	439920	H05430	Hs.288433	neurotrophin	1.91
	432542	AW083920	Hs.16098	claudin 2	3.47

	410418	D31382	Hs.63325	transmembrane protease, serine 4	3.82
	415989	AI267700	Hs.317584	ESTs	182.50
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.84
	400024			AFFX control - HUMRGE/M10098_5	4.82
5	418067	AI127958	Hs.83393	cystatin E/M	4.19
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.92
	405909	NA		Target Exon	71.80
	448811	AI590371	Hs.174759	ESTs	6.74
	430044	AA464510	Hs.152812	ESTs	14.91
10	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	757.80
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	1.65
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapi	104.70
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	143.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	311.80
15	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	63.00
	422330	D30783	Hs.115263	epiregulin	141.70
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	2.59
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	181.90
	430691	C14187	Hs.103538	ESTs	95.80
20	401682	NA		Target Exon	6.17
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	318.60
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.51
	442560	AA365042	Hs.228598	ESTs, Weakly similar to 2004399A chromos	3.90
25	414812	X72755	Hs.77367	monokine induced by gamma interferon	434.60
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	6.58
	421430	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	35.10
	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	2.45
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	8.58
30	448437	AW470125		gb:wx60c04.x1 NCL_CGAP_Pan1 Homo sapiens	79.80
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	147.30
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	30.07
	424586	NM_003401	Hs.150930	X-ray repair complementing defective rep	55.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (CX	405.20
35	438746	AI885815	Hs.184727	ESTs	3.57
	456032	AW957446	Hs.301711	ESTs	136.80
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	35.10
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	9.93
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	146.40
40	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	20.60
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.58
	437157	BE048860	Hs.120655	ESTs	91.80
	404285	NA		C6001909:gil704441 dbj BAA18909.1 (D298	123.80
	424036	AA770688	Hs.28777	H2A histone family, member L	5.26
45	422026	U80736	Hs.110826	trinucleotide repeat containing 9	130.40
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	48.80
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	3.15
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	253.20
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	80.00
50	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	3.05
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.66
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	23.02
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	78.10
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	1.74
55	421298	AW172431	Hs.13012	ESTs	133.10
	422424	AI186431	Hs.296638	prostate differentiation factor	2.65
	421582	AI910275	Hs.1406	trefol factor 1 (pS2)	5.17
	401480	NA		Target Exon	73.70
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	137.70
60	409757	NM_001898	Hs.123114	cystatin SN	9.36
	449722	BE280074	Hs.23960	cyclin B1	162.70
	452240	AI591147	Hs.61232	ESTs	151.90
	415165	AW887604	Hs.78065	complement component 7	2.85
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	290.30
65	428450	NM_014791	Hs.184339	KIAA0175 gene product	6.89
	409041	AB033025	Hs.50081	KIAA1199 protein	334.10
	453331	AI240665	Hs.8895	ESTs	12.85
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	12.42
	453160	AI263307	Hs.239884	H2B histone family, member L	156.40
70	444015	AI472865	Hs.135534	ESTs	14.60
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	87.20
	448045	AJ297436	Hs.20166	prostate stem cell antigen	526.20
	422426	W79117	Hs.58559	ESTs	58.30
	450737	AW007152	Hs.203330	ESTs	281.00
75	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	31.25
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	78.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	212.10
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	3.40
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	3.48
80	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	281.50
	431753	X76029	Hs.2841	neuromedin U	60.50
	428651	AF196478	Hs.188401	annexin A10	508.30
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	85.80
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	55.30

5	435039	AW043921	Hs.130526	ESTs	64.00
	447033	AI357412	Hs.157601	ESTs	123.20
	433578	BE336886	Hs.3416	adipose differentiation-related protein	9.22
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	525.70
	411274	NM_002776	Hs.69423	kalikrein 10 (KLK10) (PRSSL1) (nes1)	44.36
10	452705	H49805	Hs.246005	ESTs	120.10
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	92.30
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	29.37
	422562	AI962060	Hs.118397	AE-binding protein 1	3.84
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	27.80
15	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	4.09
	440868	R79707	Hs.263339	ESTs, Moderately similar to I38022 hypot	76.30
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.37
	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fis, clone H	3.44
	426320	W47595	Hs.169300	transforming growth factor, beta 2	138.10
20	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	3.45
	459309	AA040620	Hs.5672	hypothetical protein AF140225	127.80
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	361.20
	422553	AI697720	Hs.171455	ESTs, Weakly similar to T31613 hypothe	136.60
	423275	BE536069	Hs.2962	S100 calcium-binding protein P	6.87
25	400534	#(NOCAT)		C22000015:gil12741327[ref]XP_008833.2] z	89.00
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.78
	423739	AA398155	Hs.97600	ESTs	135.60
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	148.50
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	87.70
30	407001	U12471	Hs.247954	Human thrombospondin-1 gene, partial cds	76.80
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	110.60
	419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (234.60
	428471	X57348	Hs.184510	stratifin	3.72
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	437.90
35	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	219.20
	419842	AA765489	Hs.104350	ESTs	3.80
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (MMP1; inters	606.80
	444207	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl protease	2.62
	424232	BE093589	Hs.38178	hypothetical protein FLJ23468	258.70
40	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	304.80
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	8.78
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	10.95
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	199.70
	438199	AW016531	Hs.122147	ESTs	67.70
45	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	107.20
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.59
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	3.45
	421937	AI878857	Hs.109706	hematological and neurological expressed	3.17
	427961	AW293165	Hs.143134	ESTs	109.30
50	422043	AL133649	Hs.110953	retinoic acid induced 1	2.98
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	276.50
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	5.28
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	27.85
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	342.30
55	424086	AI351010	Hs.102267	lysyl oxidase	213.50
	432731	R31178	Hs.287820	fibronectin 1	185.10
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	106.10
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	2.27
	417308	H60720	Hs.81892	KIAA0101 gene product	405.30
60	438146	Z36842	Hs.57548	ESTs	8.38
	424800	AL035588	Hs.153203	MyoD family inhibitor	172.10
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	45.70
	408380	AF123050	Hs.44532	diubiquitin	11.18
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	149.10
65	422963	M79141	Hs.13234	ESTs	33.60
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	6.73
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	8.96
	424897	D63216	Hs.153684	frizzled-related protein	312.40
	421110	AJ250717	Hs.1355	cathepsin E	790.80
70	411789	AF245505	Hs.72157	DKFZP564I1922 protein	3.17
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	8.52
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	558.00
	406837	R70292	Hs.156110	immunoglobulin kappa constant	4.36
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.83
75	421470	R27496	Hs.1378	annexin A3	242.90
	407242	M18728		gb:Human nonspecific crossreacting antig	36.91
	432101	AI918950	Hs.123642	EphA3	221.60
	406687	M31126	Hs.272620	matrix metalloproteinase 11 (MMP11; stro	5.34
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	292.00
80	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	184.90
	435202	AI971313	Hs.170204	KIAA0551 protein	64.80
	407216	N91773	Hs.102267	lysyl oxidase	73.70
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	3.20
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	288.70
80	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	502.60
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	6.13
	441020	W79283	Hs.35962	ESTs	178.90

	453857	AL080235	Hs.35861	DKFZP586E1621 protein	504.30
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	242.10
	413435	X51405	Hs.75360	carboxypeptidase E	7.30
5	436476	AA326108	Hs.33829	bHLH protein DEC2	247.20
	406747	AI925153	Hs.217493	annexin A2	110.00
	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	112.10
	431211	M85849	Hs.323733	gap junction protein, beta 2, 26kD (conn	583.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	6.56
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	460.90
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	204.40
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	7.75
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	14.61
	424560	AA158727	Hs.150555	protein predicted by clone 23733	99.80
15	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	242.20
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	17.88
	410668	BE379794	Hs.65403	hypothetical protein	4.18
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	116.40
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	60.30
20	442577	AA292998	Hs.163900	ESTs	4.18
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	334.20
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	8.16
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	375.30
	445133	AW157646	Hs.153506	ESTs	292.40
25	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	4.38
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	89.00
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	322.10
	410687	U24389	Hs.65436	lysyl oxidase-like 1	9.10
	417409	BE272506	Hs.82109	syndecan 1	4.05
30	426471	M22440	Hs.170009	transforming growth factor, alpha	138.60
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	250.50
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.89
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	11.76
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.79
35	408491	AI088063	Hs.7882	ESTs	8.25
	437802	AI475995	Hs.122910	ESTs	4.54
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	175.10
	421155	H87879	Hs.102267	lysyl oxidase	170.10
	451310	AW250651	Hs.26213	Human DNA sequence from clone RP3-447F3	2.91
40	439867	AA847510	Hs.161292	ESTs	261.60
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	723.00
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	251.70
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	155.50
	457180	R26022	Hs.194662	calponin 3, acidic	68.00
45	424408	AI754813	Hs.146428	collagen, type V, alpha 1	17.19
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	5.32
	425139	AW630488	Hs.325820	protease, serine, 23	371.90
	432978	AF126743	Hs.279884	DNAJ domain-containing	7.27
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	19.30
50	421991	NM_014918	Hs.110488	KIAA0990 protein	190.50
	421814	L12350	Hs.108623	thrombospondin 2	15.02
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	28.57
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	519.20
	413048	M93221	Hs.75182	mannose receptor, C type 1	240.60
55	404210	#(NOCAT)		NM_005936:Homo sapiens myeloid/lymphoid	404.60
	452862	AW378065	Hs.8687	ESTs	364.20
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	226.20
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	4.31
	427390	AI432163	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L	10.41
60	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	22.46
	451295	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene	23.74
	448569	BE382657	Hs.21486	signal transducer and activator of trans	5.68
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	190.80
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	230.50
65	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	361.90
	422545	X02761	Hs.287820	fibronectin 1	8.81
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	7.30
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	267.20
	422110	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	5.07
70	431512	BE270734	Hs.2795	lactate dehydrogenase A	270.10
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	504.60
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zip	10.62
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.80
	417944	AJ077196	Hs.82985	collagen, type V, alpha 2	14.01
75	428797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f	9.15
	434423	NM_006769	Hs.3844	LIM domain only 4	297.30
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	486.20
	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	9.73
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	762.90
80	424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	7.81
	400133	NA		Eos Control	357.00
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1150.30
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.50
	446019	AI362520	Hs.279789	histone deacetylase 3	11.26

426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	459.50
422687	AW068823	Hs.119206	insulin-like growth factor binding prote	2.68
432401	NM_013330	Hs.274479	NME7	4.99
437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	7.65

Table 41B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
419570	1860604_1	W68738 W68831
423733	231476_1	AA330281 OAA330232 AW962521
434665	390530_1	AA642125 AA654516
448437	763310_1	AW470125 AI734872 AI749559 AW856504 AI583942 AW779036 AW843429 AW844876 AI520713 AW847236

Table 41C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400534	6981826	Minus	278637-279292
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400836	8954179	Plus	677-1188
401201	9743387	Minus	138534-138629,139234-139294,140121-140335,142033-142479
401480	7321503	Plus	166120-166347,166451-166557,169651-169832
401541	8072607	Minus	50018-50158
401682	4755167	Plus	13022-13473
401732	1200312	Plus	19346-19525,19625-19708,19897-19973,20067-20130,20215-20414
403207	7630829	Plus	89914-90033,90729-90855,91131-91198
403574	8101156	Plus	5542-6176
403776	7770611	Minus	1414-1513,1624-1756
404142	9856692	Minus	80316-80459
404210	5006246	Plus	169926-170121
404285	2326514	Plus	32282-32416
404286	2326514	Plus	51086-51301
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404866	9366919	Minus	11743-11929
405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
405849	7651817	Minus	17705-18287
405909	7705180	Minus	86985-87233
406173	7230224	Plus	12925-13213
406293	5686274	Minus	17646-17953
406319	9211730	Minus	82320-82561
406399	9256288	Minus	63448-63554

TABLE 42A: 574 genes upregulated in pancreatic cancer relative to normal body tissues

Table 42A lists about 574 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1 90th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs
 R2 90th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prot.Domains; R1; R2

426230; AA367019; Hs.241395; proleaze, serine, 1 (trypsin 1); trypsin,toxin_4;SS=M; 107.29; 1.07
 415934; NM_000928; Hs.992; phospholipase A2, group IB (pancreas); phoslip;SS=M; 83.67; 1.06
 421996; AW583807; Hs.1460; glucagon; hormone2;SS=M; 59.35; 1.61
 406399; ; NM_003122; Homo sapiens serine protease; kazal;SS=M; 55.49; 1.08
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 53.65; 43.61

- 406685; M18728; ; gb:Human nonspecific crossreacting antigen; ig; TM=M; SS=M; 52.73; 22.83
 428698; AA852773; Hs.334838; KIAA1866 protein; none; NA; NA; 32.44; 13.11
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbonate; HCO₃ cotransp; TM=Y; 29.80; 1.46
 428874; W32133; Hs.194366; transthyretin (prealbumin, amyloidosis t; Transthyretin; SS=M; 29.42; 1.94
 444754; T83911; Hs.374341; transmembrane 4 superfamily member 4; none; TM=Y; SS=M; 28.78; 3.13
 418068; AW971155; Hs.293902; ESTs, Weakly similar to ISHUS protein d; none; TM=M; SS=M; 28.61; 0.98
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zfc4, none; 25.38; 3.63
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; SS=M; 24.64; 7.21
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarot; none, none; 23.77; 6.74
 414998; NM_002543; Hs.77729; oxidized low density lipoprotein (lectin; lectin_c; TM=Y; SS=M; 22.96; 4.57
 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4; TM=Y; SS=M; 22.31; 5.42
 425573; AB006423; Hs.158308; serine (or cysteine) proteinase inhibitor; serpin, GCV_H; TM=M; SS=M; 21.91; 1.03
 433110; D56494; Hs.3191; rat regenerating islet-derived-like, hum; lectin_c; TM=M; SS=M; 21.90; 0.60
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC, PAS; TM=M; 21.41; 19.89
 453863; X02544; Hs.572; orosomucoid 1; lipocalin, aldehyd, ubiquitin, IRK; SS=M; 20.80; 8.12
 421126; M74587; Hs.102122; insulin-like growth factor binding prote; thyroglobulin_1, IGFBP; SS=Y; 20.60; 8.48
 451035; AU076785; Hs.430; plasmin 1 (I isoform); efhand, CH, Adaptin_N; SS=M; 19.25; 3.53
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT, none; 18.38; 2.53
 420332; NM_001756; Hs.1305; serine (or cysteine) proteinase inhibitor; serpin; TM=M; SS=M; 18.19; 2.29
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zfc4, none; 17.67; 4.80
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Nterm, integrin_B; SS=M; 17.08; 6.37
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm_1; TM=Y; SS=M; 16.89; 7.15
 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C, G-alpha, arf; TM=M; SS=M; 16.59; 7.74
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 16.28; 9.22
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept; TM=M; SS=M; 15.96; 2.38
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodi; Somatomedin_B, Endonuclease, Phosphodiect; TM=Y; SS=M; 15.65; 1.33
 408243; Y00787; Hs.624; interleukin 8; HLH, PAS, IL8; TM=M; 15.53; 4.34
 419355; AA428520; Hs.90061; progesterone binding protein; heme_1; TM=Y; SS=M; 15.45; 10.50
 426006; R49031; Hs.22627; ESTs; pkinase, TBC; 15.17; 0.58
 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD, ICE_p10, ICE_p20; SS=M; 14.84; 3.04
 422260; AA315993; Hs.105484; regenerating gene type IV; lectin_c; SS=M; 14.71; 2.89
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3, none; 14.28; 11.47
 408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC_tran, ABC_membrane, PRK, Bac_export_3; TM=Y; 13.98; 1.18
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 13.81; 7.69
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese, DSPC, Y_phosphatase, Ribosomal_S3_N; TM=M; 13.59; 2.24
 425988; BE045897; Hs.53985; ESTs, Weakly similar to 138022 hypotheti; none, none; 13.54; 0.95
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M; 13.48; 3.59
 429556; AW139399; Hs.98988; ESTs; none; TM=M; 13.20; 1.16
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; SS=M; 12.83; 7.72
 427286; AW732802; Hs.2132; epidermal growth factor receptor pathway; SH3, TonB_boxC; TM=M; 12.72; 9.01
 431912; A1660552; Hs.356183; ESTs, Weakly similar to A56154 Abl subst; none, Acyl-CoA_dh, Acyl-CoA_dh_M, Acyl-CoA_dh_N; 12.72; 6.72
 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7tm_1; TM=Y; SS=M; 12.71; 12.56
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB, DNA_topoisolv, HATPase_c; SS=M; 12.52; 4.92
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, M_SMC_N, SMC_C, DUF164, none; 12.38; 7.59
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase, hexokinase2, none; 12.34; 11.53
 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip; TM=M; SS=Y; 12.32; 3.02
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 12.29; 2.21
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3, TPR; TM=M; 12.16; 4.14
 427283; AL119796; Hs.174185; ectonucleotide pyrophosphatase/phosphodi; Sulfatase, Somatomedin_B, Phosphodiect, Endonuclease; TM=M; SS=Y; 11.97; 5.93
 434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK; TM=Y; 11.76; 1.58
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 11.75; 3.56
 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vi; sushi; TM=Y; SS=M; 11.67; 3.77
 450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin, Idl_recept_La, none; 11.65; 4.52
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C, IMPDH_N, CBS, Integrin_B, Ricin_B_lectin; 11.56; 5.46
 431512; BE270734; Hs.27195; lactate dehydrogenase A; Idh, Idh_C, SH3, pkinase, UBA; TM=M; 11.55; 5.11
 429638; A1916662; Hs.21577; kinesin 1 (kinesin receptor); bZIP, Tropomyosin, spectrin, LBP_BPI, CETP, B56, M; TM=Y; SS=M; 11.47; 4.65
 445133; AW157646; Hs.198689; ESTs; efhand, spectrin, GAS2, SH3, Plectin, RA, Xylose_isom, F1D, bZIP, Tropomyosin, Myc-LZ, M, Idh_C, CH, AIP3; TM=M; 11.41; 12.62
 411352; NM_002890; Hs.758; RAS p21 protein activator (GTPase activa; SH2, SH3, C2, PH, RasGAP; TM=M; SS=M; 11.24; 9.95
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none, none; 11.19; 4.16
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS, AIRS_C; TM=M; 11.17; 5.98
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, fn3, Y_phosphatase; TM=M; 11.14; 9.09
 440594; AW445167; Hs.126036; ESTs; none, none; 11.05; 16.45
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD, DAPIN, HIN; SS=M; 11.05; 10.38
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese, DSPC; TM=M; 11.05; 4.70
 448811; A1590371; Hs.199460; ESTs; none; TM=Y; 10.85; 9.69
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2, SH3, pkinase; TM=M; 10.72; 8.65
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; 10.51; 12.97
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, ig, FAD_Synth, Idh, Idh_C, pkinase; SS=M; 10.37; 6.35
 436856; A1469355; Hs.127310; ESTs; pkinase, rrm; TM=M; 10.36; 2.74
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 10.34; 3.14
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2, SH3, pkinase; TM=M; 10.34; 4.47
 418299; AA279530; Hs.83968; Integrin, beta 2 (antigen CD18 (p95), ly; integrin_B, EGF, PSI; TM=Y; SS=M; 10.21; 4.58
 451820; AW058357; Hs.199248; ESTs; 7tm_1; TM=Y; SS=M; 10.18; 2.67
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2, lectin_c, Ricin_B_lectin, Xlink; TM=Y; SS=M; 10.17; 8.35
 429752; H52348; Hs.36636; ESTs; pkinase, pkinase; 10.13; 12.35
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-pho; MORN, sugar_tr; TM=Y; SS=M; 10.08; 8.74
 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 10.05; 6.06
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1; TM=Y; SS=M; 9.98; 3.16
 416389; AA180072; Hs.149846; Integrin, beta 5; integrin_B, none; 9.85; 9.59
 421044; AF051871; Hs.101302; Human DNA sequence from clone RP1-238D15; fn3, vwa, Collagen, TSPN; TM=M; SS=M; 9.78; 5.96
 446620; AA128808; Hs.179902; transporter-like protein; none; TM=Y; SS=M; 9.75; 2.64
 405102; ; C15001220; gij4469558[gb]AAD21311.1[AF]; DAG, PE-bind, PH, RhoGEF, DC1; SS=M; 9.74; 1.88
 418693; A1750878; Hs.87409; thrombospondin 1; EGF, isp_1, vwc, TSPN, isp_3; SS=M; 9.72; 6.94

- 426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR m; Kunitz_BPTI,Kunitz_BPTI,7tm_2,HRM; 9.68; 10.58
 448105; AW591433; Hs.298241; Transmembrane protease, serine 3; ldl_recept_a,trypsin;TM=Y;SS=M; 9.67; 4.06
 456266; L29073; Hs.198726; cold shock domain protein A; 7tm_2,HRM,CSD;TM=Y;SS=M; 9.62; 2.36
 410240; AL157424; Hs.61289; synaptotagmin 2; Exo_endo_phos,Syja_N,rm,Gram-ve_porins;TM=M;; 9.62; 3.77
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;; 9.60; 8.05
 456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A; none;TM=Y;; 9.57; 3.77
 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3;TM=M;; 9.56; 10.50
 437158; AW090198; Hs.348709; KIAA1150 protein; none;NA;NA; 9.55; 8.87
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;; 9.47; 5.67
 403344; ; NM_000341;Homo sapiens solute carrier fa; alpha-amylase;TM=Y;; 9.47; 1.42
 449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K_tetra,ion_trans,none; 9.46; 3.12
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M;; 9.42; 4.01
 444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP,none; 9.42; 1.87
 439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none,none; 9.41; 5.55
 428505; AL035461; Hs.2281; chromogranin B (secretogranin 1); Granin;SS=M; 9.40; 3.46
 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 9.38; 6.32
 432810; AA863400; Hs.374489; ESTs; none,Skp1,AAA; 9.38; 4.36
 427581; NM_014788; Hs.179703; KIAA0129 gene product; SPRY,zf-B_box;TM=M;; 9.34; 8.26
 413109; AW389845; Hs.110855; ESTs, similar to leukemia virus receptor; PHO4,none; 9.34; 4.67
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;; 9.31; 4.24
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3,none; 9.24; 7.12
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.23; 6.03
 437672; AW748265; Hs.5741; flavohemoprotein b57; heme_1,NAD_binding,lipoxygenase,FAD_binding_6;TM=M;; 9.22; 10.72
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 9.20; 4.46
 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta,TGFb_propeptide,Tub;SS=M; 9.19; 16.46
 413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-rel; none,START; 9.15; 2.18
 418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodi; Phosphodiester;TM=Y;SS=M; 9.14; 3.03
 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor t; Y_phosphatase,none; 9.14; 11.75
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; coflin_ADF;SS=M; 9.11; 4.29
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;; 9.06; 9.68
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit,; proteasome;TM=M;; 9.05; 5.61
 413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;; 9.04; 5.79
 437296; AA350994; Hs.20281; KIAA1700; Rhodanese,DSPC;TM=M;; 9.02; 5.75
 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestin; cadherin;TM=Y;SS=M; 8.94; 5.01
 446406; AI553681; Hs.348490; Arg/Abl-interacting protein ArgBP2; Sorb,none; 8.91; 1.77
 428820; AA436187; Hs.172631; integrin, alpha M (complement component ; vva,integrin_A,FG-GAP;TM=Y;SS=M; 8.85; 4.74
 434398; AA121098; Hs.3838; serum-inducible kinase (SNK); pkinase,POLO_box;TM=M;; 8.78; 4.54
 453902; BE502341; Hs.3402; ESTs; none,none; 8.72; 3.71
 433334; AI927208; Hs.231958; matrix metalloproteinase 28; Peptidase_M10,none; 8.71; 4.28
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;SS=M; 8.70; 3.71
 450247; AF123303; Hs.24713; hypothetical protein; ehand,milo_carr;TM=Y;SS=M; 8.68; 3.40
 432101; AI918950; Hs.123642; EphA3; fn3,pkinase,SAM,EPH_1bd;TM=Y;SS=M; 8.62; 5.62
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; none,none; 8.61; 13.53
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 8.55; 4.82
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;; 8.50; 3.18
 419111; AA234172; Hs.137418; ESTs; none,IRK; 8.47; 7.51
 430024; AI808780; Hs.227730; integrin, alpha 6; integrin_A,FG-GAP;TM=Y;SS=M; 8.45; 3.46
 447574; AF162666; Hs.18895; tousel-like kinase 1; pkinase;TM=M;; 8.45; 5.30
 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C;TM=M;SS=M; 8.44; 6.30
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M;; 8.43; 4.87
 405555; ; homeodomain-interacting protein kinase 3; trypsin;TM=M;; 8.39; 0.68
 417412; X16896; Hs.82112; interleukin 1 receptor, type I; ig,TIR;TM=M;SS=M; 8.35; 4.74
 405556; ; homeodomain-interacting protein kinase 3; trypsin;TM=M;; 8.31; 0.87
 407687; AK002011; Hs.37558; hypothetical protein FLJ11149; lys,ig,FAD_Synth,ldh_C,pkinase;SS=M; 8.28; 3.12
 408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 8.27; 5.65
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.26; 5.49
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 doma; SH2;SS=M; 8.24; 8.91
 405204; ; NM_002086;Homo sapiens growth factor re; SH2,SH3;TM=M;; 8.23; 6.43
 426806; T19228; Hs.172572; hypothetical protein FLJ20093; ank,pkinase,UPF0073;SS=M; 8.20; 6.11
 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xe; pkinase;TM=M;; 8.18; 8.37
 450375; AA009647; Hs.352537; a disintegrin and metalloproteinase doma; Reprolysin,Pep_M12B_propep,disintegrin,Reprolysin,Pep_M12B_propep,disintegrin; 8.17; 12.24
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 8.15; 4.61
 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalyti; PKI;SS=M; 8.15; 11.12
 428513; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI,none; 8.13; 13.28
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 8.13; 1.15
 425838; NM_014071; Hs.159613; nuclear receptor coactivator RAP250; per; none;TM=M;; 8.12; 4.54
 425836; AW955696; Hs.90960; ESTs; Cbl_N,Cbl_N2,Cbl_N3,UBA,zf-C3HC4,none; 8.11; 7.47
 406366; ; secreted frizzled-related protein 4; trypsin;SS=M; 8.05; 0.69
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic; C2,PLA2_B;TM=M;; 8.04; 5.20
 458946; AA009716; Hs.42311; ESTs; none,DSPC,Y_phosphatase; 8.02; 1.93
 425280; U31519; Hs.1872; phosphoenolpyruvate carboxykinase 1 (sol; PEPCCK;TM=M;; 7.97; 19.33
 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, ty; none,none; 7.90; 11.44
 449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.89; 7.00
 426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo_seg,HEAT_PBS;; 7.83; 11.16
 400408; S75765; ; Homo sapiens delta CCK-B gene, partial c; 7tm_1,none; 7.81; 0.78
 448362; AA641767; Hs.21015; hypothetical protein DKFZp564L0864 simil; sugar_tr;TM=Y;SS=M; 7.78; 7.02
 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substra; SH3;TM=M;; 7.75; 2.63
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;; 7.72; 2.68
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;; 7.68; 2.40
 421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo_seg;SS=M; 7.49; 6.57
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside_tra2,none; 7.47; 2.53
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin_c,sushi;TM=M;SS=M; 7.38; 5.60
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 7.29; 5.78

428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm_3; TM=Y; SS=M; 7.26; 11.00
 426761; AI015709; Hs.172089; PORIMIN Pro-oncogenesis receptor inducing me; none; TM=Y; SS=M; 7.25; 7.22
 413880; AI660842; Hs.110915; interleukin 22 receptor; Tissue_fac; TM=Y; SS=M; 7.24; 0.98
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase; PLAT; TM=M; 7.22; 6.45
 413441; AI929374; Hs.75367; Src-like-adaptor; SH2,SH3; TM=M; 7.20; 5.72
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep_L_domain, Furin-like, pkinase, Recep_L_domain, Peptidase_M24; 7.13; 3.97
 428474; AB023182; Hs.184523; KIAA0965 protein; pkinase; TM=M; 7.13; 5.43
 421582; AI910275; Hs.350470; trefoil factor 1 (breast cancer, estrogen; trefoil, Gastrin; SS=M; 7.08; 21.61
 449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none; TM=Y; SS=M; 7.07; 6.18
 452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PL; pkinase, Activin_rec, none; 6.94; 4.82
 451295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene; pkinase, DAG_PE-bind, pkinase_C, OPR, none; 6.92; 15.34
 430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7_HUMAN ALU S; Y_phosphatase, Adaptorin_N_Y_phosphatase; 6.88; 1.94
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZS1G; 7tm_1, Idl_recept_L, LRR; SS=M; 6.86; 0.97
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; SS=M; 6.83; 7.24
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t, fn3, ig, Y_phosphatase, MAM; TM=Y; SS=M; 6.83; 11.43
 400539; ; Target Exon; none; TM=M; 6.70; 1.19
 431113; AK000673; Hs.274337; hypothetical protein FLJ20666; pkinase; TM=M; 6.65; 2.21
 445280; AW050603; Hs.343220; v-erb-b2 avian sarcoma virus CT10 oncogene; SH2, SH3, none; 6.61; 10.66
 425834; NM_001639; Hs.1957; amyloid P component, serum; pentaxin; TM=M; SS=M; 6.57; 2.20
 435706; W31254; Hs.7045; GL004 protein; PDEase, GAF, none; 6.55; 11.44
 415906; AI751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fis, clone H; Ephrin, none; 6.45; 5.25
 408308; AI033377; Hs.44197; hypothetical protein DKFZp564D0462; none, none; 6.42; 9.14
 432336; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm, pkinase; TM=M; 6.42; 4.12
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y; 6.42; 2.26
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm_1; TM=Y; SS=M; 6.41; 4.54
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; Idl_recept_a, PKD, MHC_I; TM=M; SS=Y; 6.38; 3.55
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese, DSPc; SS=M; 6.35; 4.95
 422583; AA410506; Hs.27973; KIAA0874 protein; ank, G-alpha; TM=M; 6.35; 3.56
 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1, OATP_C; TM=Y; 6.32; 11.02
 422282; AF019225; Hs.114309; apolipoprotein L; MotA, ExbB; TM=Y; SS=M; 6.32; 5.15
 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, y; none, Ribosomal_S13, Galactosyl_T, Zip, adh_short, zf-C3HC4; 6.30; 8.35
 428486; AW583497; Hs.184604; pancreatic polypeptide; hormone3; TM=M; SS=Y; 6.29; 3.51
 408847; AW290997; Hs.30348; ESTs; pkinase, ig, none; 6.28; 3.63
 428179; AI127772; Hs.279696; serum/glucocorticoid regulated kinase-II; pkinase, PX, pkinase_C; SS=M; 6.28; 3.50
 443614; AV655386; Hs.7645; fibrinogen, B beta polypeptide; none, none; 6.26; 7.48
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1; TM=Y; SS=M; 6.25; 3.98
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 6.21; 4.10
 428180; AI129767; Hs.182874; guanine nucleotide binding protein (G pr; G-alpha, arf; TM=M; 6.18; 4.62
 409245; AA361037; Hs.356436; tRNA isopentenylpyrophosphate transferase; Armadillo_seg; TM=M; 6.17; 11.15
 417952; AI192838; Hs.372643; dual-specificity tyrosine-(Y)-phosphoryl; pkinase, none; 6.17; 3.05
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2, PH; TM=M; 6.16; 11.90
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none; TM=M; 6.10; 2.96
 426797; AW936258; Hs.342849; ADP-ribosylation factor-like 5; arf, Ca_channel_B, SH3; 6.03; 3.17
 408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc; TM=M; 5.99; 2.55
 441384; AA447849; Hs.288660; Homo sapiens cDNA: FLJ22182 fis, clone H; 7tm_3, none; 5.97; 13.12
 414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none; NA; NA; 5.92; 6.47
 418506; AA084248; Hs.85339; Unknown protein for MGC:29643; none, none; 5.91; 1.94
 436345; AA873008; Hs.121572; ESTs; CARD, BIR, zf-C3HC4, CARD, BIR, zf-C3HC4; 5.90; 1.40
 414087; W19712; ; gb:zb36d03.r1 Soares_parathyroid_tumor_N; pkinase, none; 5.85; 0.90
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank, death, ZU5, EGF, kringle, trypsin, Nebulin, LIM; SS=M; 5.77; 1.24
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A; none, none; 5.71; 4.00
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR_LY6, ET, PLA2_inh; SS=M; 5.71; 3.83
 414171; AA360328; Hs.865; RAP1A, member of RAS oncogene family; pkinase, DAG_PE-bind, RBD, ras, DC1, GFP; TM=M; 5.69; 3.07
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1, 7tm_2; TM=Y; SS=M; 5.68; 12.92
 425317; AW205118; Hs.210546; interleukin 21 receptor; none; TM=Y; SS=M; 5.60; 5.45
 417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase; TM=M; 5.59; 4.19
 400151; ; Eos Control; AT_hook, DNA_mis_repair, HATPase_c, UQ_con; TM=M; 5.53; 8.13
 450139; AK001838; Hs.355608; serum/glucocorticoid regulated kinase; none, none; 5.52; 8.61
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 5.52; 10.04
 433556; W56321; Hs.111460; calcium/calmodulin-dependent protein kin; pkinase, none; 5.51; 6.75
 424701; NM_005923; Hs.151988; mitogen-activated protein kinase kinase; pkinase; TM=M; 5.47; 4.58
 415875; AA894876; Hs.5687; protein phosphatase 1B (formerly 2C), ma; PP2C; TM=M; 5.43; 5.30
 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not ava; 7tm_1, none; 5.42; 2.59
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4, LIM; TM=M; 5.37; 8.69
 444184; T87841; Hs.282990; Human DNA sequence from clone RP1-28H20; pkinase, RIO1, APH, KOW; TM=M; 5.36; 3.32
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR, LRRCT, TIR; TM=M; SS=M; 5.36; 3.94
 429023; NM_000312; Hs.2351; protein C (inactivator of coagulation fa; EGF, trypsin, gla; SS=M; 5.31; 4.30
 421559; NM_014720; Hs.105751; Ste20-related serine/threonine kinase; pkinase, UVR; TM=M; 5.31; 3.26
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone; TM=M; 5.27; 3.12
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin, bZIP; TM=M; 5.26; 4.82
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A recepto; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 5.25; 11.26
 428234; U93553; Hs.183123; nuclear receptor subfamily 5, group A, m; hormone_rec, zf-C4; SS=M; 5.20; 1.11
 408683; R58665; Hs.46847; TRAF and TNF receptor-associated protein; Exo_endo_phos; TM=M; 5.19; 6.25
 408657; AA782601; Hs.173328; ESTs; B56, none; 5.18; 5.47
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin, Guanylate_kin, PDZ, SH3; 5.17; 4.02
 438698; AW297855; Hs.361171; ESTs, Weakly similar to I38022 hypotheti; lipoxygenase, PLAT, none; 5.16; 2.91
 442200; AW590572; Hs.235768; ESTs; none, none; 5.11; 4.22
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 5.08; 2.71
 419088; AI538323; Hs.367688; integrin, beta 8; integrin_B, none; 5.07; 3.53
 414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets, ; phoslip; TM=M; SS=Y; 5.05; 3.42
 408414; AI114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell ; fn3, ig; TM=Y; SS=M; 5.05; 3.41
 430407; H23551; Hs.30974; ESTs; pkinase, PBD, none; 5.03; 1.63
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C, none; 5.00; 5.14

- 452194; A1694413; Hs.373599; Ubiquitin-like protein FAT107?? - diubiq; none,none; 4.98; 2.65
 410073; AW408163; Hs.58488; catenin (cadherin-associated protein), α ; Stathmin,Vinculin;SS=M; 4.97; 10.60
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 4.96; 2.87
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept; Y_phosphatase;SS=M; 4.88; 21.69
 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.88; 4.60
 418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 4.79; 5.47
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand,kazal,arf,ras,7tm_1;TM=M;; 4.75; 5.41
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y_phosphatase;TM=M;; 4.74; 9.76
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 4.73; 4.68
 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M;; 4.66; 5.61
 452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none,none; 4.63; 6.62
 427333; AF067797; Hs.176658; aquaporin 8; MIP;TM=Y;SS=M; 4.63; 0.80
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit); vwa,integrin_A,FG-GAP;TM=Y;SS=M; 4.58; 11.38
 428065; A1634046; Hs.157313; ESTs; ICE_p20,DED,ICE_p10,ICE_p20,DED; 4.55; 4.51
 428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 4.54; 8.76
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand;SS=M; 4.54; 19.57
 450056; BE047394; Hs.8208; ESTs, Weakly similar to S71512 hypothet; ABC_tran,ABC_membrane,ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.49; 10.47
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;; 4.41; 7.27
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 4.41; 10.25
 433208; AW002834; Hs.24095; ESTs; arf,Ca_channel_B,SH3; 4.39; 12.14
 403208; ; ; Target Exon; lectin_c,none; 4.37; 0.76
 440486; BE243513; Hs.7212; hypothetical protein PP1044; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC;NA;NA; 4.36; 10.34
 414278; AA330116; Hs.355877; Human glucose transporter pseudogene; none,none; 4.35; 7.95
 424833; NM_003894; Hs.153405; period (Drosophila) homolog 2; PAS;SS=M; 4.34; 6.23
 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin receptor; FG-GAP,integrin_A,none; 4.32; 5.85
 418721; NM_002731; Hs.87773; protein kinase, cAMP-dependent, catalytic; pkinase,pkinase_C;SS=M; 4.31; 3.09
 412330; NM_005100; Hs.788; A kinase (PRKA) anchor protein (gravin); none;TM=M;; 4.25; 12.74
 421939; BE169531; Hs.109727; TAK1-binding protein 2; KIAA0733 protein; zf-RanBP,CUE;TM=M;; 4.25; 12.54
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant_thionins;SS=M; 4.24; 6.91
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 4.22; 5.27
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb; re; ig;TM=Y;; 4.16; 7.22
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;SS=M; 4.16; 9.27
 445496; AB007860; Hs.12802; development and differentiation enhancin; SH3,ank,PH,ArfGAP;TM=M;; 4.15; 23.43
 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 4.14; 3.76
 414462; BE622743; Hs.301064; arfaptin 1; none,none; 4.08; 13.43
 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase,TrkA-N,2-Hacid_DH_C;TM=M;; 4.06; 9.12
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_lr;TM=Y;; 4.04; 10.05
 429379; NM_014840; Hs.200598; KIAA0537 gene product; pkinase,RIOT;TM=M;; 4.00; 6.35
 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M;; 3.98; 5.66
 405203; ; ; NM_002086; Homo sapiens growth factor re; SH2,SH3;TM=M;; 3.95; 17.71
 409335; NM_001502; Hs.53985; glycoprotein 2 (zymogen granule membrane; zona_pellucida;TM=M;SS=M; 3.94; 0.58
 446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 3.89; 7.59
 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3,PDZ,Guanylate_kin;TM=M;; 3.84; 8.89
 438000; A1825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M;; 3.83; 4.22
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 3.81; 6.45
 450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M;; 3.78; 8.49
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone_rec,zf-C4;SS=M; 3.77; 4.22
 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M;; 3.68; 4.92
 438113; A1467908; Hs.8882; ESTs; 7tm_1,none; 3.59; 12.12
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 3.58; 10.93
 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin_A,PHO4,pkinase,ubiquitin; 3.57; 5.10
 415088; A1077288; Hs.374374; serum/glucocorticoid regulated kinase; none,none; 3.56; 4.60
 418478; X38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 3.55; 4.52
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;; 3.54; 8.19
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 3.52; 9.70
 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor.; integrin_A,FG-GAP;TM=Y;; 3.45; 6.44
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2;TM=M;; 3.41; 6.03
 418255; AW135405; Hs.37251; ESTs; pkinase,none; 3.41; 13.97
 408822; AW500715; Hs.57079; Homo sapiens cDNA FLJ13267 fis, clone OV; PIP5K,none; 3.40; 8.97
 426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase;TM=M;; 3.39; 11.24
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none;TM=M;SS=Y; 3.39; 5.10
 414291; A1289619; Hs.13040; G protein-coupled receptor 86; 7tm_1;TM=Y;SS=M; 3.38; 10.25
 457329; A1634860; Hs.247043; type 1 tumor necrosis factor receptor sh; Peptidase_M1;SS=M; 3.38; 13.78
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 3.36; 4.17
 443710; A1928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha,none; 3.32; 20.33
 454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M;; 3.31; 6.94
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg;TM=M;SS=M; 3.29; 3.07
 426728; NM_007118; Hs.367689; triple functional domain (PTPRF interact; SH3,ig,pkinase,PH,spectrin,RhoGEF;TM=M;; 3.27; 14.90
 427202; BE272922; Hs.173936; interleukin 10 receptor, beta; Tissue_fac;TM=Y;SS=M; 3.24; 4.49
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M;; 3.24; 12.27
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 3.23; 13.40
 417534; NM_004998; Hs.82251; myosin IE; SH3,myosin_head,IQ;TM=M;; 3.21; 15.21
 458097; AW341135; Hs.58104; ESTs; none,SH3,PID; 3.21; 7.34
 437928; NM_005476; Hs.5920; UDP-N-acetylglucosamine-2-epimerase/N-ac; hexokinase,FGGY,ROK,Epimerase_2;SS=M; 3.20; 8.38
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 3.19; 5.09
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none,none; 3.18; 4.17
 453489; AA300067; Hs.102000; hypothetical protein DKFZp434N185; F5_F8_type_C,pkinase,Ets,F5_F8_type_C,pkinase,Ets; 3.17; 7.88
 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3_PI4_kinase;TM=M;; 3.16; 4.71
 412767; AA233808; Hs.286241; protein kinase, cAMP-dependent, regulator; SH3,7tm_2,cadherin,GPS,laminin_G,EGF,laminin_EGF,Sulfate_transp,STAS,cNMP_binding,Rlla; 3.16; 7.19
 415662; AW972481; Hs.170610; ESTs, Highly similar to G01887 MEK kinas; pkinase,none; 3.16; 7.21
 407786; AA687538; Hs.38972; telraspan 1; transmembrane4;TM=Y;SS=M; 3.15; 22.66

- 437175; AW968078; Hs.87773; protein kinase, cAMP-dependent, catalytic; pkinase, pkinase_C, none; 3.14; 11.72
 409270; BE090051; Hs.23120; PIST1; fn3, pkinase, PDZ, DUF139; TM=Y; SS=M; 3.09; 7.81
 419591; AF090900; Hs.91393; Homo sapiens cDNA: FLJ21887 fis, clone H; PDZ, L27; TM=M; 3.06; 5.46
 447225; R62676; Hs.17820; Rho-associated, coiled-coil containing p; PH, pkinase, HR1, none; 3.04; 13.05
 412692; AF044288; Hs.74515; aryl hydrocarbon receptor nuclear trans; HLH, PAS, PAC; TM=M; 2.95; 12.28
 409274; NM_003930; Hs.52644; SKAP55 homologue; SH3, PH; SS=M; 2.90; 14.62
 417707; AL035786; Hs.82425; actin related protein 2/3 complex, subunit; none; TM=M; 2.90; 11.00
 427045; H86504; Hs.173328; protein phosphatase 2, regulatory subunit; B56; TM=M; 2.89; 6.12
 431177; NM_003304; Hs.250687; transient receptor potential channel 1; ion_trans, ank; TM=Y; 2.89; 6.53
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none; TM=M; 2.87; 9.18
 418546; AA224827; gb:nc32g04.s1 NCL_CGAP_Pr2 Homo sapiens; vwa, integrin_A, FG-GAP, none; 2.86; 9.94
 446668; W58353; Hs.285123; Homo sapiens mRNA full length insert cDN; NDK, PH, Oxysterol_BP; SS=M; 2.85; 14.25
 454080; AI199711; Hs.576; fucosidase, alpha-L-1, tissue; Alpha_L_fucos; TM=M; SS=M; 2.81; 28.84
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3; TM=M; SS=Y; 2.80; 10.53
 433000; U26710; Hs.3144; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4, UBA, Cbl_N, Cbl_N3; 2.77; 10.93
 444488; AW192879; Hs.355660; ancient conserved domain protein 4; none, none; 2.77; 12.58
 417904; AJ750762; Hs.82911; protein tyrosine phosphatase type IVA, m; Y_phosphatase, DSPc; TM=M; 2.76; 12.78
 425204; NM_002436; Hs.1861; membrane protein, palmitoylated 1 (55kD); SH3, PDZ, Guanylate_kin; SS=M; 2.74; 5.71
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS, zf-C2H2, SET; 2.73; 12.50
 410793; AW581906; Hs.66392; intersectin 1 (SH3 domain protein); SH3, ehfand, C2, PH, RhoGEF, M; SS=M; 2.73; 9.84
 446081; AA972412; Hs.13755; f-box and WD-40 domain protein 2; WD40, F-box, Ribosomal_L14; TM=M; 2.71; 12.29
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor; ig, pkinase; TM=Y; 2.71; 10.53
 452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox, none; 2.69; 12.53
 423533; NM_014339; Hs.129751; interleukin 17 receptor; none; TM=Y; SS=M; 2.67; 8.59
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 2.67; 12.22
 453915; AA588721; Hs.12284; ribosomal protein L44; none, T-box; 2.65; 6.38
 416810; AF035606; Hs.80019; programmed cell death 6; ehfand; TM=M; 2.61; 13.89
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none; TM=M; SS=M; 2.58; 10.19
 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3, none; 2.56; 19.04
 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS; SS=M; 2.55; 14.99
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP; none; 2.52; 14.71
 409098; AA132672; Hs.7984; pleckstrin homology, Sec7 and coiled/coi; PH, Sec7; TM=M; 2.51; 14.51
 413040; AA193338; Hs.12321; sodium calcium exchanger; Na_Ca_Ex; TM=Y; SS=M; 2.49; 9.28
 422070; AF149785; Hs.111126; pituitary tumor-transforming 1 interact; TCTP; TM=M; SS=Y; 2.45; 12.49
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase; pkinase; TM=M; 2.44; 6.68
 427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none; TM=M; 2.43; 7.97
 446287; BE247683; Hs.14611; dual specificity phosphatase 11 (RNA/RNP); DSPc; SS=M; 2.41; 9.51
 410017; AW952426; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none, none; 2.41; 14.01
 424756; AW504657; Hs.152931; lamin B receptor; ERG4_ERG24, FKBP; TM=Y; 2.40; 5.98
 447580; AI953360; Hs.88201; ESTs; none, none; 2.36; 11.63
 426276; AW881411; Hs.169078; hypothetical protein FLJ23018; hormone_rec, zf-C4; TM=M; 2.34; 13.34
 424441; X14850; Hs.147097; H2A histone family, member X; histone, CBFD_NFYB_HMF; 2.33; 12.17
 429623; NM_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase, RGS; TM=M; 2.32; 15.80
 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm, NTF2; TM=M; 2.32; 12.48
 453648; W21493; Hs.28329; hypothetical protein FLJ14005; none, none; 2.31; 13.19
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22_Claudin, none; 2.31; 8.51
 453327; AW500180; Hs.356109; tryptophanyl-tRNA synthetase; rrm, vwa, FG-GAP; 2.30; 13.02
 439256; AA322302; Hs.183302; PCTAIRE protein kinase 2; none, none; 2.26; 10.36
 424467; AI929392; Hs.350026; DnaJ (Hsp40) homolog, subfamily B, member; DnaJ, pkinase, UBA, pkinase_C; SS=M; 2.26; 11.82
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; SS=M; 2.26; 12.54
 456607; AI660190; Hs.106070; cyclin-dependent kinase inhibitor 1C (p5; CDI; TM=M; 2.25; 13.11
 423960; AA164516; Hs.136309; SH3-containing protein SH3GLB1; SH3, none; 2.20; 20.05
 424058; AL121516; Hs.138617; thyroid hormone receptor interactor 12; HECT, WWE; TM=M; 2.20; 13.38
 446644; NM_003272; Hs.15791; transmembrane 7 superfamily member 1 (up; none; TM=Y; SS=M; 2.18; 15.68
 411218; H46440; Hs.180528; dynamin 1-like; dynamin_2, dynamin, GED, none; 2.18; 13.83
 414721; X90392; Hs.77091; ribosomal protein L10; Exo_endo_phos, Ribosomal_L10e, Acyltransferase, SCP; TM=M; SS=M; 2.14; 11.24
 421759; AA027968; Hs.107979; small membrane protein 1; none; TM=Y; SS=M; 2.14; 14.03
 416240; NM_001981; Hs.79095; epidermal growth factor receptor pathway; ehfand, DUF164; TM=M; 2.13; 12.86
 435521; W23814; Hs.6361; mitogen-activated protein kinase kinase; none, none; 2.12; 11.08
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_P14_kinase, FAT, FATC, BclA, RUN; TM=M; 2.12; 14.05
 453064; R40334; Hs.89463; potassium large conductance calcium-acti; none, none; 2.12; 8.96
 409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory su; SH2, SH3, RhoGAP, none; 2.08; 11.60
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1; TM=Y; SS=M; 2.06; 14.23
 414496; W73853; Hs.355424; ESTs; pkinase, F5_F8_type_C, adh_short, none; 2.05; 13.45
 450455; AL117424; Hs.25035; chloride intracellular channel 4; none, TNF; 2.05; 19.04
 449906; NM_005638; Hs.24167; synaptobrevin-like 1; synaptobrevin, NTF2; TM=Y; 2.04; 13.34
 422112; BE540240; Hs.111783; Lsm1 protein; Sm, BAG; SS=M; 2.03; 12.60
 434935; BE561824; Hs.273369; uncharacterized hematopoietic stem/proge; none; TM=M; 2.02; 10.52
 433427; AI816449; Hs.171889; cholinephosphotransferase 1; SH2, CDP-OH_P_transf; TM=M; 2.02; 16.87
 410850; AW362867; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp, STAS, HMG_box; 2.02; 9.37
 440481; AA182907; Hs.7200; Homo sapiens, clone MGC16714, mRNA, com; pkinase, RCC1; TM=M; 2.02; 12.31
 434645; AF255303; Hs.112227; membrane-associated nucleic acid binding; zf-CCH1, gpdh, Adeno_E1B_55K, zf-C3HC4; TM=M; 2.00; 9.15
 410113; AW996564; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone H; pkinase, none; 1.99; 10.64
 414636; AL120259; Hs.76691; stannin; none; TM=M; SS=Y; 1.95; 7.72
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylate kinase, none; 1.95; 14.95
 422690; AU077275; Hs.119222; suppression of tumorigenicity 13 (colon); TPR; TM=M; 1.94; 10.91
 427881; BE538296; Hs.323834; cytochrome c oxidase subunit Va; none, GKAP; 1.93; 20.57
 433387; L76528; Hs.3260; presenilin 1 (Alzheimer disease 3); Presenilin, 7tm_3, oxidored_q5_N; TM=Y; 1.92; 12.58
 453938; AF082569; Hs.36794; D-type cyclin-interacting protein 1; B56; TM=M; 1.90; 12.74
 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog); none; TM=M; 1.89; 23.27
 447791; BE241859; Hs.19575; CGI-11 protein; V-ATPase_H, Armadillo_seg; TM=M; 1.88; 12.82
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone H; adenylate kinase, none; 1.88; 14.95

- 432650; D00860; Hs.56; phosphoribosyl pyrophosphate synthetase ; none,none; 1.88; 12.70
 424250; AF073310; Hs.143648; insulin receptor substrate 2; PH,IRS;TM=M;; 1.86; 19.50
 424482; BE268621; Hs.149155; voltage-dependent anion channel 1; Euk_porin;SS=M; 1.85; 11.29
 425335; BE394327; Hs.296267; follistatin-like 1; efhand,kazal,arf,ras,7tm_1;TM=M;; 1.85; 13.62
 426122; NM_006925; Hs.166975; splicing factor, arginine/serine-rich 5; rrm;SS=M; 1.83; 10.88
 451579; AW607731; Hs.26670; Human PAC clone RP3-515N1 from 22q11.2-q; kringle;TM=Y;SS=M; 1.83; 20.35
 428901; AI929568; Hs.146668; KIAA1253 protein; 7tm_2,UPF0073,TMS_TDE;TM=Y;SS=M; 1.83; 19.00
 453963; AA040311; Hs.28959; ESTs; pkinase,Activin_recpt,none; 1.82; 15.25
 417414; AA434589; Hs.367676; dUTP pyrophosphatase; dUTPase,KRAB;; 1.81; 14.20
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 1.81; 22.29
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2;TM=M;; 1.80; 18.30
 417733; AL048678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown prot; none;NA;NA; 1.80; 6.28
 424805; AF230904; Hs.153260; c-Cbl-interacting protein; SH3;TM=M;; 1.80; 11.99
 420747; BE294407; Hs.99910; phosphofructokinase, platelet; PFK;TM=M;; 1.79; 25.25
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase;SS=M; 1.78; 15.25
 437708; AB033020; Hs.5801; KIAA1194 protein; LRR,Exo_endo_phos;TM=M;; 1.77; 11.11
 439877; H39685; Hs.258730; trypsin beta 1; pkinase;SS=M; 1.77; 21.91
 440256; U23841; Hs.18851; hypothetical protein FLJ10875; none,UBA,UBX; 1.76; 12.95
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor I; none;TM=M;SS=Y; 1.76; 21.01
 414703; BE243877; Hs.374366; ATPase, Na⁺ transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 1.75; 20.03
 443693; AI344782; Hs.349261; DnaJ (Hsp40) homolog, subfamily C, membe; rrm,DnaJ,TPR;TM=M;; 1.75; 13.29
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFp547C136 (fr; ABC_tran,GTP_EFTU,ABC_membrane,none; 1.75; 8.75
 413796; AW408094; Hs.75545; interleukin 4 receptor; fn3,granulin;TM=M;SS=M; 1.74; 14.73
 438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyrosine kinase; pkinase,SH2,adenylatekinase,none; 1.73; 24.10
 429655; U48959; Hs.211582; myosin, light polypeptide kinase; pkinase,fn3,ig,none; 1.73; 31.59
 421456; AW579842; Hs.104557; hypothetical protein FLJ10697; zf-C2H2,DUF18,efhand,C2,PI-PLC-Y,PI-PLC-X;TM=M;; 1.73; 16.87
 444252; R21135; Hs.54985; ESTs; none,none; 1.71; 10.40
 442819; BE622721; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; none,pkinase,PBD; 1.69; 14.02
 447918; AI129320; Hs.115175; ESTs, Highly similar to JC5818 gamma-act; pkinase,SAM,none; 1.69; 17.14
 429279; AB018271; Hs.198689; KIAA0728 protein; Myosin_tail,efhand,spectrin,GAS2,Myosin_tail; 1.68; 14.21
 450440; AB024334; Hs.25001; tyrosine 3-monooxygenase/tryptophan 5-mo; 14-3-3;TM=M;; 1.67; 24.67
 413423; AU076684; Hs.75350; vinculin; Vinculin,none; 1.65; 29.28
 420972; AW814616; Hs.31431; hypothetical protein FLJ12171; Fructosamin_kin;SS=M; 1.65; 10.75
 416884; M60484; Hs.80350; protein phosphatase 2 (formerly 2A), cat; Metallophos;SS=M; 1.63; 24.55
 436719; Y11192; Hs.5299; aldehyde dehydrogenase 5 family, member ; lipocalin,aldedh,ubiquitin,IRK;SS=M; 1.61; 11.20
 419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4;TM=Y;SS=M; 1.61; 14.93
 414176; BE140638; Hs.75794; EDG-2 (endothelial differentiation, lys; 7tm_1,CROB;TM=Y;; 1.61; 8.03
 431476; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT;SS=M; 1.60; 24.37
 412347; AW970026; Hs.73818; ubiquinol-cytochrome c reductase hinge p; UCR_hinge,G-alpha,arf;TM=M;; 1.59; 18.09
 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;; 1.59; 10.99
 426552; BE297660; Hs.170328; moesin; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 1.58; 25.97
 428216; M18468; Hs.183037; protein kinase, cAMP-dependent, regulator; cNMP_binding,Rlla;SS=M; 1.56; 10.58
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ;SS=M; 1.56; 13.51
 448581; NM_002709; Hs.21537; protein phosphatase 1, catalytic subunit; none,none; 1.55; 12.33
 417098; AB017365; Hs.173859; frizzled (Drosophila) homolog 7; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 1.55; 13.77
 437076; AA961260; Hs.5443; BCL2-associated athanogene 5; BAG,Hanta_nucleocap;TM=M;; 1.54; 10.93
 426653; AA530892; Hs.171695; dual specificity phosphatase 1; Rhodanese,DSPPc,Y_phosphatase;TM=M;; 1.54; 11.88
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing le; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 1.53; 23.05
 414457; AW514320; Hs.76159; ATPase, H transporting, lysosomal (vacuo; pkinase,ATP-synt_C,none; 1.53; 32.59
 414382; AW380339; Hs.8068; hematopoietic PBX-interacting protein; M;TM=M;; 1.52; 8.66
 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; rrm;TM=M;; 1.52; 11.74
 402705; ; ; activator of S phase kinase; AhpC-TSA;TM=M;SS=M; 1.51; 26.85
 426268; AF083420; Hs.168913; serine/threonine kinase 24 (Ste20, yeast; pkinase;SS=M; 1.50; 24.04
 414604; AU076649; Hs.76556; growth arrest and DNA-damage-inducible 3; none;TM=M;; 1.50; 14.35
 445584; AF217518; Hs.8360; PTD012 protein; none;SS=M; 1.49; 12.00
 407232; X04526; ; gb:Human liver mRNA for beta-subunit sig; WD40;TM=M;; 1.49; 19.32
 424206; NM_003734; Hs.198241; amine oxidase, copper containing 3 (vasc; Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3;TM=M;SS=M; 1.48; 13.21
 458761; AF090922; Hs.152738; mitochondrial ribosomal protein L11; ER_lumen_recept,Ribosomal_L11,Ribosomal_L11_N;TM=Y;SS=M; 1.48; 12.50
 426340; Z97989; Hs.169370; FYN oncogene related to SRC, FGR, YES; BNR,SH2,SH3,pkinase;TM=Y;SS=M; 1.48; 17.75
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPPc,isp_1,Ribosomal_S21,rvp;TM=M;; 1.46; 20.47
 452516; AA058630; Hs.29759; RNA POLYMERASE I AND TRANSCRIPT RELEASE ; none;SS=M; 1.46; 12.72
 414240; AL046742; Hs.75842; dual-specificity tyrosine-(Y)-phosphoryl; pkinase;SS=M; 1.45; 14.38
 420532; AA248016; Hs.194110; hypothetical protein PRO2730; pkinase,WD40;SS=M; 1.43; 13.92
 402575; ; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.43; 13.71
 414765; X07854; Hs.77269; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M;; 1.41; 24.62
 448423; BE390905; Hs.21198; translocase of outer mitochondrial membr; TPR;TM=M;SS=M; 1.41; 10.70
 422587; AI879352; Hs.118625; hexokinase 1; hexokinase,hexokinase2;TM=M;; 1.41; 19.31
 415995; NM_004573; Hs.355888; phospholipase C, beta 2; C2,PI-PLC-Y,PI-PLC-X;TM=M;; 1.40; 11.21
 446108; AL036596; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemm;TM=M;; 1.40; 13.98
 427721; AI582843; Hs.180455; RAD23 (S. cerevisiae) homolog A; ubiquitin,UBA,integrin_B;SS=M; 1.39; 15.01
 417891; W79410; Hs.82887; protein phosphatase 1, regulatory (inhib; none;TM=M;; 1.39; 15.97
 427373; AB007972; Hs.130760; myosin phosphatase, target subunit 2; ank;TM=M;; 1.39; 14.49
 446334; U52427; Hs.14839; polymerase (RNA) II (DNA directed) polyp; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rrm,PAP_assoc;TM=Y;SS=M; 1.38; 12.58
 447042; AB035863; Hs.182217; succinate-CoA ligase, ADP-forming, beta ; ligase-CoA,ATP-grasp,Zip,CPSase_L_D2,GARS_B;TM=Y;SS=M; 1.37; 11.37
 427705; AI870421; Hs.180394; signal recognition particle 14kD (homolo; SRP14,TNFR_c6;SS=M; 1.37; 22.05
 425969; AW576265; Hs.301763; KIAA0554 protein; SH3,FCH,HR1;TM=M;; 1.37; 13.68
 433572; AL046859; Hs.3407; protein kinase (cAMP-dependent, catalyti; PKI;SS=M; 1.35; 12.43
 410597; W16518; Hs.279518; amyloid beta (A4) precursor-like protein; Kunitz_BPTI,AA_EXTRA,Coprogen_oxidas;TM=Y;SS=M; 1.35; 22.54
 418424; Y13622; Hs.85807; latent transforming growth factor beta b; EGF,TB,spidertoxin,granulin,ANF_receptor;SS=M; 1.34; 12.09
 442603; AL035719; Hs.303091; pleckstrin homology, Sec7 and coiled/coi; PH,Sec7;TM=M;; 1.34; 11.40
 418043; AW377752; Hs.83341; AXL receptor tyrosine kinase; fn3,ig,pkinase;TM=Y;SS=M; 1.31; 10.79

439278; AF077046; Hs.6518; ganglioside expression factor 2; MAP1_LC3,aminotran_3;TM=M; 1.31; 15.89
 425875; AU077333; Hs.160483; erythrocyte membrane protein band 7.2 (s; PBP,Band_7;TM=M; 1.31; 17.93
 407744; AB020629; Hs.38095; ATP-binding cassette, sub-family A (ABC1; ABC_tran,PRK;TM=Y;SS=M; 1.29; 10.95
 420679; X57152; Hs.99853; fibrillarin; CK_II_beta,Fibrillarin,WD40;TM=M; 1.29; 18.69
 5 427397; AI929685; Hs.177656; calmodulin 1 (phosphorylase kinase, delt; efhand,RmaAD;SS=M; 1.29; 15.68
 424661; M29551; Hs.151531; protein phosphatase 3 (formerly 2B), cat; Metallophos;TM=M; 1.28; 13.39
 428950; BE311879; Hs.194673; phosphoprotein enriched in astrocytes 15; DED;TM=M; 1.27; 11.15
 440820; AL031846; Hs.356416; plakophilin 4; none,none; 1.26; 10.65
 10 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevi; NusG;SS=M; 1.25; 12.07
 447386; NM_006289; Hs.375001; KIAA1027 protein; Band_41,L_LWEQ,Apolipoprotein,IRS;SS=M; 1.22; 10.65
 433053; BE301909; Hs.279952; glutathione S-transferase subunit 13 hom; HCCA_isomerase;TM=M; 1.20; 15.78
 440708; AF038962; Hs.7381; voltage-dependent anion channel 3; Euk_porin,Enterotoxin_A,PHO4,none; 1.20; 14.06
 417069; AA442192; Hs.374980; cytochrome c oxidase subunit VIII; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rrm,PAP_assoc;TM=Y;SS=M; 1.18; 16.91
 15 402559; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.16; 15.49
 426636; BE242634; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; ThiF,UBACT;TM=M; 1.14; 10.99
 428773; BE256238; Hs.193163; bridging integrator 1; BAR,SH3;SS=M; 1.14; 11.38
 406906; Z25424; ; gb:H.sapiens protein-serine/threonine ki; none,none; 1.13; 12.97
 443932; AW888222; Hs.9973; tensin; SH2,WW,PID,none; 1.07; 15.41
 20 421996; AW583807; Hs.1460; glucagon; hormone2;SS=M; 59.35; 1.61
 414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 22.96; 4.57
 442573; H93366; Hs.7567; branched chain aminotransferase 1, cytos; aminotran_4,none; 21.41; 1.15
 451035; AU076785; Hs.430; plastin 1 (i isoform); efhand,CH,Adaptin_N;SS=M; 19.25; 3.53
 408243; Y00787; Hs.624; Interleukin 8; HLH,PAS,IL8;TM=M; 15.53; 4.34
 25 421340; F07783; Hs.1369; decay accelerating factor for complement; sushi;SS=M; 14.84; 19.59
 422260; AA315993; Hs.105484; regenerating gene type IV; lectin_c;SS=M; 14.71; 2.89
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 14.28; 11.47
 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7tm_1;TM=Y;SS=M; 12.71; 12.56
 451820; AW058357; Hs.199248; ESTs; 7tm_1;TM=Y;SS=M; 10.18; 2.67
 30 418693; AI750878; Hs.87409; thrombospondin 1; EGF,isp_1,vwc,TSPN,isp_3;SS=M; 9.72; 6.94
 448105; AW591433; Hs.298241; Transmembrane protease, serine 3; ldl_recept_a,trypsin;TM=Y;SS=M; 9.67; 4.06
 456266; L29073; Hs.198728; cold shock domain protein A; 7tm_2,HRM,CSD;TM=Y;SS=M; 9.62; 2.36
 413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-rel; none,START; 9.15; 2.18
 417933; X02308; Hs.82962; thymidylate synthetase; thymidylat_synt,MR_MLE,MR_MLE_N;SS=M; 8.97; 5.01
 35 433334; AI927208; Hs.231958; matrix metalloproteinase 28; Peptidase_M10,none; 8.71; 4.28
 418030; BE207573; Hs.83321; neuromedin B; Bombesin;TM=M;SS=Y; 8.38; 1.55
 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20;SS=M; 8.31; 4.23
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.26; 5.49
 428513; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI,none; 8.13; 13.28
 40 449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.89; 7.00
 453459; BE047032; Hs.257789; ESTs; none,none; 7.40; 0.60
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 7.29; 5.78
 426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 7.25; 7.22
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 7.13; 3.97
 45 419968; X04430; Hs.93913; interleukin 6 (interferon, beta 2); IL6;SS=Y; 6.93; 3.43
 457133; M54968; Hs.351221; v-Ki-ras2 Kirsten rat sarcoma 2 viral on; ras,ldh;SS=M; 6.90; 2.85
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 6.88; 3.10
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=Y; 6.42; 2.26
 427969; NM_001963; Hs.82226; epidermal growth factor (beta-urogastron; EGF,ldl_recept_b,EB;TM=M;SS=M; 6.37; 1.07
 50 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 5.77; 1.24
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR,LY6,ET,PLA2_inh;SS=M; 5.71; 3.83
 418283; S79895; Hs.83942; cathepsin K (pseudosynthesis); Peptidase_C1;SS=M; 5.59; 38.68
 458471; AV648609; Hs.194240; ESTs; none,none; 5.23; 1.05
 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.88; 4.60
 55 433293; AF007835; Hs.32417; hypothetical protein MGC4309; none;TM=M; 4.56; 4.96
 410867; X63556; Hs.750; fibrillin 1 (Marfan syndrome); EGF,TB,wnt,EB,TIL;SS=M; 4.32; 26.87
 417512; X76534; Hs.82226; glycoprotein (transmembrane) nmb; PKD;TM=Y;SS=M; 4.26; 9.04
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian ; Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 3.94; 1.16
 439180; AI93742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 3.76; 2.21
 60 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 3.47; 2.24
 419749; X73608; Hs.93029; sparco/osteonection, cwcv and kazal-like d; kazal,thyroglobulin_1;SS=M; 3.37; 7.10
 436576; AI458213; Hs.77542; ESTs; 7tm_1,DnaJ; 3.15; 3.27
 428093; AW594506; Hs.104830; ESTs; none,none; 2.81; 3.40
 459683; AI674906; Hs.199460; gb:wc73f02.x1 NCL_CGAP_Pan1 Homo sapiens; none;TM=Y; 2.77; 1.36
 65 414443; AU077268; Hs.76144; platelet-derived growth factor receptor; ig,pkinase;TM=Y; 2.71; 10.53
 430451; AA836472; Hs.297939; cathepsin B; Peptidase_C1,pro_isomerase;SS=M; 2.28; 14.59
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfam; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD; 2.21; 6.33
 435496; AW840171; Hs.265398; PAR-6 beta; none,none; 2.17; 2.00
 70 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin,Repolyisin,Pep_M12B_propep,EGF;TM=Y;SS=M; 1.91; 13.06
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigeni; DAN;TM=M;SS=M; 1.81; 22.29
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 1.52; 8.40
 452795; AW392555; Hs.18878; hypothetical protein FLJ21620; 2OG-Fel1_Oxy;TM=M; 1.49; 3.29
 432199; AI693815; Hs.127179; cryptic gene; none;TM=M;SS=M; 1.23; 1.60
 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin,ldl_recept_a,none; 1.00; 3.92
 75 445418; AW139377; Hs.127179; cryptic gene; none,none; 1.00; 2.45
 451106; BE382701; Hs.25960; N-MYC oncogene; HLH,Myc_N_term;TM=M; 1.00; 1.87
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00; 1.30

TABLE 42B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
5	406685	0_0 M18728
	414087	1632850_1 W19712 BE247277
	400151	9575_21 BC006850 U07418 NM_000249 U07343 AL574783 BI090482 BG684481 AA385302 BG196167 BI091720 BG195132 AI680106 AI457552 AA402478
		BG249688 AA347119 BG755996 BG822578
	418546	242836_1 T59708 AA224827 T59843 BE156903

TABLE 42C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
20	406399	9256288	Minus 63448-63554
	405102	8076881	Minus 120922-121296
	403344	8569726	Plus 70823-70990
	405555	1552511	Plus 153405-153564,154623-154876,155272-15540
25	405556	1552511	Plus 163497-163623,164715-164968,165369-16550
	405204	7230116	Plus 126569-126754
	406366	9256126	Minus 10639-10800,10890-11023,11113-11293
	400539	7574902	Plus 8559-8721
	403208	7630829	Minus 147706-147903,148667-148804
30	405203	7230116	Plus 125295-125463
	402705	8782736	Plus 89961-90114,90773-90895,91131-91261
	402575	9884830	Minus 109742-109883
	402559	9864273	Plus 33539-33715

TABLE 43A: 43 genes upregulated in pancreatic cancer relative to normal body tissues

Table 43A lists about 43 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins particularly useful for diagnostic or prognostic applications. These genes were selected from 59680 probesets on the Eos/Affymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1 90th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs
 R2 90th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prot.Domains; R1; R2

446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin;SS=M; 44.95; 2.17
 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;SS=M; 35.40; 29.13
 411274; NM_002776; Hs.69423; kallikrein 10; trypsin;TM=M; 30.10; 13.59
 446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL8;SS=Y; 29.33; 16.08
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8;SS=M; 24.64; 7.21
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide,TGF-beta,none; 23.81; 10.74
 407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagonist; TGF-beta,DAN;SS=Y; 22.33; 10.20
 404682; ; C9001188*gi12738842[ref]NP_073725.1| p; none;TM=M; 17.72; 1.40
 413554; AA319146; Hs.75426; secretogranin II (chromogranin C); Granin;TM=M;SS=Y; 17.36; 2.01
 428392; H10233; Hs.2265; secretory granule, neuroendocrine protein; none;TM=M;SS=M; 16.82; 1.70
 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M; 15.53; 4.34
 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8;SS=M; 15.40; 3.70
 428242; H55709; Hs.2250; leukemia inhibitory factor (cholinergic ; LIF_OSM;SS=M; 14.85; 6.58
 421340; F07783; Hs.1369; decay accelerating factor for complement; sushi;SS=M; 14.84; 19.59
 409757; NM_001898; Hs.123114; cystatin SN; cystatin;SS=M; 14.61; 12.75
 425071; NM_013989; Hs.154424; deiodinase, iodothyronine, type II; T4_deiodinase;TM=M;SS=Y; 14.35; 17.22
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 13.81; 7.69
 409420; Z15008; Hs.54451; laminin, gamma 2 (nicein (100kD), kalini; laminin_B,laminin_EGF;SS=M; 13.05; 7.72
 432596; AJ224741; Hs.278461; matrilin 3; EGF,vwa;SS=M; 12.80; 9.91
 422109; S73265; Hs.1473; gastrin-releasing peptide; Bombesin,Defensin_propep;TM=M;SS=M; 12.79; 4.69
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 11.36; 2.22
 429547; AW009166; Hs.99376; FGENESH predicted novel secreted protein; none,none; 10.25; 5.62
 422424; AI186431; Hs.296638; prostate differentiation factor; TGF-beta;SS=M; 9.96; 1.88
 428505; AL035461; Hs.2281; chromogranin B (secretogranin 1); Granin;SS=M; 9.40; 3.46
 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta,TGFb_propeptide,Tub;SS=M; 9.19; 16.46
 418030; BE207573; Hs.83321; neuromedin B; Bombesin;TM=M;SS=Y; 8.38; 1.55
 452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-induced pro; Xlink,CUB;SS=M; 7.46; 4.96

421582; AI910275; Hs.350470; trefoil factor 1 (breast cancer, estroge; trefoil; Gastrin; SS=M; 7.08; 21.61
 423634; AW959908; Hs.1690; heparin-binding growth factor binding pr; none; TM=M; SS=M; 6.78; 12.19
 428486; AW583497; Hs.184604; pancreatic polypeptide; hormone3; TM=M; SS=Y; 6.29; 3.51
 443646; AI085198; Hs.164226; ESTs; EGF; tsp_1; vwc; TSPN; tsp_3; none; 6.17; 4.25
 457489; AI693815; Hs.127179; cryptic gene; none; TM=M; SS=M; 5.19; 2.79
 450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; none; SS=M; 5.01; 7.43
 422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; tsp_3; EGF; SS=M; 4.87; 9.40
 426322; J05068; Hs.2012; transcobalamin I (vitamin B12 binding pr; Cobalamin_bind; SS=M; 4.71; 11.74
 414774; X02419; Hs.77274; plasminogen activator; urokinase; kringle; trypsin; plant_thionins; SS=M; 4.24; 6.91
 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA; TM=Y; 3.52; 8.43
 422048; NM_012445; Hs.288126; spondin 2, extracellular matrix protein; tsp_1; TM=M; SS=M; 3.45; 7.69
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2; hemopexin; Peptidase_M10; SS=M; 3.43; 10.37
 417931; W95642; Hs.82961; trefoil factor 3 (intestinal); trefoil; SS=M; 2.98; 9.65
 445417; AK001058; Hs.12680; Homo sapiens cDNA FLJ10196 fis, clone HE; tsp_1; Reprolysin; Pep_M12B_propep; none; 2.97; 5.74
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3; TM=M; SS=Y; 2.80; 10.53
 431462; AW583672; Hs.256311; granin-like neuroendocrine peptide precu; none; none; 2.70; 1.99

TABLE 43C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404682	9797231	Minus	40977-41150

TABLE 44A: 754 GENES UP-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

Table 44A lists about 754 genes up-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title

Pkey	ExAccn	UnigenelD	Unigene Title
100042	M10098		AFFX control - HUMRGE/M10098_3
101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h
103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa
104743	AA021157	Hs.33619	Homo sapiens cDNA FLJ20096 fis, clone CO
104996	AA112307	Hs.105894	hypothetical protein FLJ21919
105437	AA252191	Hs.25199	hypothetical protein
108258	AA063269		gb:zm02a09.s1 Stralagene corneal stroma
109086	AA166695	Hs.270737	tumor necrosis factor (ligand) superfamI
109279	AA196625	Hs.86080	ESTs
109779	F10527	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur
111794	R32647	Hs.23545	ESTs
112531	R69798	Hs.29036	ESTs
112784	R96306	Hs.191290	ESTs
113293	T67026	Hs.187403	ESTs
115416	AA283893	Hs.337079	ESTs
116548	D20433		gb:HUMGS01407 Human promyelocyte Homo sa
116565	D45533	Hs.129691	hypothetical protein FLJ21603
118104	N55332	Hs.39785	ESTs
119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa
119336	T55340	Hs.208238	ESTs
120101	W95414	Hs.55497	EST
120715	AA292700		gb:zs59a06.s1 NCL_CGAP_GCB1 Homo sapiens
120872	AA357993	Hs.96996	ESTs
121010	AA398355	Hs.97330	ESTs
121509	AA412092	Hs.97888	ESTs
121722	AA419482	Hs.98874	similar to proline-rich protein 48
122265	AA436838	Hs.98906	EST
123206	AA489681	Hs.102248	Homo sapiens cDNA: FLJ22105 fis, clone H
123490	AA599723		gb:ag11c07.s1 Gessler Wilms tumor Homo s
124198	H53099	Hs.198271	NADH dehydrogenase (ubiquinone) 1 alpha
124294	H90573	Hs.102298	EST
125067	T86429	Hs.111725	ESTs
125153	W38294		
125330	AA401804	Hs.114574	ESTs
125335	T86620	Hs.16230	hypothetical protein FLJ20619
125361	T90348	Hs.183404	ESTs
125439	AA826305		gb:PM0-LT0017-031299-001-c07 LT0017 Homo
125535	R17430	Hs.22215	secretogranin III
125583	R22272	Hs.86022	ESTs
125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,
125742	H81181	Hs.261023	hypothetical protein FLJ20958

	125795	T98190	Hs.7756	proteasome (prosome, macropain) 26S subu
	125858	H11549	Hs.31066	ESTs
	125865	H12876	Hs.283078	hOAT4
5	126039	AA160575	Hs.181102	p30 DBC protein
	126143	N29315	Hs.266331	hypothetical protein MGC4595
	126177	H93164	Hs.129750	hypothetical protein FLJ10546
	126219	N36368	Hs.293483	ESTs, Weakly similar to similar to C. el
	126221	AI248169	Hs.172965	ESTs
10	126262	C75147	Hs.143764	ESTs, Weakly similar to unknown [H.sapi
	126277	N39132	Hs.15441	Crm (Cramped Drosophila)-like
	126292	AA491328		gb:aa65d09.r1 NCI_CGAP_GCB1 Homo sapiens
	126293	Z18870	Hs.248121	G protein-coupled receptor 22
	126353	AI243114	Hs.94031	ESTs
15	126556	AA491325	Hs.112227	membrane-associated nucleic acid binding
	126559	R15866	Hs.170263	tumor protein p53-binding protein, 1
	126609	W87435	Hs.186802	ESTs
	126616	AA348581	Hs.134605	ESTs
	126628	AI357886	Hs.170994	hypothetical protein MGC10946
20	126636	AA001527		gb:zf56g09.r1 Soares retina N2b4HR Homo
	126861	AA742428	Hs.144432	ESTs
	126990	AA215510	Hs.191650	ESTs
	127017	AA740146	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I
	127049	AA235966	Hs.291811	ESTs
25	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil
	127331	F20186		gb:HSPD05873 HM3 Homo sapiens cDNA clone
	127357	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
	127368	AA434362	Hs.193326	fibroblast growth factor receptor-like 1
	127374	AA448728	Hs.312110	ESTs, Weakly similar to I38022 hypothet
30	127429	AA961490	Hs.293751	ESTs, Moderately similar to TPTE_HUMAN P
	127490	W52891	Hs.7278	cryptochrome 2 (photolyase-like)
	127502	AA614422	Hs.183502	ESTs
	127647	AI087279	Hs.148410	ESTs
	127650	AA873776	Hs.261957	ESTs
35	127676	D31237	Hs.279938	HSPC067 protein
	127746	AI239495	Hs.120189	ESTs
	127812	AA749094	Hs.291434	ESTs
	127824	AI208365	Hs.127811	ESTs
	127933	AA811102	Hs.303581	ESTs, Moderately similar to ALU1_HUMAN A
40	128006	AA058693	Hs.129908	KIAA0591 protein
	128011	AI347067	Hs.124636	ESTs
	128038	AA868782	Hs.137024	ESTs
	128058	AI126617	Hs.132449	ESTs
	128199	AI073548	Hs.164597	ESTs
45	128308	AI079496	Hs.134169	ESTs
	128389	AI142639	Hs.146662	ESTs
	128410	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
	129199	H90914	Hs.200332	hypothetical protein FLJ20651
	130998	C00810	Hs.293981	guanine nucleotide binding protein (G pr
50	134409	AA281600	Hs.164915	small nuclear RNA activating complex, p
	134578	AA194724	Hs.224137	hypothetical protein
	134644	S83308	Hs.87224	SRY (sex determining region Y)-box 5
	100262	D38500	Hs.278468	postmeiotic segregation increased 2-like
	100676	HG3044-HT3742	Hs.287820	fibronectin 1
55	100704	HG3242-HT3419	Hs.166110	calcium channel, voltage-dependent, alph
	100787	HG3872-HT4142	Hs.302063	immunoglobulin heavy constant mu
	100873	HG4333-HT4603	Hs.17364	zinc finger protein 79 (pT7)
	100943	HG880-HT880		gb:PM0-SN0019-280300-001-D11 SN0019 Homo
	100996	J03909	Hs.14623	interferon, gamma-inducible protein 30
60	101046	K01160		
	101371	M13232	Hs.36989	coagulation factor VII (serum prothrombi
	101461	M22430	Hs.76422	phospholipase A2, group IIA (platelets,
	101697	M64358		gb:Human rhom-3 gene, exon.
	101909	S69265		
65	102199	U21128	Hs.79914	lumican
	102275	U30998	Hs.17752	phosphatidylserine-specific phospholipas
	102295	U32581	Hs.168052	KIAA0421 protein
	102319	U34587	Hs.66578	corticotropin releasing hormone receptor
	102383	U40622	Hs.150930	X-ray repair complementing defective rep
70	102470	U49835	Hs.154138	chitinase 3-like 2
	102544	U57721	Hs.169139	kynureninase (L-kynurenine hydrolase)
	102649	U68133		gb:U68133 Human cell line PCI-O6A Homo s
	102798	U88898		gb:Human endogenous retrovirus H proteas
	102804	U89942	Hs.83354	lysyl oxidase-like 2
75	102851	V00532	Hs.93907	interferon, alpha 14
	102852	V00571	Hs.75294	corticotropin releasing hormone
	102860	X00368		gb:Human prolactin gene 5' region.
	103262	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)
	103484	Y08374	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
80	103559	Z19585	Hs.75774	thrombospondin 4
	103658	Z74615	Hs.172928	collagen, type I, alpha 1
	103719	AA054109	Hs.4273	hypothetical protein FLJ13159
	103876	AA226865	Hs.8203	endomembrane protein emp70 precursor iso
	103897	AA248870	Hs.55058	EH-domain containing 4

	103906	AA249437	Hs.317403	hypothetical protein MGC2744
	103985	AA313880	Hs.99872	fetal Alzheimer antigen
	104056	AA397529	Hs.58297	CLLL8 protein
5	104209	AB000221	Hs.16530	small inducible cytokine subfamily A (Cy
	104386	H41895	Hs.144164	ESTs, Moderately similar to ALU8_HUMAN A
	104398	H53555	Hs.36790	ESTs, Weakly similar to putative p150 [H
	104422	H86858	Hs.132909	ESTs
	104561	R60100	Hs.323817	DKFZP547E1010 protein
10	104593	R81267	Hs.98640	hypothetical protein FLJ21069
	104643	AA004701	Hs.18978	Homo sapiens cDNA: FLJ22822 fis, clone K
	104673	AA007633	Hs.20010	ESTs
	104681	AA009832	Hs.34500	ESTs
	104711	AA017254	Hs.32794	ESTs
	104812	AA034111	Hs.124187	ESTs
15	104877	AA047437	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se
	104886	AA053348	Hs.339699	growth differentiation factor 11
	104924	AA058532	Hs.28774	ESTs, Weakly similar to I38022 hypotheti
	105071	AA136532	Hs.29475	ESTs
	105105	AA151872	Hs.87016	hypothetical protein FLJ22938
20	105203	AA195660	Hs.7882	ESTs
	105317	AA233926	Hs.52620	integrin, beta 8
	105617	AA280687	Hs.4069	glucocorticoid modulatory element bindin
	105707	AA291012	Hs.37617	ESTs, Weakly similar to A53933 myosin I
	105754	AA302657	Hs.192028	ESTs
25	105770	AA347964	Hs.269873	Homo sapiens clone IMAGE:297403, mRNA se
	105882	AA400292	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	105883	AA400490	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com
	105890	AA400766	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,
30	106080	AA418046	Hs.35124	ESTs
	106090	AA418909	Hs.169333	hypothetical protein DKFZp761E2110
	106096	AA419609	Hs.170121	protein tyrosine phosphatase, receptor t
	106124	AA423987	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H
	106308	AA436186	Hs.30662	ESTs
	106438	AA449199	Hs.21342	ESTs
35	106660	AA460936	Hs.27056	KIAA1284 protein
	106731	AA465657	Hs.29205	alpha integrin binding protein 63
	106880	AA488889	Hs.32425	ESTs
	107055	AA600152	Hs.29419	ESTs
	107151	AA621169	Hs.8687	ESTs
40	107183	C20974	Hs.12114	varin 1
	107231	D59299	Hs.34727	ESTs, Moderately similar to I38759 zinc
	107490	W74158	Hs.103189	lipopolysaccharide specific response-68
	107572	AA001903	Hs.59962	ESTs
	107620	AA005039	Hs.60171	ESTs
45	107801	AA019433	Hs.285803	Homo sapiens cDNA FLJ10674 fis, clone NT
	107817	AA020781	Hs.60847	ESTs
	107823	AA021057	Hs.60836	ESTs
	107857	AA024687	Hs.61208	ESTs
	107882	AA025630	Hs.231967	ALL1 fused gene from 5q31
50	108005	AA037769	Hs.194293	ESTs, Weakly similar to I54374 gene NF2
	108092	AA045961	Hs.184029	hypothetical protein DKFZp761A052
	108115	AA047291	Hs.165216	ESTs
	108214	AA058661	Hs.60764	ESTs
	108382	AA074885	Hs.67726	macrophage receptor with collagenous str
55	108409	AA075578		gb:zm88h03.r1 Stratagene ovarian cancer
	108436	AA078801		gb:zm94a09.s1 Stratagene colon HT29 (937
	108625	AA101983	Hs.283022	triggering receptor expressed on myeloid
	108631	AA102553	Hs.334337	ESTs
	108763	AA127539	Hs.281397	hypothetical protein AD034
60	108852	AA133131		gb:zm25d03.s1 Stratagene pancreas (93720
	108931	AA147186		gb:zo38d01.s1 Stratagene endothelial cel
	108976	AA151480	Hs.91202	ESTs
	109026	AA157811		gb:zo35d07.s1 Stratagene colon (937204)
	109170	AA180352	Hs.191472	ESTs, Weakly similar to ALU1_HUMAN ALU
65	109303	AA206126	Hs.269291	ESTs
	109326	AA210719		gb:zr88e04.s1 NCI_CGAP_GCB1 Homo sapiens
	109345	AA213774	Hs.203396	ESTs
	109404	AA224594	Hs.86941	ESTs
	109473	AA233151	Hs.81796	ESTs
70	109725	F10003	Hs.79658	casein kinase 1, epsilon
	109794	F10684	Hs.23687	ESTs
	109835	H00615	Hs.170044	ESTs
	109896	H04794	Hs.30489	ESTs
	109918	H05641	Hs.216701	Homo sapiens mRNA; cDNA DKFZp564I0816 (f
75	109950	H08200	Hs.268770	ESTs, Weakly similar to 2004399A chromos
	110078	H15054	Hs.318773	KIAA1836 protein
	110182	H20402	Hs.31746	hypothetical protein DKFZp547F072
	110213	H23216	Hs.86905	ATPase, H+ transporting, lysosomal (vacu
80	110310	H38209	Hs.32728	EST
	110354	H41280	Hs.22586	ESTs
	110413	H48124	Hs.279454	ESTs
	110422	H48467	Hs.36094	EST
	110433	H49425	Hs.301062	UDP-N-acetyl-alpha-D-galactosamine:polyp

	110434	H49446	Hs.26299	ESTs
	110553	H58934	Hs.124990	ESTs
	110750	N20522	Hs.30981	ESTs
5	110827	N30077	Hs.14855	ESTs
	110829	N30198	Hs.28625	ESTs
	110917	N46363	Hs.5170	ESTs
	111100	N62522	Hs.20450	BCM-like membrane protein precursor
	111112	N63281	Hs.35452	ESTs
10	111179	N67239	Hs.10760	asporin (LRR class 1)
	111185	N67551	Hs.12844	EGF-like-domain, multiple 6
	111223	N68921	Hs.334838	KIAA1866 protein
	111275	N70970	Hs.35006	ESTs
	111443	R01901		gb:Homo sapiens endogenous retrovirus W
15	111573	R10305	Hs.185683	ESTs
	111590	R11157	Hs.75425	ubiquitin associated protein
	111671	R19368	Hs.229084	Homo sapiens cDNA FLJ11666 fis, clone H
	111732	R25153	Hs.163813	ESTs
	111809	R33616	Hs.24688	EST
20	111829	R36070		gb:Homo sapiens full length insert cDNA
	111944	R40606	Hs.21263	suppressor of potassium transport defect
	112015	R42836	Hs.23198	ESTs
	112023	R43020	Hs.236223	EST
	112055	R43621	Hs.26139	ESTs
25	112334	R56239	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S
	112340	R56602	Hs.8904	Ig superfamily protein
	112353	R58986	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (f
	112467	R65706		gb:yi16g12.s1 Soares placenta Nb2HP Homo
	112478	R66067	Hs.28664	ESTs
30	112533	R69886		gb:yi47f03.s1 Soares placenta Nb2HP Homo
	112588	R77302		gb:yi75h08.s1 Soares placenta Nb2HP Homo
	112595	R77783	Hs.22404	protease, serine, 12 (neurotrypsin, moto
	112676	R86976	Hs.34060	ESTs
	112744	R93206	Hs.293762	ESTs, Weakly similar to I38022 hypotheti
35	112777	R95869	Hs.35467	EST
	112817	R98491	Hs.14584	ESTs
	112902	T09262	Hs.129190	Human DNA sequence from clone RP5-1046G1
	113009	T23699	Hs.7246	ESTs
	113151	T51620	Hs.9326	EST
40	113297	T67161	Hs.13059	ESTs
	113398	T82280	Hs.87016	hypothetical protein FLJ22938
	113484	T87795	Hs.187543	ESTs
	113769	U55966	Hs.22985	alpha2,8-sialyltransferase
	113794	W37382	Hs.11090	membrane-spanning 4-domains, subfamily A
45	113971	W86760	Hs.269172	ESTs
	114066	Z38152	Hs.26920	ESTs
	114178	Z39063	Hs.17930	chromosome 6 open reading frame 11
	114206	Z39294	Hs.27339	EST
	114371	Z41835	Hs.27810	ESTs
50	114428	AA017130	Hs.84790	KIAA0225 protein
	114466	AA026970	Hs.135150	lung type-I cell membrane-associated gly
	114625	AA084362		gb:zn05b10.r1 Stratagene hNT neuron (937
	114862	AA235174	Hs.106432	Homo sapiens cDNA FLJ13410 fis, clone PL
	114908	AA236545	Hs.54973	cadherin-like protein VR20
55	114973	AA250845	Hs.87762	ESTs
	115009	AA251561	Hs.48689	ESTs
	115055	AA253005	Hs.61753	ESTs
	115098	AA256161	Hs.161729	ESTs
	115321	AA280805	Hs.191540	ESTs
60	115385	AA282540	Hs.109694	KIAA1451 protein
	115466	AA287008	Hs.285655	ESTs
	115479	AA287596	Hs.278188	ESTs, Moderately similar to I54374 gene
	115663	AA405838	Hs.40507	ESTs
	115689	AA410645	Hs.199014	ESTs, Moderately similar to ALU7_HUMAN A
65	115748	AA418835	Hs.90286	ESTs
	115810	AA426026	Hs.187615	ESTs
	115827	AA427890	Hs.83583	actin related protein 2/3 complex, subun
	115881	AA435577	Hs.184942	G protein-coupled receptor 64
	116148	AA460708	Hs.62905	hypothetical protein FLJ14834
70	116257	AA481493	Hs.88537	ESTs
	116365	AA521080	Hs.46765	ESTs
	116941	H77395	Hs.39749	ESTs
	116982	H81933	Hs.312582	ESTs
	116995	H83928		gb:ys64b03.s1 Soares retina N2b4HR Homo
75	116997	H84214	Hs.40594	ESTs
	117016	H87171	Hs.52170	ESTs
	117097	H93608	Hs.41919	EST
	117101	H94043	Hs.24341	transcriptional co-activator with PDZ-bi
	117238	N20815	Hs.173337	ESTs
80	117303	N22776	Hs.264079	ESTs
	117399	N26480	Hs.43805	lipoma HMGIC fusion partner-like 3
	117503	N31963	Hs.44286	ESTs
	117544	N33222	Hs.44451	ESTs
	117594	N34929	Hs.171984	ESTs

5	117627	N36113	Hs.44789	ESTs, Weakly similar to B34087 hypothet
	117653	N38970	Hs.194214	ESTs
	117695	N40953	Hs.45093	EST
	117697	N40976		gb:yy80b06.s1 Soares_multiple_sclerosis_
	117766	N47807	Hs.46767	EST
10	117807	N48701	Hs.46523	EST
	117816	N48872		gb:yy77a05.s1 Soares_multiple_sclerosis_
	117882	N50101	Hs.301406	hypothetical protein PP3501
	117987	N51935	Hs.47374	Homo sapiens cDNA FLJ13561 fis, clone PL
	118074	N54188	Hs.130323	Homo sapiens, clone IMAGE:3960432, mRNA
15	118114	N56875	Hs.143212	cystatin F (leukocystatin)
	118151	N58276	Hs.229119	EST
	118270	N62868	Hs.48653	ESTs
	118291	N63076	Hs.138746	EST
	118358	N64017	Hs.144633	hypothetical protein DKFZp434F2322
20	118383	N64529	Hs.49001	EST
	118412	N64856	Hs.97437	centrosomal protein 1
	118433	N66248	Hs.141609	EST
	118600	N69222	Hs.238936	ESTs, Weakly similar to (define not av
	118641	N70298	Hs.49829	ESTs
25	118643	N70324	Hs.49840	ESTs
	118695	N71781	Hs.50081	KIAA1199 protein
	118915	N91481	Hs.54713	ESTs
	119041	R02591	Hs.284294	Breakpoint cluster region protein, uteri
	119069	R27619	Hs.231046	EST
30	119105	R42357	Hs.91453	ESTs
	119154	R61293		gb:yh07a05.s1 Soares infant brain 1NIB H
	119241	T12559		gb:CHR90079 Chromosome 9 exon II Homo sa
	119269	T16367	Hs.65327	EST
	119310	T40427		gb:ya01a06.s2 Stratagene lung (937210) H
35	119345	T63474	Hs.90696	EST
	119353	T66867	Hs.187402	ESTs
	119390	T89122	Hs.249712	ESTs, Weakly similar to ALU1_HUMAN ALU
	119423	T99544	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU
	119428	W02129	Hs.55242	EST
40	119529	W38053		ESTs, Highly similar to S03917 fibronec
	119795	W73370	Hs.339722	ESTs
	119817	W74257	Hs.159690	DKFZP586L2024 protein
	119831	W78050	Hs.58419	hypocretin (orexin) receptor 2
	119930	W86471	Hs.151624	ESTs
45	120039	W92548	Hs.94985	hypothetical protein
	120256	AA169801	Hs.98710	gb:zp54e11.s1 Stratagene NT2 neuronal pr
	120284	AA182626		KIAA0627 protein; Drosophila multiple as
	120350	AA211300	Hs.108614	gb:DKFZp434B1822_r1 434 (synonym: hles3)
	120379	AA227849		FSH primary response (LRPR1, rat) homolo
50	120383	AA228030	Hs.123122	spinal cord-derived growth factor-B
	120420	AA236031	Hs.112885	novel protein with MAM domain
	120437	AA243427	Hs.104311	ESTs
	120461	AA251301	Hs.293369	ring finger protein 10
	120594	AA282054	Hs.5094	homeo box A10
55	120611	AA284178	Hs.110637	EST
	120626	AA285064	Hs.104485	ESTs
	120696	AA291503	Hs.97249	ESTs
	120747	AA302976	Hs.96672	ESTs
	120749	AA303235		gb:EST14544 Testis tumor Homo sapiens cD
60	120752	AA311972	Hs.22895	hypothetical protein FLJ23548
	120851	AA349662	Hs.174248	ESTs
	120866	AA350718	Hs.291272	ESTs
	120949	AA397830	Hs.98347	ESTs, Weakly similar to JC5308 testis-sp
	120996	AA398281	Hs.308114	ESTs
65	121038	AA398536	Hs.97365	ESTs
	121065	AA398658	Hs.97300	ESTs
	121067	AA398662	Hs.97302	ESTs
	121071	AA398678	Hs.139355	ESTs
	121082	AA398722		gb:zl75h07.s1 Soares_testis_NHT Homo sap
70	121172	AA400013	Hs.97750	EST, Weakly similar to MPL3 RAT MICROTUB
	121191	AA400205	Hs.104447	ESTs
	121354	AA405384	Hs.193737	ESTs
	121393	AA405981	Hs.262643	ESTs
	121399	AA406059	Hs.332700	EST
75	121479	AA411911	Hs.98110	ESTs
	121498	AA412033	Hs.178045	ESTs
	121704	AA418743	Hs.98306	KIAA1862 protein
	121736	AA421131	Hs.148515	Human clone 23564 mRNA sequence
	122198	AA435892	Hs.97541	ESTs
80	122220	AA436011	Hs.98187	ESTs
	122250	AA436692	Hs.98892	EST
	122279	AA437209	Hs.234016	ESTs
	122286	AA437259	Hs.104944	ESTs
	122330	AA442870	Hs.98628	Homo sapiens, clone IMAGE:4214491, mRNA,
	122338	AA443311	Hs.98998	ESTs
	122355	AA443789	Hs.19978	CGI-30 protein
	122590	AA453264	Hs.99310	ESTs

	122746	AA458791		gb:aa88c02.s1 Stratagene fetal retina 93
	122805	AA460702	Hs.82772	collagen, type XI, alpha 1
	122841	AA461536	Hs.288908	WASP protein family, member 2
5	122899	AA469960	Hs.178420	ESTs, Highly similar to WASP interacting
	122933	AA476728	Hs.107537	chromosome 7 open reading frame 2
	123005	AA479726	Hs.52620	integrin, beta 8
	123142	AA487504	Hs.105718	EST
	123153	AA488349	Hs.334808	hypothetical protein MGC4189
10	123168	AA488881	Hs.105218	EST
	123188	AA489092	Hs.177726	ESTs
	123276	AA491270	Hs.187946	ESTs
	123305	AA496133		gb:zv51e12.s1 Soares_testis_NHT Homo sap
	123328	AA496968		gb:aa42g03.s1 Soares_NhHMPu_S1 Homo sapi
15	123450	AA598913	Hs.111207	ESTs
	123464	AA599014	Hs.153321	Homo sapiens cDNA FLJ10577 fis, clone NT
	123650	AA609332	Hs.180696	ESTs
	123700	AA609606	Hs.191956	ESTs
	123858	AA620821	Hs.112911	EST
20	123863	AA620873	Hs.112916	ESTs
	124046	F10243		gb:HSC3CC122 normalized infant brain cDN
	124059	F13673	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	124196	H52617	Hs.144167	ESTs
	124197	H52921		gb:yq76c09.s1 Soares fetal liver spleen
25	124229	H62793	Hs.268945	ESTs
	124230	H63111	Hs.6655	Homo sapiens EST from clone 208499, full
	124241	H65947	Hs.165355	ESTs, Moderately similar to ZN91_HUMAN Z
	124251	H68286	Hs.107924	ESTs
	124400	N30597	Hs.179152	loll-like receptor 7
30	124416	N34042	Hs.271674	ESTs
	124570	N67117	Hs.102808	ESTs
	124575	N68168		gb:za11c01.s1 Soares fetal liver spleen
	124588	N69197	Hs.191361	ESTs, Weakly similar to I38022 hypotheti
	124598	N70294	Hs.269137	ESTs, Weakly similar to A56194 thromboxa
35	124655	N93176	Hs.102914	ESTs
	124706	R07499	Hs.193612	ESTs, Weakly similar to ALU8_HUMAN ALU
	124848	R60135	Hs.203498	EST
	124882	R74041	Hs.101539	ESTs
	124898	R82846	Hs.273789	ESTs
40	125086	T91161	Hs.173880	interleukin 1 receptor accessory protein
	125145	W38001		
	125216	W73409	Hs.103185	ESTs
	125342	AI055916	Hs.133552	ESTs
	125351	T96520	Hs.324746	alpha-2-HS-glycoprotein
45	125419	AI076822	Hs.134544	ESTs
	125424	T99667	Hs.18564	ESTs
	125526	R14487	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f
	125539	R17870	Hs.248120	G protein-coupled receptor 21
	125633	AA908225	Hs.15463	Homo sapiens, clone IMAGE:2959994, mRNA
50	125689	R48940	Hs.108043	Friend leukemia virus integration 1
	125707	C14616	Hs.284122	Wnt inhibitory factor-1
	125790	AA868325	Hs.99962	proteoglycan 2, bone marrow (natural kil
	125876	AA324967	Hs.7298	biphenyl hydrolase-like (serine hydrolase
	125969	R94247	Hs.88414	BTB and CNC homology 1, basic leucine zi
55	125970	AI400964	Hs.177516	high density lipoprotein binding protein
	125975	AA495891	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv
	125985	H54857	Hs.35981	ESTs
	126018	H54866	Hs.167583	ESTs
	126032	H59735	Hs.269065	ESTs, Highly similar to KIAA0349 [H.sapi
60	126059	H66582	Hs.308486	ESTs
	126107	H79155	Hs.93361	ESTs
	126154	AI004105	Hs.190488	Homo sapiens, Similar to nuclear localiz
	126199	AI000492	Hs.125829	ESTs
	126207	W77936	Hs.83583	actin related protein 2/3 complex, subun
65	126227	N27236	Hs.269034	ESTs
	126269	AA830432	Hs.44701	ESTs
	126373	F11606	Hs.6079	B cell RAG associated protein
	126378	AA347842		gb:yy62a11.s1 Soares_multiple_sclerosis_
	126383	AA885594	Hs.6298	KIAA1151 protein
70	126403	N73388	Hs.125976	ESTs, Weakly similar to S71949 metallop
	126525	AA884833	Hs.166432	ESTs
	126527	AA548559	Hs.103853	hypothetical protein FLJ20043
	126566	W67245	Hs.103142	ESTs
	126583	W92895	Hs.279746	vanilloid receptor-like protein 1
75	126610	AA460338	Hs.191391	ESTs
	126622	AA699443	Hs.193213	ESTs
	126633	AA206993	Hs.315367	Homo sapiens, Similar to hypothetical pr
	126727	AA037230	Hs.135084	cystatin C (amyloid angiopathy and cereb
	126762	AA064671		gb:zm13b04.s1 Stratagene pancreas (93720
80	126775	S86382	Hs.957	putative opioid receptor, neuromedin K (
	126783	AA126047		gb:zn09d10.s1 Stratagene hNT neuron (937
	126882	AA761143	Hs.250581	SWI/SNF related, matrix associated, acti
	126945	R51877	Hs.25845	ESTs
	126968	AI311457	Hs.99472	ESTs

5	127070	AA641812	Hs.190037	ESTs
	127087	AA380418	Hs.88012	SHP2 interacting transmembrane adaptor
	127187	AA297138	Hs.207422	ESTs, Weakly similar to S71949 metallopro
	127215	AI246377	Hs.127675	ceroid-lipofuscinosis, neuronal 8 (epile
	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of
10	127278	AA342715		gb:EST48309 Fetal spleen Homo sapiens cD
	127299	AA360710	Hs.158480	ESTs
	127325	AA393073	Hs.126099	ESTs
	127347	AA428350	Hs.58389	hypothetical protein MGC4090
	127401	AA921944	Hs.127639	ESTs
15	127420	AA699582	Hs.82171	Homo sapiens clone 191B7 placenta expres
	127438	AI224421	Hs.77100	general transcription factor IIe, polype
	127441	AA835684	Hs.287601	Homo sapiens cDNA FLJ13830 fis, clone TH
	127449	AI421866	Hs.75722	ribophorin II
	127493	AA808081	Hs.291701	ESTs
20	127505	AA594244	Hs.292245	ESTs, Weakly similar to ALU1_HUMAN ALU S
	127620	AI025699	Hs.116200	ESTs
	127623	AA773234	Hs.271877	angiopoietin-like 2
	127633	AI339609	Hs.268538	potassium voltage-gated channel, Isk-rel
	127701	AA935466		gb:zf84c06.s1 Soares_pineal_gland_N3HPG
25	127713	AA688322	Hs.150683	ESTs
	127722	AA700444	Hs.189186	ESTs, Weakly similar to ALUD_HUMAN !!!!
	127733	AA704680	Hs.189005	ESTs
	127816	AA743646	Hs.120604	ESTs, Weakly similar to YA02_HUMAN HYPOT
	127966	AI493406	Hs.292514	ESTs
30	127973	AI336794	Hs.129117	ESTs
	127989	AA909267	Hs.132413	ESTs
	127997	AI281549	Hs.311054	Homo sapiens mRNA full length insert cDN
	128016	N92597	Hs.82689	tumor rejection antigen (gp96) 1
	128037	AA868394	Hs.181129	ESTs, Weakly similar to S18968 cyritesti
35	128053	T65605	Hs.65377	ESTs, Moderately similar to KIAA1399 pro
	128066	AA884838	Hs.189171	ESTs
	128071	AA889398	Hs.189241	ESTs
	128091	AA904559	Hs.129329	ESTs
	128113	AI341423	Hs.288433	neurotrimin
40	128145	AI498467	Hs.166669	solute carrier family 4, sodium bicarbon
	128167	AA932961	Hs.85752	uncharacterized hematopoietic stem/proge
	128195	AI143866	Hs.127778	ESTs
	128265	T95851	Hs.17691	ESTs
	128283	AI076570	Hs.134053	ESTs
45	128309	AI457235	Hs.166479	ESTs
	128313	AI051250	Hs.157775	ESTs
	128346	AI088907	Hs.160189	ESTs
	128359	AI096526	Hs.270244	ESTs, Weakly similar to I38022 hypotheti
	128369	F12681	Hs.30445	Homo sapiens cDNA FLJ14687 fis, clone NT
50	128371	H12876	Hs.283078	hOAT4
	128421	T77876	Hs.268589	ESTs
	128453	X02761	Hs.287820	fibronectin 1
	128496	T83496	Hs.32944	inositol polyphosphate-4-phosphatase, ty
	128514	H84261	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA,
55	128551	H09058	Hs.278398	KIAA1117 protein
	128683	AA316862	Hs.9605	cleavage and polyadenylation specific fa
	128731	AF005271	Hs.104555	neuropeptide FF-amide peptide precursor
	128843	AA234141	Hs.275675	katanin p80 (WD40-containing) subunit B
	128988	AA411040	Hs.294140	ESTs
60	129016	W84524	Hs.184194	transmembrane 4 superfamily member 5
	129021	AA426406	Hs.173081	KIAA0530 protein
	129095	L12350	Hs.108623	thrombospondin 2
	129171	AA234048	Hs.7753	calumenin
	129188	M30257	Hs.109225	vascular cell adhesion molecule 1
65	129410	U25987	Hs.272620	pregnancy specific beta-1-glycoprotein 9
	129467	AA410311	Hs.44208	hypothetical protein FLJ23153
	129518	AA369807	Hs.112238	ESTs
	129534	R73640	Hs.11260	hypothetical protein FLJ11264
	129632	L27213	Hs.11176	solute carrier family 4, anion exchanger
70	129691	X06700	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl
	129881	AA458952	Hs.181406	hypothetical protein FLJ22301
	129990	N30316		gb:yw75b05.s1 Soares_placenta_8to9weeks_
	130049	V01515	Hs.1460	glucagon
	130171	AA454177	Hs.245257	ESTs, Weakly similar to A46010 X-linked
75	130411	AA505009	Hs.169910	KIAA0173 gene product
	130479	R44163	Hs.12457	hypothetical protein FLJ10814
	130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
	130521	U92971	Hs.194351	coagulation factor II (thrombin) recepto
	130645	AA020942	Hs.17200	STAM-like protein containing SH3 and ITA
80	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)
	130656	Z20481	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro
	130889	D57622	Hs.20985	sin3-associated polypeptide, 30kD
	131064	AA598441	Hs.22583	DKFZP434K2235 protein
	131070	F13694	Hs.22607	ESTs
	131189	L16782	Hs.240	M-phase phosphoprotein 1
	131318	X51699	Hs.2558	bone gamma-carboxyglutamate (gla) protei
	131506	W47579	Hs.5801	KIAA1194 protein

	131551	AA127867	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H
	131563	C20547	Hs.302810	Novel human gene mapping to chromosome 20
	131830	U33054	Hs.32959	G protein-coupled receptor kinase 2 (Dro
5	131879	AA017161	Hs.33792	ESTs
	132017	W67251	Hs.267659	vav 3 oncogene
	132025	U58516	Hs.3745	milk fat globule-EGF factor 8 protein
	132096	AA131410	Hs.3964	Homo sapiens clone 24877 mRNA sequence
10	132159	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi
	132164	U84573	Hs.41270	procollagen-llysine, 2-oxoglutarate 5-dio
	132180	AA405569	Hs.418	fibroblast activation protein, alpha
	132223	R77451	Hs.4245	chromosome 11 hypothetical protein ORF3
	132238	AA453446	Hs.42673	ESTs
	132406	F09979	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f
15	132945	N40559	Hs.6129	ATP-binding cassette, sub-family B (MDR/
	133185	AA481404	Hs.6686	hypothetical protein DKFZp564O1664
	133193	C14015	Hs.303075	EST
	133370	AA156897	Hs.72157	DKFZP564I1922 protein
	133406	U22172	Hs.179697	Human DNA damage repair and recombatio
20	133409	U65918	Hs.73078	deleted in azoospermia-like
	133591	T82292	Hs.75111	protease, serine, 11 (IGF binding)
	133899	X00588	Hs.77432	epidermal growth factor receptor (avian
	134137	F10045	Hs.79347	KIAA0211 gene product
	134339	AA478971	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
25	134421	AA122386	Hs.82985	collagen, type V, alpha 2
	134462	U11037	Hs.181300	sel-1 (suppressor of lin-12, C.elegans)-
	134515	C20737	Hs.84469	ESTs
	134527	T40835	Hs.322978	EST
	134711	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro
30	134824	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor
	134854	J03464	Hs.179573	collagen, type I, alpha 2
	134921	W60186	Hs.125511	Homo sapiens mRNA; cDNA DKFZp434P1530 (f
	135003	H42527	Hs.26102	trichorhinophalangeal syndrome 1
	135210	W90522	Hs.93589	hypothetical protein DKFZp564B1162
35	135348	AA442054	Hs.268177	phospholipase C, gamma 1 (formerly subty
	100547	HG2149-HT2219		gb:Homo sapiens mucin (mucin) mRNA, part
	100572	HG2271-HT2367	Hs.73995	filaggrin
	100687	HG3115-HT3291		gb:Human Golli-mbp gene, exon 2.
40	100695	HG315-HT315	Hs.272620	pregnancy specific beta-1-glycoprotein 9
	101447	M21305		gb:Human alpha satellite and satellite 3
	102329	U35407	Hs.158084	peroxisome receptor 1
	102892	X05232	Hs.83326	matrix metalloproteinase 3 (stromelysin
	103036	X54925	Hs.83169	matrix metalloproteinase 1 (interstitial
	103206	X72755	Hs.77367	monokine induced by gamma interferon
45	103260	X78416	Hs.3155	casein, alpha
	103751	AA082824		gb:zo08b08.s1 Stratagene neuroepithelium
	104113	AA427510	Hs.181202	hypothetical protein FLJ10038
	104316	D61871	Hs.330821	EST
	104453	M19169	Hs.123114	cystatin SN
50	104668	AA007312		gb:EST376458 MAGE resequences, MAGH Homo
	104916	AA056588	Hs.155489	NS1-associated protein 1
	106151	AA424958	Hs.294132	ESTs
	106899	AA490107	Hs.21753	JM5 protein
	107379	U93868	Hs.333861	polymerase (RNA) III (DNA directed) (32k
55	107412	W26105	Hs.287797	integrin, beta 1 (fibronectin receptor,
	107652	AA010195	Hs.52642	ESTs, Weakly similar to ALUF_HUMAN !!!!
	107754	AA017462	Hs.269244	ESTs
	107897	AA026240		gb:nc077a05.s1 NCI_CGAP_AA1 Homo sapiens
	108238	AA059473	Hs.66783	EST
60	108497	AA083070		gb:zm85a05.r1 Stratagene ovarian cancer
	108710	AA121960		gb:zm24g09.r1 Stratagene pancreas (93720
	109012	AA156576	Hs.5947	mel transforming oncogene (derived from
	109043	AA159605	Hs.72580	ESTs
	109560	F01778	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H
65	110572	H60523	Hs.37844	EST
	110687	H93005	Hs.177311	ESTs
	111418	R01084	Hs.19081	ESTs
	111507	R07728	Hs.268668	ESTs
	111644	R16539	Hs.223649	EST, Moderately similar to Cd-7 Metallo
	111919	R39926	Hs.21031	ESTs, Weakly similar to I78885 serine/th
70	112102	R44840	Hs.326475	ESTs
	112229	R50938	Hs.24949	ESTs
	112309	R55021		gb:yj76d05.s1 Soares breast 2NbHBst Homo
	112368	R59371	Hs.26653	ESTs
75	112397	R60822	Hs.26805	ESTs, Weakly similar to putative p150 [
	112532	R69824	Hs.28313	ESTs
	112858	T02963	Hs.4454	ESTs
	113170	T54342	Hs.270373	ESTs, Weakly similar to S65657 alpha-1C
	113321	T70580	Hs.13759	RAB3A interacting protein (rabin3)-like
80	113404	T82323	Hs.70337	immunoglobulin superfamily, member 4
	113420	T83964	Hs.15400	ESTs, Weakly similar to S65824 reverse
	113613	T93337	Hs.17167	ESTs, Highly similar to LRR FLI-I intera
	113663	T95909		gb:ye47g07.s1 Soares fetal liver spleen
	113790	W33178	Hs.26912	ESTs

	113889	W72720		gb:zd61c03.s1 Soares_fetal_heart_NbHH19W
	114016	W90671	Hs.11087	ESTs
	114251	Z39898	Hs.21948	ESTs
5	115187	AA261805	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,
	115722	AA417297	Hs.59609	ESTs
	115775	AA424030	Hs.46627	ESTs
	116380	AA598455	Hs.66817	ESTs
	116551	D20458	Hs.229071	EST
10	117009	H85422	Hs.108556	ESTs
	117329	N23680	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone H
	117523	N32626	Hs.145532	ESTs, Weakly similar to FV1 MOUSE FRIEND
	118387	N64579		gb:yz51d11.s1 Morton Fetal Cochlea Homo
	118456	N66580		gb:yy69f01.s1 Soares_multiple_sclerosis_
15	118741	N74042	Hs.50421	KIAA0203 gene product
	118771	N74690	Hs.50547	ESTs
	119075	R36451	Hs.287820	fibronectin 1
	119217	R95778	Hs.237309	EST
	119306	T26914	Hs.132785	EAP30 subunit of ELL complex
20	119347	T64349		gb:yc10d08.s1 Stratagene lung (937210) H
	120006	W90108	Hs.10848	KIAA0187 gene product
	120441	AA243588	Hs.190035	ESTs
	120651	AA287286	Hs.99657	ESTs
	120811	AA346854	Hs.52788	fragile X mental retardation, autosomal
25	121186	AA400156	Hs.339808	hypothetical protein FLJ10120
	121599	AA416770	Hs.98255	EST
	122146	AA435584	Hs.250173	hypothetical protein FLJ13158
	122261	AA436830	Hs.98902	ESTs
	122352	AA443725	Hs.159677	ESTs
30	122433	AA447417	Hs.285491	ESTs
	122489	AA448342	Hs.178551	ribosomal protein L8
	122554	AA451886	Hs.154654	cytochrome P450, subfamily I (dioxin-ind
	122857	AA463879	Hs.99606	EST, Weakly similar to STK2_HUMAN SERIN
	122889	AA465704	Hs.287687	Homo sapiens cDNA: FLJ21960 fis, clone H
35	123399	AA521274	Hs.105516	EST
	123662	AA609385	Hs.112703	ESTs, Moderately similar to AF171102 1 r
	123762	AA610013		gb:af18d04.s1 Soares_testis_NHT Homo sap
	123792	AA620333	Hs.112857	ESTs
	123900	AA621223	Hs.112953	EST
40	123981	C20797	Hs.95481	ESTs
	124126	H18517	Hs.164568	fibroblast growth factor 7 (keratinocyte
	124404	N31998	Hs.164256	hypothetical protein FLJ20657
	124557	N66025	Hs.141604	ESTs, Moderately similar to ALU1_HUMAN A
	124703	R07294	Hs.300076	solute carrier family 22 (organic cation
45	124867	R68971	Hs.168500	ESTs
	125092	T92544	Hs.137548	CD84 antigen (leukocyte antigen)
	125111	T96240	Hs.178658	RAD23 (S. cerevisiae) homolog B
	125331	AI422996	Hs.161378	ESTs
	125349	T87826	Hs.164480	ESTs, Weakly similar to T50609 hypotheti
50	125426	R43963	Hs.184029	hypothetical protein DKFZp761A052
	125436	R64472	Hs.16131	hypothetical protein FLJ12876
	125465	AI375276	Hs.158732	ESTs
	125515	R13353		gb:yf76c04.r1 Soares infant brain 1NIB H
	125626	AI038854	Hs.180789	S164 protein
55	125656	AA040118	Hs.78687	neutral sphingomyelinase (N-SMase) activ
	125743	H17151		gb:ym37a05.r1 Soares infant brain 1NIB H
	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass
	125760	W03020	Hs.40300	calpain 3, (p94)
	125804	R79519	Hs.16899	ESTs
60	125967	AI341206	Hs.173770	ESTs
	126068	AI190171	Hs.144413	ESTs
	126081	AI346024	Hs.227835	KIAA1049 protein
	126150	AA018427	Hs.64616	chromosome 12 open reading frame 3
	126171	AA704771	Hs.191942	ESTs
65	126198	AI693555	Hs.127310	ESTs
	126224	AI097280	Hs.44493	Human DNA sequence from clone 462023 on
	126289	AA194603	Hs.73451	ESTs, Weakly similar to S55024 nebulin,
	126343	AA628890	Hs.158701	ESTs
	126406	AA034096		gb:yy41h02.r1 Soares fetal liver spleen
70	126419	AA451775	Hs.129064	Homo sapiens chromosome 19, cosmid F2216
	126479	T78141	Hs.12285	ESTs, Weakly similar to I55214 salivary
	126500	AA885306	Hs.184376	synaptosomal-associated protein, 23kD
	126520	AA292988	Hs.72071	hypothetical protein FLJ20038
	126701	AA515212	Hs.339670	ESTs, Weakly similar to AF147790 1 trans
75	126718	AA322718	Hs.309435	ESTs, Weakly similar to KIAA0927 protein
	126739	AI160709	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE
	126745	AA057506		gb:zf49g04.r1 Soares retina N2b4HR Homo
	126846	AA663527	Hs.116910	ESTs
	126872	AA136653		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su
80	126952	AA195575	Hs.85962	hyaluronan synthase 3
	127036	AI468598	Hs.276916	nuclear receptor subfamily 1, group D, m
	127039	AA233366	Hs.168103	prp28, U5 snRNP 100 kd protein
	127067	F06732		gb:HSC1JA051 normalized infant brain cDN
	127083	Z44079	Hs.91608	otoferlin

5	127116	AA278492	Hs.288304	Homo sapiens cDNA FLJ11529 fis, clone HE
	127282	AA347547	Hs.185780	ESTs
	127349	AA412108	Hs.269350	ESTs
	127352	AA416577	Hs.189105	ESTs, Weakly similar to NBR13 [H.sapiens
	127482	AI337294	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I
	127543	AI364367	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO
	127553	AA282433		gb:aa63g02.r1 NCI_CGAP_GCB1 Homo sapiens
10	127556	AA679831	Hs.190228	ESTs
	127859	AA806837	Hs.291559	ESTs
	127993	AA847856	Hs.124565	ESTs
	128277	AI018275	Hs.269791	ESTs
	128285	AA634569	Hs.13351	LanC (bacterial lantibiotic synthetase c
	128317	AI051960	Hs.303754	ESTs
15	128334	AI080130	Hs.134207	ESTs
	128428	AI185718	Hs.143900	ESTs
	128582	U22963	Hs.101840	major histocompatibility complex, class
	128592	AA470056	Hs.113994	Homo sapiens cDNA FLJ20796 fis, clone CO
	128751	AA442274	Hs.183176	ESTs
20	129105	AA224351	Hs.108681	Homo sapiens brain tumor associated prot
	129161	N27334	Hs.181780	hypothetical protein FLJ20241
	129246	N99174	Hs.206063	ESTs
	129361	X64229	Hs.110713	DEK oncogene (DNA binding)
	129577	AA424952	Hs.82906	CDC20 (cell division cycle 20, S. cerevi
25	129600	N78980	Hs.271599	hypothetical protein MGC10500
	129989	AF005887	Hs.247433	activating transcription factor 6
	130024	U15197	Hs.113271	ABO blood group (transferase A, alpha 1-
	130292	U70136	Hs.218791	proteoglycan 4, (megakaryocyte stimulati
	130589	AA234308	Hs.16441	DKFZP434H204 protein
30	130736	T99385		gb:ow89g07.s1 Soares_fetal_liver_spleen_
	131238	R82327	Hs.24625	ESTs
	131378	AA463886	Hs.203910	small glutamine-rich tetralricopeptide r
	131601	M31165	Hs.29352	tumor necrosis factor, alpha-induced pro
	131605	AA256220	Hs.29383	Homo sapiens mRNA; cDNA DKFZp434E2321 (f
35	131676	C20785	Hs.30514	ESTs
	131861	D11925	Hs.184245	KIAA0929 protein Msx2 interacting nuclea
	131873	H39997	Hs.166852	KIAA1683 protein
	132023	F01927	Hs.3743	matrix metalloproteinase 24 (membrane-in
	132273	AA489716	Hs.43658	DKFZP586L151 protein
40	132770	AA425647	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL
	132859	D20925	Hs.69235	transportin-SR
	133052	R40166	Hs.106826	KIAA1696 protein
	133373	S72487	Hs.73946	endothelial cell growth factor 1 (platelet
	133446	M25322	Hs.73800	selectin P (granule membrane protein 140
45	134693	N70361	Hs.8854	Human transcription unit PVT gene, exons
	134733	U03644	Hs.89421	CBF1 interacting corepressor
	134965	J05480	Hs.272458	protein phosphatase 3 (formerly 2B), cat
	135327	AA477989	Hs.98800	ESTs
	135377	C21382	Hs.99766	Homo sapiens mRNA; cDNA DKFZp564J0323 (f
50	135398	AA194075	Hs.287270	ret proto-oncogene (multiple endocrine

TABLE 44B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

60	Pkey	CAT number	Accessions
	108497	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204 AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070 AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209 AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053 AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA065051 AA079143 AA071110 AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200 AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929
70	107897	91776_1	AA604872 AA026240
	130736	611414_1	AI168326 T99385
	108710	133560_1	AA121959 AA121960
	100943	45976_1	AW864944 L07517 AW869606
75	124575	1666649_1	N68168 N69188 N90450
	125439	465590_1	AW835829 AA826305 R01759
	117697	499877_1	N40976 AA902795
	125515	181_2	R13353 R13890 H11359
	118387	65081_5	N64579
80	126292	327512_1	AA491328 N42312
	102798	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
	126378	244444_1	N58924 AA347842
	125743	5025_5	H17151 H11956
	126406	95703_1	N76683 AA034096 AA034082

127067	1534978_1	F06732 Z43705
119243	1774795_1	T12603 T12604
111443	31528_18	AF072503 AF208161 AA613238 H12439 N76991 D78692 BE019603 AA776439 R37932 T93615 AF072508 R00744 R01948 R68685 AI128496 AA865193 AI797629 H13302 AF072506 NM_014590 AF072505 R00743 T93661 T39519 R68740 H13097 N58614 N77302 H01372 N41878 H04136 AA426511 AW971553 AW900030 R76136 T52094 AI598135 AA781423 R76086 R77278 AI393478 AA837267 AI570707 R01901 R27412 N53177 AI379210 AI128526 AA250958 R79323 R27389 H01325 N55091 T69704 AA868777 T47345 R27591 AA860368 AA729556 H04137 T87297 C17420 AA293243 AA419144 AA342715 AA367634 AA131367 AA082824 AA057531 AA001527 F20186 AA622352 AA424107 AA452788 AA047854 AA057506 AA053841 AA064613 AA064671 AA083531 AA126047 AA074915 AA148649 R55021 H26613 AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363 AA179656 AA182626 AA182603 AF074991 R36070 AW964385 AA007312 AI081711 AA318253 AW891655 T99192 AA505046 AW969109 AA505047 AL042725 BE063316 AW975610 AA457591 BE062092 AI655202 AA714296 AI267264 AI075321 AA223286 AA071122 AA227849 AA216700 AI696002 AA101867 AA099426 AA135997 AL041698 T02815 T51824 AA207189 T59230 T51868 AA663341 BE165757 AW818104 AW392886 AA584918 AA099408 AW856396 AW861859 AA053045 AA679064 AA935466 AA424107 AA452788 AA081507 AA070071 AA070840 AA084362 AA157811 AA836869 AA075631 AA075578 L18862 AA210719 AA610013 D20433 W38001 W38294 H83928 U68133 N66580 X00368 AA292700 AA303235 T95909 W72720 AA063269 K01160 N30316 AA458791 F10243 AA078801 H52921 M21305 AA133131 M64358 AA147186 S69265 N48872 R61293 T12559 T40427 T64349 W38053 R65706 R69886 R77302 AA398722 AA496133 AA496968 M57417 AA599723
127278	240640_1	
103751	118557_1	
126636	80804_1	
127331	379388_1	
127357	288073_1	
126745	104479_1	
126762	110350_1	
126783	113388_1	
112309	1576900_1	
126872	142696_1	
120284	158963_1	
111829	46636_1	
104668	82752_1	
127553	202308_2	
120379	34624_3	
127701	405284_1	
128410	288073_1	
114625	111686_1	
109026	150431_1	
108409	113869_1	
100687	tigr_HT3291	
109326	genbank_AA210719	
123762	genbank_AA610013	
116548	genbank_D20433	
125145	entrez_W38001	
125153	entrez_W38294	
116995	genbank_H83928	
102649	genbank_U68133	
118456	genbank_N66580	
102860	entrez_X00368	
120715	genbank_AA292700	
120749	genbank_AA303235	
113663	genbank_T95909	
113889	genbank_W72720	
108258	genbank_AA063269	
101046	entrez_K01160	
129990	genbank_N30316	
122746	genbank_AA458791	
124046	genbank_F10243	
108436	genbank_AA078801	
124197	genbank_H52921	
101447	entrez_M21305	
108852	genbank_AA133131	
101697	entrez_M64358	
108931	genbank_AA147186	
101909	entrez_S69265	
117816	genbank_N48872	
119154	genbank_R61293	
119241	genbank_T12559	
119310	genbank_T40427	
119347	genbank_T64349	
119529	entrez_W38053	
112467	genbank_R65706	
112533	genbank_R69886	
112588	genbank_R77302	
121082	genbank_AA398722	
123305	genbank_AA496133	
123328	genbank_AA496968	
100547	tigr_HT2219	
123490	genbank_AA599723	

75 TABLE 45A: 90 GENES DOWN-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

Table 45A lists about 90 genes down-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip.

80 Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

	Pkey	ExAccn	UnigenelD	Unigene Title
5	100137	D13627	Hs.15071	chaperonin containing TCP1, subunit 8 (t
	100240	D31767	Hs.75416	DAZ associated protein 2
	100289	D45248	Hs.179774	proteasome (prosome, macropain) activato
	100658	HG2855-HT2995	Hs.75452	heat shock 70kD protein 2
	100763	HG3597-HT3800		gb:Human major histocompatibility comple
10	100779	HG3731-HT4001	Hs.302063	immunoglobulin heavy constant mu
	101091	L06132	Hs.149155	voltage-dependent anion channel 1
	101155	L13972	Hs.301698	sialyltransferase 4A (beta-galactosidase
	102223	U24685		gb:Homo sapiens immunoglobulin heavy cha
	102282	U31383	Hs.79126	guanine nucleotide binding protein 10
15	102378	U40369	Hs.28491	spermidine/spermine N1-acetyltransferase
	102386	U40998	Hs.81728	unc119 (C.elegans) homolog
	102389	U41371	Hs.75916	splicing factor 3b, subunit 2, 145kD
	102480	U50327	Hs.1432	protein kinase C substrate 80K-H
	102566	U59752	Hs.303091	pleckstrin homology, Sec7 and coiled/coi
20	102605	U64444	Hs.181369	ubiquitin fusion degradation 1-like
	102693	U73824	Hs.183684	eukaryotic translation initiation factor
	102710	U77827	Hs.113207	G protein-coupled receptor 30
	102920	X12451	Hs.78056	cathepsin L
	102929	X13238	Hs.74649	cytochrome c oxidase subunit VIc
25	103166	X67951	Hs.180909	peroxiredoxin 1
	103283	X80199	Hs.83422	MLN51 protein
	103463	Y00281	Hs.2280	ribophorin I
	103835	AA172215	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT
	104796	AA029368	Hs.33026	hypothetical protein PP2447
30	105714	AA291429	Hs.12211	GDP-fucose transporter 1
	105927	AA402968	Hs.332040	hypothetical protein MGC13010
	105945	AA404512	Hs.14453	interferon consensus sequence binding pr
	106001	AA410986	Hs.8963	Homo sapiens mRNA full length insert cDN
	106027	AA412119	Hs.234799	breakpoint cluster region
35	106227	AA429262	Hs.19613	ESTs
	106295	AA435664	Hs.8583	similar to APOBEC1
	106417	AA448008	Hs.261828	G protein-coupled receptor kinase 7
	107391	W02877	Hs.284294	Breakpoint cluster region protein, uteri
	109107	AA169180	Hs.269280	ESTs
40	109885	F09325	Hs.28102	ESTs
	110021	H11252	Hs.31037	ESTs
	110738	H99370	Hs.139648	kinesin family member 1C
	112746	R93237	Hs.74170	metallothionein 1E (functional)
	113059	T26925	Hs.172684	vesicle-associated membrane protein 8 (e
45	113822	W47350	Hs.17466	retinoic acid receptor responder (tazaro
	113859	W67225	Hs.13273	KIAA0592 protein
	113909	W78127	Hs.9956	hypothetical protein FLJ20259
	114693	AA122158	Hs.300683	Homo sapiens cDNA FLJ12825 fis, clone NT
	115399	AA283182	Hs.92023	core histone macroH2A2.2
50	116606	D80217	Hs.259842	protein kinase, AMP-activated, gamma 2 n
	116633	F02702	Hs.268726	ESTs, Highly similar to ZN91_HUMAN ZINC
	119254	T15837	Hs.279009	matrix Gla protein
	119493	W35384	Hs.50477	RAB27A, member RAS oncogene family
	120108	W95696	Hs.16803	LUC7 (S. cerevisiae)-like
55	120886	AA365566	Hs.301342	hypothetical protein MGC4342
	120953	AA397911	Hs.97499	ESTs, Weakly similar to unknown [H.sapie
	121303	AA402441	Hs.303197	B-cell CLL/lymphoma 7C
	121547	AA412448	Hs.104777	ESTs
	123495	AA599850	Hs.106747	serine carboxypeptidase 1 precursor prot
60	123608	AA609144	Hs.112851	ESTs
	123749	AA609949	Hs.112790	EST
	124763	R39610	Hs.76288	calpain 2, (mII) large subunit
	125366	H60192	Hs.76853	Homo sapiens mRNA; cDNA DKFZp434N1728 (f
	125657	AA481719	Hs.150540	Homo sapiens, clone IMAGE:3954961, mRNA,
65	125670	AI432621	Hs.82685	CD47 antigen (Rh-related antigen, integr
	125882	H45538	Hs.101448	metastasis associated 1
	126541	AA204913	Hs.7854	zinc/iron regulated transporter-like
	126715	R70160	Hs.241552	KIAA0268 protein
	126817	AA478642	Hs.291623	ESTs, Weakly similar to unnamed protein
70	127112	AI143906	Hs.125103	ESTs
	127273	AA335263	Hs.144950	ESTs
	127615	AA718919		gb:zv88a04.s1 Soares_NhHMPu_S1 Homo sapi
	127635	AA766903	Hs.116346	ESTs, Highly similar to A46297 beta-1,6-
	128528	R39234	Hs.251699	ESTs, Weakly similar to IDN4-GGTR14 [H.s
75	129398	AA437374	Hs.234573	Homo sapiens mRNA for TL132
	129621	AA489459	Hs.301005	purine-rich element binding protein B
	131037	AA256171	Hs.22391	chromosome 20open reading frame 3
	131328	V01512	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131631	AA486868	Hs.29802	slit (Drosophila) homolog 2
80	132079	H67964	Hs.38694	ESTs
	132455	T15774	Hs.4892	Homo sapiens clone 24841 mRNA sequence
	132582	AA318547	Hs.278712	eukaryotic translation initiation factor
	132610	AA443114	Hs.5326	amino acid system N transporter 2; porcu
	132755	AA609201	Hs.182635	ESTs
	133192	AA393804	Hs.67052	vacuolar protein sorting 26 (yeast homol

5	133437	R57419	Hs.7370	phosphatidylinositol transfer protein, b
	133449	AA094989	Hs.7381	voltage-dependent anion channel 3
	133649	AA479139	Hs.75393	acid phosphatase 1, soluble
	133814	M33882	Hs.76391	myxovirus (influenza) resistance 1, homo
	134378	AF006088	Hs.82425	actin related protein 2/3 complex, subun
	134419	L08044	Hs.82961	trefoil factor 3 (intestinal)
	134548	U41515	Hs.333495	Deleted in split-hand/split-foot 1 regio
	134776	J05582	Hs.89603	mucin 1, transmembrane
10	135032	AA243497	Hs.173685	hypothetical protein FLJ12619

TABLE 45B

15	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
20	Pkey	CAT number	Accessions
	127615	380951_1	AA626215 AA718919
	100763	tigr_HT3800	X12432 Y08693
	102223	221_265	AF013616 AA300945 X65907 AF062264 AF062250 Z47228 Z75389 Z75374 AF062152 AF062146 Z75398 X64153 AF062101 AF062218 S59161 Z75392 AF062196 AF062192 X65904 U24685 AF062181 Z47241 Z75376 AF062217 Z47234 X64152 AF062187 AF062173 AF062158 Z47229 M74018 M74021 X54441 M84512 L29115 M84508 Z75384 AJ244983 AJ245240 AJ245030 AJ245042 M26998 L03635 S64473 AJ244997 AJ245013 AJ279535 U89766 AF174049 AF174085 AF174086 U97246 AJ245011 AJ245017 AJ245028 AJ245041 AJ245051 AJ245065 AJ245236 U22391 Z49143 Z74665 AF087428 S66098 Z70650 AJ244929 AF006528 AF022004 AF021983 U00556 AJ245035 Z70617 Z70605 AJ245052 AJ245046 AF087424 AF174054 S67110 U21257 U21267 U21268 Z35492 U71103 AF021991 L23518 Z70644 AJ245036 Z49141 AF089001 Z74695 Z46304 AF021957 AF021990 AF022005 AF052527 AF021947 Z70604 Z70610 AF062104 Z49135 X64235 Z46341 Z46305 Z46307 Z49136 AJ244996 Z46342 AJ244931 AJ244935 AJ244937 AJ244938 L12192 AJ244939 AJ244940 AJ244941 Z46308 AJ244962 AF062234 AJ244973 AJ244984 AJ244985 AF174088 AJ279519 AJ279521 AJ279526 AJ245009 AJ279531 AJ245008 AJ244994 AJ244991 AJ244990 AJ244988 AJ244987 X87440 AJ245238 Z70625 Z70626 Z70641 Z70640 Z70643 AJ244975 Z70616 Z70637 AJ244982 AJ244967 AJ239377 AJ245057 AF021948 AF107239 AJ245040 L34163 AF062231 Z70627 AF062113 AF006527 AF174041 AJ279537 Z70642 U00497 Z70639 AJ245054 AJ244960 AJ279524 AJ244943 AJ249631 AF035041 AJ245039 AJ245050 AF107233 AJ239362 AJ244969 Z46278 Z46290 Z46274 Z46281 AJ239351 L25293 AJ244944 AJ244951 Z46280 Z46270 AJ245043 Z46276 AF107241 Z46271 Z46277 AJ245034 Z46273 AJ244992 Z46282 Z70638 Z46275 AJ244972 Z46272 Z46279 Z46269 AF087422 M74469 X64159 AF103243 X64156 AJ244942 Z46316 AJ222547 Z46322 Z46324 Z46326 Z46327 AJ222556 Z46329 Z46330 Z46302 AJ222561 AJ222549 AJ222568 AJ222570 AJ222571 Z49139 AJ222578 AJ222562 AJ222577 Z46323 AJ222576 AJ222566 Z46315 AJ222557 AJ222564 AJ222559 AJ222573 AJ222575 Z46318 AJ222548 Z46319 AJ222552 AJ222550 AJ222567 AJ222558 AJ222563 Z46317 X87438 AJ222555 AJ240581 AF103161 AJ240580 AJ240594 Y17929 AJ240553 AJ240573 AJ240558 AJ240555 Y17927 Y17949 AJ240561 Y17948 Y17933 Y17947 Y17944 Y17928 Y17931 Y17934 AJ240595 Y17943 Y17932 Y17930 AJ240590 AJ240560 Y17945 AJ240556 S79918 AF103278 AW364256 AF103299 AF103122 X75022 AF004937 Z30557 Z30677 Z30573 Z30576 Z30561 Z30674 Z30562 Z30675 AW403129 AI203192 AW404253 AW237246 AI654630 H61354
25			
30			
35			
40			

Table 46A lists about 714 genes upregulated in esophageal cancer relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 47A lists about 113 genes upregulated in esophageal tumors relative to normal esophagus. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 48A lists about 162 genes downregulated in esophageal tumors relative to normal esophagus. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

TABLE 46A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of esophageal tumor AIs divided by the 70th percentile of normal tissue AIs, where the 15th percentile of the normal tissue AIs was subtracted from both the numerator and denominator.

Pkey	ExAccn	UnigenelD	Unigene Title	R1
413808	J00287		Homo sapiens mRNA for caldesmon, 3' UTR	31.57
411243	AB039886	Hs.69319	CA11	26.06
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias)	25.65
401781			Target Exon	23.23
424098	AF077374	Hs.139322	small proline-rich protein 3	21.35
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	20.37
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	20.33
401780			NM_005557*:Homo sapiens keratin 16 (foca	18.94
421948	L42583	Hs.334309	keratin 6A	18.13
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	18.01
429538	BE182592	Hs.11261	small proline-rich protein 2A	17.31
400666			NM_002425:Homo sapiens matrix metallopro	17.28
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	16.96

	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	16.35
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	16.22
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	15.64
5	421582	AI910275		trefoil factor 1 (breast cancer, estroge	14.86
	425679	X05997	Hs.159177	lipase, gastric	14.53
	421773	W69233	Hs.112457	ESTs	14.26
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	14.26
10	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	13.93
	444325	AW152618	Hs.16757	ESTs	13.24
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	13.19
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	11.98
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.99
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	10.77
15	422239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	10.31
	446292	AF081497	Hs.279682	Rh type C glycoprotein	9.69
	421978	AJ243662	Hs.110196	NICE-1 protein	9.68
	448811	AI590371	Hs.199460	ESTs	9.38
	453331	AI240665		ESTs	9.37
20	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	9.28
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	9.18
	406687	M31126		matrix metalloproteinase 11 (stromelysin	9.13
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	9.04
	450701	H39960	Hs.288467	hypothetical protein XP_098151	8.77
25	418686	Z36830	Hs.87268	annexin A8	8.76
	421110	AJ250717	Hs.1355	cathepsin E	8.42
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	8.42
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.38
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	8.18
30	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	8.11
	450375	AA009647		a disintegrin and metalloproteinase doma	8.03
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	7.97
	445891	AW391342	Hs.199460	DPCR1 protein	7.95
	437053	AJ077018	Hs.3235	keratin 4	7.93
35	423271	W47225	Hs.126256	interleukin 1, beta	7.80
	409757	NM_001898	Hs.123114	cystatin SN	7.74
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	7.64
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.58
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	7.55
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.26
	448045	AJ297436	Hs.20166	prostate stem cell antigen	7.14
	408243	Y00787	Hs.624	interleukin 8	7.13
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	7.08
45	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	7.04
	407366	AF026942	Hs.17518	gb:Homo sapiens c1g33 mRNA, partial sequ	7.04
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.98
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	6.89
	414774	X02419	Hs.77274	plasminogen activator, urokinase	6.85
	439926	AW014875	Hs.137007	ESTs	6.84
50	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.82
	429259	AA420450	Hs.292911	Plakophilin	6.77
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	6.71
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	6.67
	429228	AI553633	Hs.326447	ESTs	6.61
55	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	6.60
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.58
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.55
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	6.54
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.53
60	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.51
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.49
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	6.48
	428471	X57348	Hs.184510	stratifin	6.46
	422511	AJ076442	Hs.117938	collagen, type XVII, alpha 1	6.45
65	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.44
	401747			Homo sapiens keratin 17 (KRT17)	6.42
	421508	NM_004833	Hs.105115	absent in melanoma 2	6.42
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	6.42
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	6.41
70	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	6.38
	422596	AF063611	Hs.118633	2'-5'-oligoadenylate synthetase-like	6.38
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	6.36
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	6.35
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antago	6.33
75	425415	M13903	Hs.157091	involucrin	6.32
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.30
	415989	AI267700		ESTs	6.23
	406673	M34996	Hs.198253	major histocompatibility complex, class	6.21
80	449228	AJ403107	Hs.148590	protein related with psoriasis	6.21
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	6.18
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	6.06
	418663	AK001100	Hs.41690	desmocollin 3	6.04
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.98
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	5.96

5	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	5.93
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	5.92
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	5.92
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum corn	5.84
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.76
10	400665			NM_002425:Homo sapiens matrix metallopro	5.75
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.72
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	5.72
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	5.71
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	5.70
15	439606	W79123	Hs.58561	G protein-coupled receptor 87	5.70
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	5.68
	433447	U29195	Hs.3281	neuronal pentraxin II	5.67
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.64
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	5.62
20	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PL	5.60
	428450	NM_014791	Hs.184339	KIAA0175 gene product	5.53
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.50
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	5.48
	447164	AF026941	Hs.17518	Homo sapiens cig 5 mRNA, partial sequence	5.47
25	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	5.44
	439223	AW238299	Hs.250618	UL16 binding protein 2	5.44
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	5.42
	402994			NM_002463*:Homo sapiens myxovirus (infl	5.40
	447333	BE090580	Hs.70704	hypothetical protein dJ616B8.3	5.40
30	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	5.36
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	5.33
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	5.32
	449722	BE280074	Hs.23960	cyclin B1	5.31
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.30
35	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	5.29
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	5.29
	417720	AA205625	Hs.208067	ESTs	5.29
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.28
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	5.27
40	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	5.26
	430280	AA361258	Hs.237868	interleukin 7 receptor	5.25
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	5.24
	402075			ENSP00000251056*:Plasma membrane calcium	5.24
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	5.24
45	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	5.22
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.22
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death domai	5.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	5.20
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epider	5.20
50	406663	U24683	Hs.293441	immunoglobulin heavy constant mu	5.19
	409178	BE393948	Hs.50915	kallikrein 5	5.15
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	5.14
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	5.10
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	5.09
55	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.09
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platel	5.08
	411274	NM_002776	Hs.69423	kallikrein 10	5.07
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	5.03
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	5.03
60	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	5.02
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	5.02
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.02
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	5.00
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	5.00
65	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.97
	405770			NM_002362:Homo sapiens melanoma antigen,	4.96
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.94
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.94
	426866	U02330	Hs.172816	neuregulin 1	4.93
70	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	4.92
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	4.91
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	4.90
	427786	BE407863	Hs.256871	ESTs	4.87
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	4.86
75	444371	BE540274	Hs.239	forkhead box M1	4.86
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	4.85
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	4.84
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	4.83
	409402	AF208234	Hs.695	cystatin B (stefin B)	4.81
80	408202	AA227710	Hs.43658	DKFZP586L151 protein	4.79
	401994			Target Exon	4.77
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.74
	421574	AJ000152	Hs.105924	defensin, beta 2	4.69
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.69
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.68
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.68
	407944	R34008	Hs.239727	desmocollin 2	4.67

	411296	BE207307	Hs.10114	growth suppressor 1	4.65
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	4.65
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.61
5	421335	X99977	Hs.103505	ARS component B	4.60
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.59
	453779	N35187	Hs.43388	28kD interferon responsive protein	4.59
	423575	C18863	Hs.163443	periostin (OSF-2os)	4.59
	417308	H60720	Hs.81892	KIAA0101 gene product	4.58
10	428651	AF196478	Hs.188401	annexin A10	4.58
	424354	NM_014314	Hs.145612	RNA helicase	4.58
	404996			Target Exon	4.56
	404240			NM_018950:Homo sapiens major histocompat	4.56
	453095	AW295660	Hs.252756	ESTs	4.55
15	410407	X66839	Hs.63287	carbonic anhydrase IX	4.55
	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	4.55
	450685	L15533	Hs.423	pancreatitis-associated protein	4.54
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	4.53
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.52
20	408380	AF123050	Hs.44532	diubiquitin	4.47
	443859	NM_013409	Hs.9914	folistatin	4.46
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	4.44
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	4.44
	421777	BE562088	Hs.108196	HSPC037 protein	4.44
25	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.43
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	4.42
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	4.42
	400419	AF084545		Target	4.42
	452571	W31518	Hs.34665	ESTs	4.41
30	430044	AA464510	Hs.152812	ESTs	4.41
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	4.39
	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	4.39
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	4.39
	453884	AA355925	Hs.36232	KIAA0186 gene product	4.38
35	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	4.37
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	4.37
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	4.37
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	4.36
	448357	N20169	Hs.108923	RAB38, member RAS oncogene family	4.36
40	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.34
	439999	AA115811	Hs.6838	ras homolog gene family, member E	4.34
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.34
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	4.32
	402447			C1000201:gi204416[gb]AA02627.1[(L0519	4.31
45	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	4.28
	432731	R31178	Hs.287820	fibronectin 1	4.27
	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	4.27
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	4.25
	425580	L11144	Hs.1907	galanin	4.25
50	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	4.23
	409433	AA074382	Hs.135255	ESTs	4.23
	430630	AW269920	Hs.2621	cystatin A (stefin A)	4.22
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	4.21
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	4.20
55	432375	BE536069	Hs.2962	S100 calcium-binding protein P	4.20
	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.19
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	4.19
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	4.18
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	4.17
60	410286	AI739159	Hs.61898	DKFZP586N2124 protein	4.16
	448844	AI581519	Hs.177164	ESTs	4.16
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	4.16
	417599	AA204688	Hs.62954	ESTs	4.16
	402992			Target Exon	4.15
65	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoactin)	4.14
	422100	AI096988	Hs.111554	ADP-ribosylation factor-like 7	4.13
	409512	AW979187	Hs.293591	melanoma differentiation associated prot	4.12
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.11
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.10
70	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	4.10
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.10
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	4.09
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.08
	417933	X02308	Hs.82962	thymidylate synthetase	4.08
75	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	4.06
	417678	X06560	Hs.82396	2',5'-oligoadenylate synthetase 1 (40-46	4.06
	451541	BE279383	Hs.26557	plakophilin 3	4.06
	433848	AF095719	Hs.93764	carboxypeptidase A4	4.06
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.04
80	429599	AA806106	Hs.123664	ESTs	4.03
	450823	T81223	Hs.22011	complement-c1q tumor necrosis factor-rel	4.02
	423787	AJ295745	Hs.236204	nuclear pore complex protein	4.00
	431250	BE264649	Hs.251377	taxol resistance associated gene 3	4.00
	416091	AF295370	Hs.283082	defensin, beta 3	3.97

	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	3.97
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.97
	402408			NM_030920*:Homo sapiens hypothetical pro	3.97
5	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.95
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	3.95
	452888	AW955454	Hs.30942	ephrin-B2	3.95
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.95
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.94
10	419693	AA133749	Hs.301350	FXFD domain-containing ion transport reg	3.94
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.94
	422094	AF129535	Hs.272027	F-box only protein 5	3.94
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	3.93
	404286			C6001909:gil704441 dbj BAA18909.1 (D298	3.93
15	423961	D13666	Hs.136348	periostin (OSF-2os)	3.92
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	3.91
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	3.91
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	3.91
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	3.91
20	421904	BE143533	Hs.109309	hypothetical protein FLJ20035	3.90
	441553	AA281219	Hs.121296	ESTs	3.90
	428093	AW594506	Hs.104830	ESTs	3.90
	441020	W79283	Hs.35962	ESTs	3.89
	447078	AW885727	Hs.9914	ESTs	3.89
25	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	3.89
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	3.87
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	3.87
	426059	BE292842	Hs.166120	interferon regulatory factor 7	3.86
	419833	AA251131	Hs.220697	ESTs	3.85
30	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	3.85
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.83
	452203	X57522		transporter 1, ATP-binding cassette, sub	3.83
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	3.83
	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	3.83
35	442599	AF078037	Hs.324051	RelA-associated inhibitor	3.82
	405387			NM_022170*:Homo sapiens Williams-Beuren	3.82
	449539	W80363	Hs.58446	ESTs	3.82
	419079	AW014836	Hs.18844	ESTs	3.81
	410434	AF051152	Hs.63668	toll-like receptor 2	3.81
40	408660	AA525775		ESTs, Moderately similar to PC4259 ferri	3.80
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.80
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.80
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.79
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp58612022 (f	3.79
45	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.78
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.78
	414561	AI064813	Hs.195155	Homo sapiens amino acid transport system	3.78
	411789	AF245505	Hs.72157	Adican	3.77
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	3.77
50	449378	AW664026	Hs.59892	ESTs	3.76
	449961	AW265634	Hs.133100	ESTs	3.76
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.75
	407242	M18728		gb:Human nonspecific crossreacting anti	3.75
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	3.75
55	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	3.75
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	3.74
	422699	BE410590	Hs.119257	ems1 sequence (mammary tumor and squamou	3.74
	441954	AI744935	Hs.8047	Fanconi anemia, complementation group G	3.74
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	3.73
60	422648	D86983	Hs.118893	Melanoma associated gene	3.72
	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfami	3.71
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	3.71
	428728	NM_016625	Hs.191381	hypothetical protein	3.71
	400245			Eos Control	3.71
65	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.70
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.70
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	3.70
	440659	AF134160	Hs.7327	claudin 1	3.69
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.67
70	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.67
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	3.66
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	3.65
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	3.63
	414883	AA926960		CDC28 protein kinase 1	3.63
75	428398	AI249368	Hs.98558	ESTs	3.63
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	3.63
	408482	NM_000676	Hs.45743	adenosine A2b receptor	3.63
	404287			C6001909:gil704441 dbj BAA18909.1 (D298	3.63
80	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.61
	414110	BE251752		gb:601112444F1 NIH_MGC_16 Homo sapiens c	3.61
	427857	AL133017	Hs.2210	hypothetical protein FLJ22865	3.61
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	3.61
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.60
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	3.60

	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.60
	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, com	3.60
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.59
5	437340	AL353935	Hs.135917	hypothetical protein DKFZp761D1823	3.59
	435793	AB037734	Hs.4993	KIAA1313 protein	3.59
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	3.59
	420247	AA256930	Hs.44680	hypothetical protein FLJ20979	3.58
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	3.57
10	422282	AF019225	Hs.114309	apolipoprotein L	3.57
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.57
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.57
	408015	AW136771	Hs.244349	epidermal differentiation complex protei	3.56
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	3.56
15	449039	AI962602	Hs.74284	hypothetical protein MGC2714	3.56
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.55
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	3.55
	428977	AK001404	Hs.194698	cyclin B2	3.55
	402995			NM_002463*:Homo sapiens myxovirus (infl	3.55
20	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.54
	432917	NM_014125	Hs.241517	PRO0327 protein	3.54
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	3.53
	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	3.52
	438113	AI467908	Hs.8882	ESTs	3.52
25	414420	AA043424	Hs.76095	immediate early response 3	3.51
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.50
	447208	BE315291	Hs.237971	hypothetical protein MGC5627	3.50
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	3.49
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	3.49
30	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	3.49
	429249	X81479	Hs.2375	egf-like module containing, mucin-like,	3.48
	413900	AW409747	Hs.75612	stress-induced-phosphoprotein 1 (Hsp70/H	3.48
	424242	AA337476	Hs.347408	hypothetical protein MGC13102	3.48
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.47
35	446480	NM_014578	Hs.15114	ras homolog gene family, member	3.46
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.46
	428865	BE544095	Hs.164960	BarH-like homeobox 1	3.46
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.46
	450506	NM_004460		fibroblast activation protein, alpha	3.46
40	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	3.45
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.45
	405545			Target Exon	3.45
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.44
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.44
45	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.44
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomatos	3.44
	431228	AB006746	Hs.198282	phospholipid scramblase 1	3.44
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.43
	440502	AI824113	Hs.78281	regulator of G-protein signalling 12	3.43
50	448741	BE614567	Hs.19574	hypothetical protein MGC5469	3.43
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.43
	406646	M33600	Hs.308026	major histocompatibility complex, class	3.42
	413281	AA861271	Hs.222024	transcription factor BMAL2	3.42
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.42
55	430890	X54232	Hs.2699	glypican 1	3.41
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.41
	412429	AV650262	Hs.75765	GRO2 oncogene	3.41
	443211	AI128388	Hs.143655	ESTs	3.41
	422209	AF005210	Hs.113222	chemokine (C-C motif) receptor 8	3.40
60	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	3.39
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	3.39
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.39
	422101	AW404176	Hs.111611	ribosomal protein L27	3.39
	457670	AF119666	Hs.23449	insulin receptor tyrosine kinase substra	3.38
65	437033	AW248364	Hs.5409	RNA polymerase I subunit	3.37
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.37
	417059	AL037672	Hs.81071	extracellular matrix protein 1	3.37
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	3.36
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.36
70	436748	BE159107	Hs.159263	collagen, type VI, alpha 2	3.36
	401797			Target Exon	3.36
	428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	3.35
	421563	NM_006433	Hs.105806	granulysin	3.35
	402294			Target Exon	3.34
75	414024	AA134712	Hs.22410	gb:zm79g08.r1 Stratagene neuroepithelium	3.34
	401961			NM_021626:Homo sapiens serine carboxypep	3.33
	418462	BE001596	Hs.85266	integrin, beta 4	3.33
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	3.33
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.33
80	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.33
	404440			NM_021048:Homo sapiens melanoma antigen,	3.33
	432398	AA307808	Hs.2979	trefoil factor 2 (spasmolytic protein 1)	3.33
	421677	H64092	Hs.38282	ESTs	3.33
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.32

	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.32
	417197	AW994561	Hs.151777	eukaryotic translation initiation factor	3.32
	429669	BE185499	Hs.2471	KIAA0020 gene product	3.32
5	409636	AA305729	Hs.18272	amino acid transporter system A1	3.32
	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3.32
	405386			Target Exon	3.32
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.31
	448275	BE514434	Hs.20830	kinesin-like 2	3.31
10	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.31
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.31
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.31
	422575	AK000546	Hs.118552	hypothetical protein FLJ20539	3.31
	404171			NM_000636*:Homo sapiens superoxide dismu	3.31
15	418464	R87580	Hs.144531	gb:ym89h07.r1 Soares adult brain N2b4HB5	3.31
	425566	AW162943	Hs.250618	UL16 binding protein 2	3.31
	410226	AI831958	Hs.61053	hypothetical protein	3.30
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.30
	443247	BE614387	Hs.333893	c-Myc target JPO1	3.30
20	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	3.30
	428336	AA503115	Hs.183752	microseminoprotein, beta-	3.29
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.29
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.28
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.28
25	405778			NM_005361:Homo sapiens melanoma antigen,	3.28
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.27
	421150	AI913562	Hs.189902	ESTs	3.27
	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	3.27
	455813	BE141577		gb:QV2-HT0083-071299-018-a11 HT0083 Homo	3.27
30	426064	BE387014	Hs.166146	Homer, neuronal immediate early gene, 3	3.27
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.27
	458791	BE615453	Hs.346509	dedicator of cyto-kinesis 1	3.27
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	3.26
	429002	AW248439	Hs.2340	junction plakoglobin	3.26
35	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	3.25
	407777	AA161071	Hs.71465	squalene epoxidase	3.25
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	3.25
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	3.24
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	3.24
40	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	3.24
	447519	U46258	Hs.339665	ESTs	3.24
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	3.24
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.24
	423198	M81933	Hs.1634	cell division cycle 25A	3.23
45	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.23
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.22
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.22
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	3.22
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	3.22
50	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.22
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.21
	409197	N54706	Hs.303025	chromosome 11 open reading frame 24	3.21
	412641	M16660	Hs.74335	heat shock 90kD protein 1, beta	3.21
	413436	AF238083	Hs.68061	sphingosine kinase 1	3.21
55	408636	BE294925	Hs.46680	CGI-12 protein	3.21
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	3.21
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.21
	411573	AB029000	Hs.70823	KIAA1077 protein	3.20
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.19
60	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	3.19
	435014	BE560898	Hs.10026	mitochondrial ribosomal protein L17	3.18
	401176			Target Exon	3.18
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.17
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.16
65	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	3.16
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	3.16
	452012	AA307703	Hs.279766	kinesin family member 4A	3.16
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.15
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	3.15
70	433020	AI375726	Hs.279918	hypothetical protein	3.14
	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	3.14
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.14
	420005	AW271106	Hs.133294	ESTs	3.14
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.13
75	412270	AC005262	Hs.73797	guanine nucleotide binding protein (G pr	3.13
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	3.13
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.12
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.11
	431722	AF161528	Hs.268049	hypothetical protein	3.11
80	427239	BE270447	Hs.174070	ubiquitin carrier protein	3.11
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.10
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.10
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1	3.10
	418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfam	3.10

	439755	AW748482	Hs.77873	B7 homolog 3	3.10
	404170			NM_000636*:Homo sapiens superoxide dismu	3.09
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	3.09
5	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.09
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	3.08
	421155	H87879	Hs.102267	lysyl oxidase	3.08
	441224	AU076964	Hs.7753	calumenin	3.08
	424326	NM_014479	Hs.145296	disintegrin protease	3.08
10	429413	NM_014058	Hs.201877	DESC1 protein	3.08
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	3.08
	446510	H58306	Hs.15165	retinoic acid induced 14	3.08
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668 protein,	3.07
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	3.07
15	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	3.07
	448853	NM_012204	Hs.22302	general transcription factor IIIC, polyp	3.07
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.07
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	3.06
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	3.06
20	412577	Z22968	Hs.74076	CD163 antigen	3.06
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.06
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	3.05
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	3.05
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	3.04
25	451578	NM_016323	Hs.26663	cyclin-E binding protein 1	3.04
	444726	NM_006147	Hs.84981	interferon regulatory factor 6	3.04
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	3.04
	437741	BE561610	Hs.5809	putative transmembrane protein; homolog	3.04
	442643	U82756	Hs.3991	PRP4/STK/WD splicing factor	3.04
30	429358	AB037825	Hs.200317	KIAA1404 protein	3.03
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	3.03
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orolat	3.03
	409154	U72882	Hs.50842	interferon-induced protein 35	3.02
	442173	N76101	Hs.8127	KIAA0144 gene product	3.02
35	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	3.01
	450962	BE535647	Hs.25723	Sjogren's syndrome/scleroderma autoantig	3.01
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	3.01
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	3.01
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	3.01
40	459107	AA811881	Hs.28505	ubiquitin-conjugating enzyme E2H (homolo	3.00
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.00
	416110	Z42262	Hs.322844	hypothetical protein DKFZp564A176	3.00
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	3.00
	448569	BE382657	Hs.21486	signal transducer and activator of trans	3.00
45	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.00
	400200			NM_002788*:Homo sapiens proteasome (pros	3.00
	403330			Target Exon	2.99
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.99
	403416	AI744626		KIAA0564 protein	2.97
50	403438			NM_031419*:Homo sapiens molecule possess	2.96
	447942	F12628	Hs.155470	hypothetical protein MGC16040	2.96
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.95
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	2.94
	440086	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom	2.94
55	429547	AW009166	Hs.99376	ESTs	2.93
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	2.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.89
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2.89
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.86
60	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	2.86
	423425	AA375756	Hs.14449	KIAA1609 protein	2.86
	412851	AI826502	Hs.106149	ESTs	2.86
	400664			NM_002425:Homo sapiens matrix metallopro	2.86
	454140	AB040888	Hs.41793	hypothetical protein FLJ10474	2.85
65	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.85
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	2.84
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.83
	423767	H18283	Hs.132753	F-box only protein 2	2.82
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	2.82
70	441801	AW242799	Hs.86366	ESTs	2.80
	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	2.80
	416539	Y07909	Hs.79368	epithelial membrane protein 1	2.79
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	2.79
	422947	AA306782	Hs.122552	G-2 and S-phase expressed 1	2.75
75	417849	AW291587	Hs.82733	nidogen 2	2.74
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.73
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.72
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	2.71
	424874	AA347951	Hs.326413	Homo sapiens cDNA FLJ20812 fis, clone AD	2.71
80	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.71
	447854	AW138454	Hs.11594	ESTs	2.71
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.70
	412636	NM_004415		desmoplakin (DPI, DPII)	2.69
	420576	AA297634	Hs.54925	KIAA1858 protein	2.68

	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	2.68
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.68
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.66
5	428698	AA852773	Hs.334838	KIAA1866 protein	2.64
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	2.64
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro	2.64
	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.63
	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.63
10	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.62
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	2.59
	452620	AA436504	Hs.119286	ESTs	2.59
	420552	AK000492	Hs.98806	hypothetical protein	2.59
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.56
15	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.56
	448454	NM_005879	Hs.21254	TRAF interacting protein	2.55
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	2.55
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.54
	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like doma	2.54
20	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.54
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.53
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	2.53
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	2.51
	411908	L27943	Hs.72924	cytidine deaminase	2.49
25	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.48
	430024	AI808780	Hs.227730	integrin, alpha 6	2.47
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.46
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.45
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	2.45
30	407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	2.45
	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.44
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.42
	413048	M93221	Hs.75182	mannose receptor, C type 1	2.40
	403851			C5002154*:gi 7299015 gb AAF54217.1 (AE0	2.39
35	433745	AF075320	Hs.28980	hypothetical protein FLJ14540	2.37
	423903	M57765	Hs.1721	interleukin 11	2.37
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.36
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	2.32
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	2.31
40	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	2.31
	406974	M57293		gb:Human parathyroid hormone-related pep	2.31
	401924			ENSP00000246632*:CDNA FLJ20261 fis, clon	2.30
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	2.29
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	2.29
45	436608	AA628980		down syndrome critical region protein DS	2.28
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	2.27
	434398	AA121098	Hs.3838	serum-inducible kinase	2.27
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	2.26
	418030	BE207573	Hs.83321	neuromedin B	2.25
50	404927			Target Exon	2.25
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	2.24
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.23
	411388	X72925	Hs.69752	desmocollin 1	2.21
	445757	AW449065	Hs.13264	KIAA0856 protein	2.18
55	405069			NM_006212*:Homo sapiens 6-phosphofructo-	2.17
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.16
	443168	AI038653	Hs.50500	ESTs	2.15
	444301	AK000136	Hs.10760	asporin (LRR class 1)	2.13
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.11
60	426471	M22440	Hs.170009	transforming growth factor, alpha	2.10
	445019	AI205540	Hs.281295	ESTs	2.08
	402021			NM_031891:Homo sapiens cadherin 20, type	2.07
	431866	NM_012098	Hs.8025	angiopoietin-like 2	2.05
65	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.04
	409571	AA504249	Hs.187585	ESTs	2.03
	450831	R37974	Hs.25255	ESTs	1.99
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.99
	445960	AI268399	Hs.140489	ESTs, Weakly similar to LIN1_HUMAN LINE-	1.98
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	1.97
70	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	1.91
	426850	BE247670	Hs.172766	MAP/microtubule affinity-regulating kina	1.90
	427335	AA448542	Hs.251677	G antigen 7B	1.90
	450649	NM_001429	Hs.25272	E1A binding protein p300	1.88
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	1.88
75	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	1.88
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	1.86
	433226	AW503733	Hs.9414	KIAA1488 protein	1.86
	413129	AF292100	Hs.104613	RP42 homolog	1.85
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.85
80	446620	AA128808	Hs.179902	transporter-like protein	1.81
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	1.79
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	1.78
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	1.77
	423482	BE280172	Hs.129228	galactokinase 2	1.77

5	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	1.76
	419125	AA642452	Hs.130881	B cell CLL/lymphoma 11A (zinc finger pro	1.75
	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	1.74
	405102			C15001220*:gij4469558[jgb]AAD21311.1[(AF	1.74
	433201	AB040896	Hs.21104	KIAA1463 protein	1.73
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	1.65
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.62
	414961	U27266	Hs.927	myosin-binding protein H	1.61
10	428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha p	1.61
	422170	AI791949	Hs.112432	anti-Mullerian hormone	1.61
	431846	BE019924	Hs.271580	uroplakin 1B	1.58
	404468			C3000442*:gij11120696[ref]NP_068518.1] c	1.57
	405779			NM_005367:Homo sapiens melanoma antigen,	1.55
15	441129	AA074904	Hs.296420	ESTs, Weakly similar to T18651 hypotheti	1.55
	427244	AA402400	Hs.178045	ESTs	1.52
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	1.52
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78855 serine/th	1.51
	418367	AA326035	Hs.59236	hypothetical protein DKFZp434L0718	1.51
20	440340	AW895503	Hs.125276	ESTs	1.48
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	1.47
	424750	D29956	Hs.152818	ubiquitin specific protease 8	1.46
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	1.44
	406374			C16001364:gij11067373[ref]NP_067689.1] C	1.43
25	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	1.40
	404405			Target Exon	1.39
	401258			NM_030932*:Homo sapiens diaphanous (Dros	1.38
	433323	AA805132	Hs.159142	ESTs	1.36
	427441	AA412605	Hs.343879	SPANX family, member C	1.33
30	444707	AI188613	Hs.41690	desmocollin 3	1.31
	409103	AF251237	Hs.112208	XAGE-1 protein	1.27
	451106	BE382701	Hs.25960	N-MYC oncogene	1.27
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	1.23
	430686	NM_001942	Hs.2633	desmoglein 1	1.21
35	429325	AW08739	Hs.243770	ESTs	1.19
	406703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	1.03
	418827	BE327311	Hs.47166	HT021	1.01
	404104			C6001378*:gij1171748[sp]P46530[NOTC_BRAR	1.00

TABLE 46B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

45	Pkey	CAT Number	Accession
	413808	2905_1	AI570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188 AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204 BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155 AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841728 BI335729 BE841739 BE841663 AW863104 AA335201 AA335143 BF906965 AW867493 BE841505 BF374250 BE841766 BF373837 AW863191 BE841705 AW863154 AW868673 AW867311 AA335896 BE841753 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI801799 AI610344 AI452852 AW131174 AI581089 AI225028 AI446689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354652 AI470250 AI536872 AI891151 AW868019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681 AA335141 AW008176 AA335223 AI888837 AW868622 AI803901 AW005718 AI538062 AI282258 AI580678 AI445803 AI445394 AI868168 AA335144 AI926349 AA335210 AA334919 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109 AI453488 AI678606 AW869289 AW869211 BE841580 AI679368 AI888882 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584 AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404 AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154 AW868815 BF373812 BE841657 BE841780 AI440394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236 AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048 AW029395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012 AA335227 AW869307 AW869350 AW868709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607 AW008153 AI520957 AI610620 AI679828 AI868151 AI537839 AI679547 T28354 AI282567 AA335207 R36555 BF906963 AW131160 AI925626 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246 AW868723 BE937150 AA955002 AW863338 BE841767
50			X00474 NM_003225 X52003 M12075 BI765761 AW950155 AI571948 BI760569 AA308400 AA568312 BI761955 AA507595 AA614579 AA614409 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA858276 BM142503 AW050700 AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418 BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 AI61014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035
55			M31126
60			BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758
65	421582	13358_1	BC013389 BC017398 AI023543 AA191424 AI287700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
70	453331	16559_1	AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF685525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635
75	406687	0_0	BE184942 BE184946 AW238414 BE144666
	450375	16559_3	
80	415989	10194_1	
	426991	29771_1	
	454241	685806_1	

452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AW1479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586 AW975281 AA664986 AA525775 AA056342 AI538978 X79449 BC017853 AL121035 BF196384 AW119044 AI028023 AW451110 AI971911 AW015069 AI079170 AI376367 AI264113 AA829646 AA737579 AA449679 AA740864 NM_001111 U18121 AL567297 BG773801 BF973874 AV687104 AA527579 AA843525 BE706355 AI074589 AI523475 BE890249 AW406263 BE074258 AV729485 BF809610 BG058619 AA677244 BE179838 AA622264 AI460106 AA740411 AI499168 AI078223 AI682923 BE696559 AW375385 AW788739 BG984978 Z40874 T17054 F09669 AW844043 U10439 BI711870 AW245957 AU158567 AA679305 AA679316 W72510 AI346029 BG059762 AW251062 AA132373 AI925621 AI860230 AI340172 AW192891 AI079980 AI094937 AI042115 AI200901 BE328452 AA644678 AA551209 BE351065 AA970761 N68609 AW002028 AA160826 AI422774 AW873114 AW073597 AW664483 AI218710 AW020550 AW190607 AI984545 AI871921 AI333970 AI452887 AI818335 AA398655 AI554424 AI274187 BE465703 AW512940 AW241366 AI923954 AA576649 AW168294 AA813181 AA912168 AI049738 AW514073 AA548255 AI569630 BE710031 AA24182 AI341697 AA563904 AI537990 AW517908 AW172943 Z39498 AI750294 AW150414 AI253293 BE825720 T31860 AW150775 D20310 AA150892 AU133933 BE781148 AL038957 BF910979 AA352297 BG988142 AW372175 BF229106 AW866705 BE093482 BG990396 AI499917 AA054452 H05484 AI828502 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418 BF998473 T92021 BI021048 BM049578 AW501366 AW501342 AW501549 BE939021 BE707147 BE160974 BE305207 N49011 AA947119 AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 BI919250 BI253018 AW130996 BE074249 BE895428 BI034862 BE083277 BF952166 AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363 BE253764 BE250764 BE255757 BE251752 BE251925 U09278 NM_004460 U76833 AF007822 AL550894 BG203919 AL575714 AI478772 AW022667 AW613820 AI435793 AI051768 AI200109 AA436611 BG208151 AI446661 BG215551 BM449645 AW630055 BG620125 AL550932 AW471133 AU136648 BE925603 BF828688 BE141577 BE141585 BE141587 AL109688 R23665 R26578 BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA448162 AA129977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI250053 AI870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 AA0506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 AI070743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AI248473 M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI688892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW995245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 BC015981 AJ301615 AA628980 AI266033 BF184719
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TABLE 46C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423

5	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
	400666	8118496	Plus	17982-18115,20297-20456
	401785	7249190	Minus	165776-165996,166189-166314,166408-16656
	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	400665	8118496	Plus	16879-17023
	402994	2996643	Minus	4727-4969
	402075	8117407	Plus	121907-122035,122804-122921,124019-12416
	405770	2735037	Plus	61057-62075
10	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	404240	5002624	Minus	116132-116407,116653-116922
	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
	402992	7767907	Minus	42137-42515
15	402408	9796239	Minus	110326-110491
	404286	2326514	Plus	51086-51301
	405387	6587915	Minus	3769-3833,5708-5895
	404287	2326514	Plus	53134-53281
	402995	2996643	Minus	5962-6216
20	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	401797	6730720	Plus	6973-7118
	402294	2282012	Minus	2575-3000
	401961	4581193	Minus	124054-124209
	404440	7528051	Plus	80430-81581
25	405386	6579238	Minus	40959-41297
	404171	9930793	Plus	173667-173783,176876-177055
	405778	7280331	Plus	18748-19757
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
	401176	9438469	Minus	20475-20734
30	404170	9930793	Plus	168836-169248

TABLE 47A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Maximum of esophageal tumor Als divided by the 98th percentile of the normal esophagus Als

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	31.70
	411243	AB039886	Hs.69319	CA11	30.12
45	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	18.46
	444325	AW152618	Hs.16757	ESTs	18.22
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	17.52
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	16.28
50	400666			NM_002425:Homo sapiens matrix metallopro	15.59
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	15.22
	425679	X05997	Hs.159177	lipase, gastric	14.60
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	13.14
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	12.60
55	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.00
	453331	AI240665		ESTs	11.20
	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	10.77
	408380	AF123050	Hs.44532	diubiquitin	10.32
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.32
60	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	10.22
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	10.18
	408243	Y00787	Hs.624	interleukin 8	9.80
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	9.75
	450375	AA009647		a disintegrin and metalloproteinase doma	9.12
65	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	8.88
	433447	U29195	Hs.3281	neuronal pentraxin II	8.64
	421508	NM_004833	Hs.105115	absent in melanoma 2	8.46
	452862	AW378065	Hs.8687	ESTs	8.34
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	7.92
70	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	7.86
	409757	NM_001898	Hs.123114	cystatin SN	7.62
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.60
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	7.58
	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	7.46
75	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	7.44
	406687	M31126		matrix metalloproteinase 11 (stromelysin	7.24
	430280	AA361258	Hs.237868	interleukin 7 receptor	7.18
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	7.13
80	429228	AI553633	Hs.326447	ESTs	7.04
	421110	AJ250717	Hs.1355	calthepsin E	6.98
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	6.88
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	6.88
	406673	M34996	Hs.198253	major histocompatibility complex, class	6.72
	421582	AI910275		trefoil factor 1 (breast cancer, estroge	6.52

5	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	6.40
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	6.32
	439926	AW014875	Hs.137007	ESTs	6.32
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.12
	411296	BE207307	Hs.10114	growth suppressor 1	6.03
	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	5.86
	413441	AI929374	Hs.75367	Src-like-adaptor	5.86
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	5.81
10	417715	AW969587	Hs.86366	ESTs	5.76
	413808	J00287		Homo sapiens mRNA for caldesmon, 3' UTR	5.63
	400665			NM_002425:Homo sapiens matrix metallopro	5.60
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.53
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	5.44
15	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.42
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.40
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	5.38
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	5.08
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	5.08
20	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	5.04
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	4.92
	436856	AI469355	Hs.127310	ESTs	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.60
	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	4.53
25	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.48
	404240			NM_018950:Homo sapiens major histocompat	4.36
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	4.34
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.29
	425139	AW630488	Hs.25338	protease, serine, 23	4.24
30	415989	AI267700		ESTs	4.20
	408202	AA227710	Hs.43658	DKFZP586L151 protein	4.11
	450701	H39960	Hs.288467	hypothetical protein XP_098151	4.06
	423271	W47225	Hs.126256	interleukin 1, beta	4.02
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.96
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	3.90
35	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.86
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.86
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	3.76
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	3.49
40	408049	AW076098	Hs.345588	desmoplakin (DPI, DPII)	3.44
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	3.37
	435370	AI964074	Hs.225838	ESTs	3.29
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.19
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.18
45	409154	U72882	Hs.50842	interferon-induced protein 35	3.13
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	3.12
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.00
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.76
	402992			Target Exon	2.57
50	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.54
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	2.52
	413945	NM_000591	Hs.75627	CD14 antigen	2.51
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	2.50
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	2.48
55	415149	X12451	Hs.78056	calhepsin L	2.47
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	2.46
	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	2.45
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.45
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.39
60	422562	AI962060	Hs.118397	AE-binding protein 1	2.35
	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	2.28
	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	2.19
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	2.19
	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	2.03
65	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.03
	428981	BE313077	Hs.93135	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.83
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	1.79
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (fr	1.70
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	1.69
70	412773	HI5785	Hs.74573	similar to vaccinia virus HindIII K4L OR	1.66
	414024	AA134712	Hs.22410	gb:zm79g08.r1 Stratagene neuroepithelium	1.65
	426530	U24578	Hs.278625	complement component 4A	1.58
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.52

TABLE 47B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993

H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620
 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665
 BF989591 BI056086 BG001590 BF107035
 450375 16559_3 BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410
 452410 59661_1 H59605 BE157601 AA113758
 10 406687 0_0 AL133619 AI435410 AA622747 AW272464 AI215594 AI673758 AI476447 AI804128 AI581345 AI026826 AI300820 AW513621 AA256162 AI559724
 421582 13358_1 AI493388 AA614641 AI125754 AI214351 AI567080 AI200813 AI476629 AI685732 AA602400 AA730140 AI565082 AI269603 AI807095 AA905453
 15 413808 2905_1 AA505909 AI204595 AI582930 AI686077 AA757863 AA730154 AA664048 BI831663 AI734138 AI734130 AI732734 AW043563 AI741241 AI732741
 20 406687 0_0 BF111446 BE677727 AA437369 AA426284 AA433997 AA425820
 25 413808 2905_1 M31126
 30 406687 0_0 X00474 NM_003225 X52003 M12075 BI765761 AW950155 AI571948 BI760569 AA308400 AA568312 BI761955 AA507595 AA614579 AA614409
 35 413808 2905_1 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA858276 BM142503 AW050700
 40 406687 0_0 AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418
 45 413808 2905_1 AI570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188
 50 406687 0_0 AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204
 55 413808 2905_1 BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155
 60 406687 0_0 AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841728 BI335729 BE841739 BE841663 AW863104 AA335201
 65 413808 2905_1 AA335143 BF906965 AW867493 BE841505 BF374250 BE841766 BF373837 AW863191 BE841705 AW863154 AW868673 AW867311 AA335896
 70 406687 0_0 BE841753 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230
 75 413808 2905_1 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI801799 AI610344 AI452852
 80 406687 0_0 AW131174 AI581069 AI225028 AI446689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354652 AI470250
 85 413808 2905_1 AI536872 AI891151 AW968019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681
 90 406687 0_0 AA335141 AW008176 AA335223 AI888837 AW868622 AI803901 AW005718 AI538062 AI282258 AI580678 AI445803 AI445394 AI868168
 95 413808 2905_1 AA335144 AI926349 AA335210 AA334919 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109
 100 406687 0_0 AI453488 AI678606 AW869289 AW869211 BE841580 AI679368 AI888882 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584
 105 413808 2905_1 AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532
 110 406687 0_0 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404
 115 413808 2905_1 AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154
 120 406687 0_0 AW868815 BF373812 BE841657 BE841780 AI440394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236
 125 413808 2905_1 AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048
 130 406687 0_0 AW029395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012
 135 413808 2905_1 AA335227 AW869307 AW869350 AW868709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607
 140 406687 0_0 AW008153 AI520957 AI610620 AI679828 AI868151 AI537839 AI679547 T28354 AI282567 AA335207 R83655 BF906963 AW131160 AI925626
 145 413808 2905_1 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246
 150 406687 0_0 AW868723 BE937150 AA955002 AW863338 BE841767
 155 413808 2905_1 BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153
 160 406687 0_0 BG285837 AI720344 BF541715 AA355086 AA172236

TABLE 47C

Pkey:	Unique number corresponding to an Eos probeset		
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.		
Strand:	Indicates DNA strand from which exons were predicted.		
NL_position:	Indicates nucleotide positions of predicted exons.		
Pkey	Ref	Strand	NL_position
400666	8118496	Plus	17982-18115,20297-20456
400665	8118496	Plus	16879-17023
404240	5002624	Minus	116132-116407,116653-116922
402992	7767907	Minus	42137-42515

TABLE 48A:

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigenelD:	Unigene number
Unigene Title:	Unigene gene title
R1:	90th percentile of normal esophagus AIs divided by the 90th percentile of esophageal tumor AIs

Pkey	ExAccn	UnigenelD	Unigene Title	R1
407245	X90568	Hs.172004	titin	37.43
426752	X69490	Hs.172004	titin	30.23
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	23.69
407013	U35637		gb:Human nebulin mRNA, partial cds	17.09
400440	X83957	Hs.83870	nebulin	15.56
406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	14.21
428087	AA100573	Hs.182421	troponin C2, fast	13.03
417070	Z19077	Hs.172004	titin	13.02
406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	12.61
405001	U58196		interleukin enhancer binding factor 1	12.53
418391	NM_003281	Hs.84673	troponin I, skeletal, slow	12.46
418205	L21715	Hs.83760	troponin I, skeletal, fast	12.40
422633	X56832	Hs.118804	enolase 3, (beta, muscle)	12.21
400499			C10001858.gij6679124[ref]NP_032759.1] ne	11.99
418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	10.53
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	10.21
417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	10.14
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	10.13
408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	10.00
416373	AA195845	Hs.73680	ESTs, Weakly similar to S12658 cysteine-	9.65
415672	N53097	Hs.193579	ESTs	9.57
409096	AA194412	Hs.50550	sarcomeric muscle protein	9.48

	431360	NM_000427	Hs.251680	loricrin	9.42
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	9.20
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	9.15
5	422089	AJ010063	Hs.343603	titin-cap (telethonin)	8.96
	409028	AB014513	Hs.49998	Z-band alternatively spliced PDZ-motif	8.64
	437206	AW975934	Hs.283382	ESTs, Weakly similar to I38344 titin, ca	8.48
	421296	NM_002666	Hs.103253	perilipin	8.47
	412129	M21984	Hs.73454	troponin T3, skeletal, fast	8.39
10	434352	AF129505	Hs.86492	small muscle protein, X-linked	8.28
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	7.93
	408591	AF015224	Hs.46452	mammaglobin 1	7.88
	435124	AA725362	Hs.120456	ESTs	7.76
	430681	AW969675	Hs.291232	ESTs	7.70
	454229	AW957744	Hs.278469	lacrimal proline rich protein	7.68
15	424734	AI217685	Hs.96844	ESTs	7.59
	428221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	7.57
	431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	7.41
	443727	Z25389	Hs.18459	ESTs	7.21
20	408753	AI337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	7.04
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	6.98
	424485	AI685069	Hs.272556	peptidylarginine deiminase type I	6.93
	403805			Target Exon	6.87
	429997	NM_006789	Hs.227457	apolipoprotein B mRNA editing enzyme, ca	6.72
25	418532	F00797	Hs.85844	neurotrophic tyrosine kinase, receptor,	6.70
	419711	C02621	Hs.159282	ESTs	6.70
	422640	M37984	Hs.118845	troponin C, slow	6.68
	433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.55
	406703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	6.34
30	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.27
	446962	AI351421	Hs.279709	muscle specific ring finger protein 1	6.20
	411102	AA401295	Hs.23926	triadin	6.17
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	6.15
	454059	NM_003154	Hs.37048	statherin	5.95
35	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	5.85
	434360	AW015415	Hs.127780	ESTs	5.57
	420813	X51501	Hs.99949	prolactin-induced protein	5.52
	417376	AA253314	Hs.154103	LIM protein (similar to rat protein kina	5.46
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	5.42
40	446523	NM_003063	Hs.334629	sarcolipin	5.41
	402270			Target Exon	5.25
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	5.24
	424982	U94777		phosphorylase, glycogen; muscle (McArdle	5.17
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	5.14
45	410621	AA194329	Hs.172004	titin	5.10
	429134	AA448953	Hs.99004	ESTs	5.06
	436519	AJ278124	Hs.238756	myozenin	5.04
	447023	AA356764	Hs.17109	integral membrane protein 2A	5.03
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	5.02
50	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	5.00
	433635	AI074502	Hs.134292	hypothetical protein MGC12921	4.98
	429892	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	4.96
	411021	F00055	Hs.172004	titin	4.95
	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	4.93
55	424897	D63216	Hs.153684	frizzled-related protein	4.92
	406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	4.92
	428824	W23624	Hs.173059	ESTs	4.78
	418692	AK000268	Hs.87383	hypothetical protein	4.74
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	4.73
60	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.66
	424049	AB014524	Hs.138380	KIAA0624 protein	4.65
	439609	AW971945	Hs.293236	ESTs	4.65
	433122	AB019391	Hs.58049	ESTs	4.62
	415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	4.59
65	415655	W05433		ESTs	4.59
	442376	W95588	Hs.129982	Homo sapiens cDNA FLJ12228 fis, clone MA	4.58
	452308	AI167560	Hs.61297	ESTs	4.57
	418072	F35210	Hs.86507	Human DNA sequence from clone RP3-353C17	4.56
	429413	NM_014058	Hs.201877	DESC1 protein	4.53
70	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.53
	438704	AI435060	Hs.32825	ESTs	4.50
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	4.49
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	4.48
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	4.46
75	422313	AF045941	Hs.115166	scellin	4.43
	417045	F01180	Hs.332030	Homo sapiens ORF1	4.41
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	4.39
	435101	AI743156	Hs.131064	ESTs	4.37
	432408	N39127		ESTs, Weakly similar to A46010 X-linked	4.35
80	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	4.35
	429930	AI580809	Hs.99569	ESTs	4.30
	429624	AA458648	Hs.99476	ESTs, Weakly similar to 1313184B alpha1	4.26
	429454	AL039940	Hs.202949	KIAA1102 protein	4.20
	411000	N40449	Hs.201619	ESTs, Weakly similar to S38383 SEB4B pro	4.11

5	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	3.99
	428560	AI243209	Hs.98669	ESTs, Weakly similar to B47411 ADPribosy	3.95
	438328	AI492261	Hs.32450	ESTs	3.84
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.84
	453876	AW021748	Hs.110406	ESTs, Weakly similar to I38022 hypotheti	3.83
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	3.82
	430171	AF086289	Hs.234766	skin-specific protein	3.80
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	3.75
10	446082	AI274139	Hs.156452	ESTs	3.74
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.70
	431205	AA194560	Hs.250763	tropomodulin 4 (muscle)	3.68
	443265	AI916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	3.68
	424747	AA346241	Hs.231887	EST	3.67
	410223	S73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	3.63
15	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.62
	453817	AW755253	Hs.61920	ESTs	3.57
	416431	AW384459	Hs.172004	titin	3.52
	425971	AF135024	Hs.165296	kallikrein 13	3.49
	412452	AA215731	Hs.79265	suppression of tumorigenicity 5	3.48
20	421512	AB007923	Hs.265848	myomegalin	3.41
	413922	AI535895	Hs.221024	ESTs	3.37
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.36
	418067	AI127958	Hs.83393	cystatin E/M	3.32
25	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	3.29
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	3.26
	420197	AW139647	Hs.88134	ESTs, Weakly similar to A57291 cytokine	3.23
	425869	AA524547	Hs.160318	FXD domain-containing ion transport reg	3.21
	404270			NM_006061:Homo sapiens specific granule	3.21
30	409169	F00991	Hs.50889	(clone PWHL2-24) myosin light chain 2	3.17
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	3.13
	452023	AB032999	Hs.27566	KIAA1173 protein	3.08
	417713	D42047	Hs.82432	KIAA0089 protein	2.99
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	2.97
	450300	AL041440	Hs.58210	ESTs, Highly similar to ITH4_HUMAN INTER	2.97
35	451814	AA847992	Hs.137003	ESTs	2.83
	452360	AI742082	Hs.98539	ESTs	2.67
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	2.57
	408104	AW972927	Hs.293968	ESTs	2.57
40	444329	W73753	Hs.209637	hypothetical protein FLJ12921	2.54
	439652	W67826	Hs.55412	ESTs, Weakly similar to K1CJ_HUMAN KERAT	2.50
	432191	AA043193	Hs.273186	hypothetical protein, clone Telethon(Ita	2.33
	425855	AF135025	Hs.159679	kallikrein 12	2.32
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	2.28
45	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.25
	411388	X72925	Hs.69752	desmocollin 1	2.25
	425721	AC002115	Hs.159309	uroplakin 1A	2.12
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	2.10
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	2.02
50	417405	W28657	Hs.5307	ESTs	2.01
	434560	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence	1.95
	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	1.79
	430513	AJ012008	Hs.241586	G6C protein	1.68
	454478	AW805749	Hs.138885	superoxide dismutase 2, mitochondrial	1.68
55	416559	AI039195	Hs.128060	ESTs	1.66
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasm	1.64
	415780	U75898	Hs.78846	heat shock 27kD protein 2	1.55
	409702	AI752244		eukaryotic translation elongation factor	1.50

60

TABLE 48B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
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70

407013	2073_7	U35637 AA192323 AA194508 BG011583 F25712 AL596820 BE185376
424982	25362_1	AK057547 BG181248 AA883756 F25670 AA778128 F27657 F18914 F25171 AA178844 F21556 F25872 F20457 F27617 F36059 F34817 F26967 F25922 F31278 F34666 F01176 F36333 F01226 F27406 F27130 F28742 F24126 F29891 AA195955 AA086351 W69291 F25880 F32791 F31311 F32380 F25216 F19679 F18656 F29700 F24954 F32741 F30404 F35470 F33989 F33141 F36382 F34118 F17714 AA176345 F24700 AA550940 F18617 F16859 F15633 F34675 F16528 F17281 AA086388 F30859 F21852 C02644 F29425 F25286 C03553 F35259 W80691 F16457 F24094 F16783 AA180319 F28443 F17763 F17448 F00542 AA197179 AA193012
415655	15499_1	AJ276240 N70563 F37502 F29200 F27903 F18577 F19683 F20867 Z28857 F30994 F31752 F17375 F15601 F17543 F17411
432408	2061_18	AV724258 AA247153 BF736219 BF513744 AW058048 AI082691 AA865520 N39127 AV724549 F20776 AA249747 AW970392 AA535433 F36964 F33894
409702	38388_1	AK056951 AK026458 BI439120 BM021106 F30243 BM055214 BM054962 BM069667 F37401 AA563621 AI752243 AI720773 AI933014 F18964 F35317 F35258 F27772 H39537 AW445222 F19408 H28557 F30608 F31797 F30960 BF837737 BF837688 AL551046 BI758668 BI765038 BI837440 BE392882 BI438801 AI093511 AI752244 AI784111 BG490221 BF338840 BF338974 BG896472 AL576843 AW966769 F25388 F37436 H28558 AI025548 AA782333 F30929 F36002 F21229 AI720539 AA719449 F21231 F18924 AA626886 F30774 F27704 F31411 F31127 F33381 F36153 F31793 F31138 F31966 F33901 AA298244 BI757347 AI810201 AI692843 F29441 H51409 F21804 AW973249 F18440 F17572 F32499 AA327152 AA534140 AI188088 F18893 F23362 AA010888 F18143 Z28500 H27651 AI720790 F22425 H13178 H28677 F21098 F37777 F21466 F16598 F23420 AL574723 R75610 F34035 F17845 F18560 F25902 R79117 F35534 F15713 AI612800 F16563 F15645 F33609 F29995 BG939623 F17385 F17384 F18660 F17922 F15523 AI093253 F18359 F31452 F00232 AI583430 BM021353 AA284108 H27650 H29935 BE708208 AA010737 H51451

80

Z19399 AI678418 AI952535 F17265 F17826 F37939 F35639 F17367 W75962 R70189 Z28755 R72106 AA335915 R75700 R79116 W72887
AI581552 R71403 F23388 C03913 BI756149 BI116109 BF790727 AL553994 R82966 W47487 AA456066 AW984608 BE708220 BG490537 W47419

TABLE 48C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405001	6015406	Minus	104646-104819
400499	9796071	Minus	148495-148806
403805	8140491	Minus	51483-51742,53429-53511
402270	3108020	Plus	117656-117822
404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965

Table 49A. 1562 genes upregulated in lung cancer relative to normal body tissues

Table 49A shows 1562 genes upregulated in lung cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
R1 90th percentile of lung tumor AIs divided by the 50th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from the numerator and denominator.

Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prod.Domains; R1

421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphate), member 2; Ribosomal_L20,Na_Pi_cotrans;TM=Y;; 24.06
439335; AA742697; Hs.62492; ESTs, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus]; none;SS=M; 21.70
406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;; 19.36
421341; AJ243212; Hs.279611; deleted in malignant brain tumors 1; zona_pellucida,CUB,SRCR;SS=M; 16.99
452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine proteinase [H.sapiens]; none,none; 16.67
429259; AA420450; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none,none; 16.50
454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member A1; aldedh; 16.24
408000; L11690; Hs.620; bulous pemphigoid antigen 1 (230/240kD); ehand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,ldh_C,CH,AIP3;TM=M;; 14.75
421798; N74880; Hs.29877; N-acylsphingosine amidohydrolase (acid ceramidase)-like; SAPA,Surfactant_B,none; 14.18
439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSOCIATED PROTEIN 1 [H.sapiens]; none,none; 13.94
431846; BE019924; Hs.271580; uropod 1B; transmembrane4;TM=Y;SS=M; 13.54
417079; U65590; Hs.81134; Interleukin 1 receptor antagonist; IL1;SS=M; 12.97
444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypothetical protein YGL050w - yeast (Saccharomyces cerevisiae) [S.cerevisiae]; Collagen;TM=M;SS=M; 12.92
408243; Y00787; Hs.624; Interleukin 8; HLH,PAS,IL8;TM=M;; 12.76
448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec,MIP;TM=M;SS=M; 12.50
414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;; 12.12
436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;; 12.00
418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none,none; 11.99
419693; AA133749; Hs.301350; FXD domain-containing ion transport regulator 3; ATP1G1_PLM_MAT8;TM=Y;SS=M; 11.88
417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;SS=M; 11.38
414998; NM_002543; Hs.77729; oxidized low density lipoprotein (lectin-like) receptor 1; lectin_c;TM=Y;SS=M; 11.21
428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm_3;TM=Y;SS=M; 11.08
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member B2; aldedh;TM=M;SS=M; 11.01
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisomIV,HATPase_c;SS=M; 10.69
418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4); ank; 10.65
439223; AW238299; Hs.250618; UL16 binding protein 2; ldl_recept_a,PKD,MHC_L;TM=M;SS=Y; 10.52
441835; AB036432; Hs.184; advanced glycosylation end product-specific receptor; homeobox,Acyltransferase,notch,EGF,ank,Acyltransferase; 10.47
451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ABC_tran,SRP54;TM=Y;SS=M; 10.33
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;; 10.21
452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhbd_glycop;TM=Y;SS=M; 10.14
417389; BE260964; Hs.82045; midline (neurite growth-promoting factor 2); PTN_MK;TM=M;SS=Y; 10.13
433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_recpt;TM=M;SS=Y; 10.12
454098; W27953; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none,none; 10.05
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 9.98
430832; A073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]; none,none; 9.79
422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; none,kinase,fn3,ig; 9.60
414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;; 9.54
439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M;; 9.52
430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 9.48

- 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); Kunitz_BPT1,fn3,vwa,Collagen,beta-lactamase;TM=M;SS=M; 9.44
- 418882; NM_004996; Hs.89433; ATP-binding cassette, sub-family C (CFTR/MRP), member 1; ABC_membrane,ABC_tran;TM=Y;SS=M; 9.32
- 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid cells 1; ig;TM=M;SS=M; 9.26
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-macroglobulin receptor precursor [H.sapiens]; none,none; 9.18
- 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR/MRP), member 3; ABC_tran,ABC_membrane;TM=Y;SS=M; 9.06
- 441384; AA447849; Hs.288660; Homo sapiens cDNA: FLJ22182 fis, clone HRC00953; 7tm_3,none; 8.98
- 446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium_transp,FecCD;TM=Y;SS=M; 8.74
- 436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin;TM=Y;SS=M; 8.71
- 421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 8.71
- 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; vwa,Cache;TM=M; 8.66
- 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1;TM=Y;SS=M; 8.63
- 438091; AW373062; ; nuclear receptor subfamily 1, group I, member 3; hormone_rec,zf-C4,none; 8.60
- 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M; 8.57
- 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin;SS=M; 8.56
- 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;SS=M; 8.52
- 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant_thionins;SS=M; 8.49
- 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M; 8.42
- 413011; AW068115; Hs.821; biglycan; LRR,LRRNT;SS=M; 8.40
- 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 8.39
- 411089; AA456454; ; cell division cycle 2-like 1 (PITSLRE proteins); none,none; 8.37
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); BIR;TM=M; 8.34
- 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; none;SS=M; 8.25
- 449019; A1949095; Hs.67776; ESTs, Weakly similar to T22341 hypothetical protein F47B8.5 - Caenorhabditis elegans [C.elegans]; none,none; 8.24
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M; 8.22
- 416819; U77735; Hs.80205; pim-2 oncogene; pkinase;SS=M; 8.19
- 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg;TM=M; 8.16
- 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 8.16
- 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg;TM=M; 8.14
- 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.14
- 421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase;SS=Y; 8.10
- 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); ig;TM=Y;SS=M; 8.03
- 439285; AL133916; ; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 7.97
- 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B; Sema,PSI,Integrin_B;TM=Y; 7.86
- 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2; pkinase;TM=M; 7.85
- 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 7.85
- 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M; 7.84
- 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); SH3,TPR;TM=M; 7.73
- 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); ig;TM=Y;SS=M; 7.72
- 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfamily, member 17; IL2;SS=M; 7.71
- 451253; H48299; Hs.26126; claudin 10; PMP22_Claudin,Peptidase_M1,K_tetra;TM=Y;SS=M; 7.70
- 435575; AF213457; Hs.44234; triggering receptor expressed on myeloid cells 2; ig;TM=Y;SS=M; 7.70
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M; 7.70
- 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; ig,ICAM_N;TM=M;SS=M; 7.67
- 422282; AF019225; Hs.114309; apolipoprotein L; MolA_ExcB;TM=Y;SS=M; 7.64
- 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; SAM_PNT,none; 7.54
- 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding protein; 7tm_1;TM=Y;SS=M; 7.52
- 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); Y_phosphatase,DSPC;TM=M; 7.46
- 421071; A1311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen alpha 1(XI) chain precursor [H.sapiens]; none;TM=Y;SS=M; 7.40
- 421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 7.39
- 438089; W05391; ; nuclear receptor subfamily 1, group I, member 3; hormone_rec,zf-C4,none; 7.38
- 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M; 7.36
- 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor, epsilon; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 7.36
- 416178; A1808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; none;TM=M; 7.31
- 418506; AA084248; Hs.85339; G protein-coupled receptor 39; none,none; 7.25
- 441553; AA281219; Hs.121296; ESTs; none,FG-GAP,Integrin_A; 7.25
- 422311; AF073515; Hs.114948; cytokine receptor-like factor 1; fn3;TM=M; 7.21
- 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-type, Z polypeptide 1; fn3,Y_phosphatase,carb_anhydrase;TM=Y;SS=M; 7.20
- 438746; A1885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; transferrin,Guanylate_kin,PDZ,SH3; 7.20
- 412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M; 7.14
- 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 7.14
- 428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 7.12
- 418462; BE001596; Hs.85266; integrin, beta 4; fn3,Integrin_B,Calx-beta,EGF;TM=M;SS=M; 7.08
- 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 7.02
- 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M; 7.00
- 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; ig,isodh,Ribosomal_L6,F-box;TM=Y;SS=M; 6.98
- 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; Furin-like,pkinase,Recep_L_domain,YLP,none; 6.97
- 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M; 6.96
- 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; ITAM;TM=Y;SS=M; 6.93
- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 6.93
- 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg,HEAT;TM=M; 6.91
- 451035; AU076785; Hs.430; plastin 1 (I isoform); ehand,CH,Adaptin_N;SS=M; 6.86
- 432407; AA221036; ; gb:z03f12.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ;, mRNA sequence; DEAD,helicase_C,rm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rila,abhydrolase,TGF-beta,DUF139,TPR,DSFc,isp_1,Ribosomal_S21,rvp;TM=M; 6.84
- 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M; 6.77
- 448243; AW369771; Hs.52620; integrin, beta 8; Integrin_B,none; 6.76
- 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_inh;SS=M; 6.75
- 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 6.74
- 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; sugar_tr;TM=Y;SS=M; 6.73

- 430397; AI924533; Hs.105607; bicarbonate transporter related protein 1; HCO3_cotransp;TM=Y;; 6.71
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 6.71
 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor); FG-GAP,Rhbd_glycop,integrin_A;TM=Y;SS=M; 6.70
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 6.69
 424925; NM_002432; Hs.153837; myeloid cell nuclear differentiation antigen; PAAD_DAPIN,HIN;; 6.69
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor); vwa,integrin_A,FG-GAP;TM=Y;SS=M; 6.65
 428157; AI738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 6.64
 430770; AA765694; Hs.123296; ESTs; none,none; 6.63
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G protein), alpha 15 (Gq class); G-alpha,arf;TM=M;; 6.59
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005735; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 6.59
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPc;TM=M;; 6.59
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin_c,Ricin_B_lectin,Xlink;TM=Y;SS=M; 6.58
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 6.58
 416110; Z42262; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 6.58
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 6.57
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); Pribosyltran,OMPdecase;TM=M;; 6.57
 402260; ; NM_001436; Homo sapiens fibrillarin (FBL), mRNA. transcript (F8A), mRNA.; pkinase,Fibrillarin,none; 6.56
 456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide); none;TM=Y;; 6.53
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ldl_recept_a,PKD,MHC_1;TM=M;SS=Y; 6.53
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; inositol_P,ig;TM=M;; 6.52
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none;TM=Y;SS=M; 6.52
 432920; U37689; Hs.3128; polymerase (RNA) II (DNA directed) polypeptide H; none;TM=M;; 6.48
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; PLDC;TM=M;; 6.48
 409208; Y00093; Hs.51077; integrin, alpha X (antigen CD11C (p150), alpha polypeptide); vwa,FG-GAP,integrin_A,vwa,integrin_A,FG-GAP; 6.43
 424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF;; 6.43
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; ig;TM=Y;SS=M; 6.41
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PLACE2000103; HLF,death,TNFR_c6,Acyl-CoA_hydro; 6.41
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;; 6.39
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBpase;TM=M;; 6.37
 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip;TM=M;SS=Y; 6.37
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;SS=M; 6.36
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 6.34
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.34
 451734; NM_006176; Hs.26944; neurogranin (protein kinase C substrate, RC3); IQ,7tm_1;TM=M;; 6.34
 443907; AU076484; Hs.8963; TYRO protein tyrosine kinase binding protein; none;TM=M;SS=Y; 6.34
 401027; ; Target Exon; none,none; 6.26
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin_B,EGF,PSI;TM=Y;SS=M; 6.22
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); SH2;SS=M; 6.21
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone ADKA02377; 7tm_3,none; 6.20
 408771; AW732573; Hs.47584; potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3; ehtand,ion_trans,K_tetra,none; 6.19
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudogene; LIM,PDZ,pkinase;SS=M; 6.18
 408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1;TM=Y;SS=M; 6.17
 426427; M86699; Hs.169840; TTK protein kinase; pkinase;; 6.17
 445019; AI205540; Hs.281295; ESTs; none,none; 6.16
 438552; AJ245820; Hs.6314; type I transmembrane receptor (seizure-related protein); none,none; 6.16
 414907; X90725; Hs.77697; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,tRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M; 6.14
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; PI3_P14_kinase,FAT,FATC;TM=M;; 6.13
 417421; AL138201; Hs.82120; nuclear receptor subfamily 4, group A, member 2; hormone_rec,zf-C4;SS=M; 6.13
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 6.12
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 6.12
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M;; 6.12
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans,K_tetra,asp; 6.11
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 thromboxane A-2 receptor, endothelial [H.sapiens]; Bcl-2,none; 6.10
 423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC_tran;TM=Y;; 6.10
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y;; 6.09
 411020; NM_006770; Hs.67726; macrophage receptor with collagenous structure; SRCR,Collagen;TM=Y;SS=M; 6.09
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1;TM=Y;SS=M; 6.08
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); PAF-AH_1b,Lipase_GDSL;TM=M;; 6.07
 421753; BE314828; Hs.107911; ATP-binding cassette, sub-family B (MDR/TAP), member 6; ABC_tran,ABC_membrane;TM=Y;SS=M; 6.07
 406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gene, complete CDS.; none,none; 6.07
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated kinase; pkinase,pkinase_C;TM=M;SS=M; 6.06
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; C1q,Collagen;SS=M; 6.05
 414883; AA926960; ; CDC28 protein kinase 1; CKS;; 6.05
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPc,isp_1,Ribosomal_S21,rvp;TM=M;; 6.03
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 6.03
 448782; AL050295; Hs.22039; KIAA0758 protein; 7tm_2,ig,GPS,SEA;TM=Y;; 6.03
 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 6.01
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 6.00
 424381; AA285249; Hs.146329; protein kinase Chk2; pkinase,FHA,DnaI;TM=M;; 6.00
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase;TM=M;; 5.99
 439310; AF086120; Hs.102793; ESTs; casein_kappa,pkinase,ig,none; 5.97
 414972; BE263782; Hs.77695; KIAA0008 gene product; GKAP;TM=M;; 5.97
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 5.94
 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase_2;TM=Y;SS=M; 5.93
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin;TM=M; 5.93
 421462; AF016495; Hs.104624; aquaporin 9; MIP;TM=Y;SS=M; 5.92
 426761; AI015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586I2022 (from clone DKFZp586I2022); none;TM=Y;SS=M; 5.92
 407792; AI077715; Hs.39384; putative secreted ligand homologous to fxi1; none;TM=M;SS=Y; 5.91
 428771; AB028992; Hs.193143; KIAA1069 protein; C2,PI-PLC-Y,PI-PLC-X;TM=M;; 5.91
 438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; ig,MHC_II_alpha,none; 5.91

- 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 5.90
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,ig,Neuregulin;TM=M;; 5.90
 408790; AW580227; Hs.47860; neurotrophic tyrosine kinase, receptor, type 2; ig,pkinase,LRR,LRRNT,LRRCT;TM=Y;SS=M; 5.89
 413186; AU077141; Hs.75231; solute carrier family 16 (monocarboxylic acid transporters), member 1; sugar_lr;TM=Y;SS=M; 5.89
 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 5.88
 422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR,SH2,SH3,pkinase;TM=Y;SS=M; 5.88
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; none;TM=M;SS=Y; 5.88
 429619; AL120751; Hs.211568; eukaryotic translation initiation factor 4 gamma, 1; none,none; 5.86
 437429; H79981; Hs.5613; Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DKFZp564E2222); SH2,SH3,BTB; 5.86
 436576; A1458213; Hs.77542; ESTs; 7tm_1,DnaJ; 5.85
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, calcium-dependent); C2,PLA2_B;TM=M;; 5.85
 419981; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 5.83
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily, member 6b, decoy; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD;; 5.83
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 5.82
 451320; AW118072; ; diacylglycerol kinase, zeta (104kD); none;TM=M;; 5.82
 400991; ; ; Target Exon; Armadillo_seg,lectin_c,none; 5.81
 456906; AF117646; Hs.156637; Cas-BR-M (murine) ectopic retroviral transforming sequence c; zfc3HC4,Cbl_N,Cbl_N2,Cbl_N3;TM=M;; 5.81
 434263; N34895; Hs.44648; ESTs; ig,none; 5.81
 428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino acid transporter), member 5; elF6,SDF;TM=M;; 5.78
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; p450;TM=Y;SS=M; 5.78
 449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep_L_domain,none; 5.77
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 5.77
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); MIF,sugar_lr,none; 5.75
 409533; AW969543; Hs.21291; mitogen-activated protein kinase kinase kinase 13; Peptidase_C48,none; 5.73
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) receptor; hormone_rec,zf-C4,Metallothio_5;TM=M;; 5.73
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kinase); none,none; 5.72
 448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; SH2,STAT,STAT_bind,STAT_prot;TM=M;; 5.72
 452295; BE379936; Hs.28866; programmed cell death 10; serpin,none; 5.72
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; NUDIX;TM=M;SS=M; 5.72
 448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitter transporter, creatine), member 8; SNF;TM=Y;; 5.71
 417015; M83772; Hs.80876; flavin containing monooxygenase 3; FMO-like,pyr_redox;TM=Y;SS=M; 5.69
 453323; AF034102; Hs.32951; solute carrier family 29 (nucleoside transporters), member 2; Nucleoside_tran;TM=Y;SS=M; 5.69
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,Integrin_B;TM=Y;SS=M; 5.69
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 46kD; rrm,hormone_rec,zf-C4,sugar_lr;; 5.69
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; none;TM=Y;SS=M; 5.66
 447250; A1878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; PP2C;TM=M;; 5.65
 438113; A1467908; Hs.8882; ESTs; 7tm_1,none; 5.65
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; ig,none; 5.64
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; Sm,pkinase;; 5.64
 406137; ; ; NM_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA. VERSION NM_000178.1 GI; MutS_C,PWWP,MutS_N;TM=M;; 5.63
 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P4_kinase,PI3Ka;TM=M;; 5.62
 445873; AA205970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-like; PABP,rrm,pkinase,14-3-3; 5.62
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; SH3,PH,RhoGEF;TM=M;; 5.61
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein coupled, 6; 7tm_1;TM=Y;SS=M; 5.59
 433662; W07162; Hs.150826; CATX-8 protein; ras,ABC_tran,arf;TM=M;SS=M; 5.59
 449029; N28989; Hs.22891; solute carrier family 7 (cationic amino acid transporter, y system), member 8; aa_permeases;TM=Y;SS=M; 5.58
 431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 5.57
 430508; A1015435; Hs.104637; ESTs; SDF;TM=Y;SS=M; 5.56
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; 7tm_1;TM=Y;SS=M; 5.55
 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 5.54
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;; 5.54
 429563; BE619413; Hs.2437; eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD); hexapep,W2,hormone2,DUF29;TM=M;; 5.52
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subunit, non-ATPase, 2; PC_rep;TM=M;; 5.51
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; pkinase;TM=M;; 5.51
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (from clone DKFZp547C136); ABC_tran,GTP_EFTU,ABC_membrane,none; 5.50
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 5.48
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); SH3,PX;TM=M;; 5.48
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304; Nucleoside_tra2,none; 5.48
 426691; NM_006201; Hs.171834; PCTAIRE protein kinase 1; pkinase;TM=M;; 5.48
 453905; NM_002314; Hs.36566; LIM domain kinase 1; pkinase,LIM,PDZ,zf-PARP;TM=M;; 5.48
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor 1 gamma; none,none; 5.44
 430486; BE062109; Hs.241551; chloride channel, calcium activated, family member 2; none;TM=Y;SS=M; 5.43
 430066; A1929659; Hs.237825; signal recognition particle 72kD; TPR,AIRC,SAICAR_synt; 5.40
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; kinesin,fn3,Y_phosphatase;TM=M;; 5.40
 411825; AK000334; Hs.72289; hypothetical protein FLJ20327; SNF,Zip;TM=Y;; 5.36
 400205; ; ; NM_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA.(APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; DUF173;SS=M; 5.35
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;SS=M; 5.34
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 5.34
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M;; 5.32
 400210; ; ; Eos Control; Adap_comp_sub,Clat_adaptor_s;TM=M;; 5.32
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog); Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 5.31
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2; serpin;SS=M; 5.30
 416000; R82342; Hs.79856; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; none,sugar_lr; 5.30
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 5.29
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; SH2,SH3,pkinase;TM=M;; 5.29
 450296; AL041949; Hs.24752; hepatocyte growth factor-regulated tyrosine kinase substrate; none,none; 5.29
 456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, complete cds; none,PK,PK_C,myosin_head,RhoGAP; 5.28
 410069; A1633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3;TM=M;; 5.28
 456629; AW891965; Hs.279789; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD,none; 5.27
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); pkinase,Sema,PSI,TIG,Integrin_B;TM=Y;SS=M; 5.26
 444051; N48373; Hs.10247; activated leucocyte cell adhesion molecule; none,none; 5.26

- 404083; ; C6002159:gij628027|pir||A53593 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor ty; none;SS=M; 5.26
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1; mito_carr;TM=M; 5.26
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M; 5.26
 427732; NM_002980; Hs.2199; secretin receptor; 7tm_2,HRM;TM=M;SS=M; 5.25
 425921; NM_007231; Hs.162211; solute carrier family 6 (neurotransmitter transporter), member 14; SNF;TM=Y;SS=M; 5.25
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A, member 4A; none;TM=Y;SS=M; 5.24
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; WD40,fn3,ig;TM=M; 5.23
 446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 5.23
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M; 5.23
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazarotene induced) 3; none;TM=Y; 5.21
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; SH3,HS1_rep;TM=M; 5.20
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M; 5.19
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; Troponin,Exo_endo_phos,IQ;TM=M; 5.19
 446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonine kinase 21); CNH,DAG_PE-bind,PH,Involucrin,M;TM=M; 5.19
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 5.19
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, subfamily J, member 15; IRK;TM=Y; 5.19
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; Ribosomal_S14,ank,pkinase,death,none; 5.18
 442200; AW590572; Hs.235768; ESTs; none,none; 5.18
 446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A, member 6A; none;TM=Y;SS=M; 5.18
 452690; AI536070; Hs.15085; ESTs; pou,homeobox,lig_chan,ANF_receptor; 5.18
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); Ion_trans,SPRY,RYDR,ITPR,RyR,MIR;TM=Y; 5.17
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 5.16
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M; 5.16
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta (Liddle syndrome); ASC;TM=Y;SS=M; 5.15
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cytotactin); EGF,fn3,fibrinogen_C,toxin_2,Keratin_B2;TM=M;SS=Y; 5.15
 411984; NM_005419; Hs.72988; signal transducer and activator of transcription 2, 113kD; SH2,STAT,STAT_bind,STAT_prot;TM=M; 5.15
 433470; AW960564; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 5.14
 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M; 5.14
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm_2;TM=Y;SS=M; 5.14
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; SRP14,TNFR_c6;SS=M; 5.14
 430563; AA481269; ; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; ABC_tran,GTP_EFTU,ABC_membrane,none; 5.13
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr;TM=Y; 5.12
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3; ER_lumen_recept;TM=M;SS=M; 5.12
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarotene induced) 1; none,none; 5.11
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase kinase 1; pkinase,CNH;TM=M; 5.11
 409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfamily, member 13; TNF;TM=Y;SS=M; 5.11
 436856; AI469355; Hs.127310; ESTs; pkinase,rm;TM=M; 5.09
 411296; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell_Oxy;TM=M;SS=M; 5.09
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; rm;TM=M; 5.09
 404440; ; NM_021048;Homo sapiens melanoma antigen, family A, 10 (MAGEA10), mRNA. VERSION NM_021049.1 GI; MAGE;TM=M; 5.08
 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; none,none; 5.08
 422100; AI096988; Hs.111554; ADP-ribosylation factor-like 7; arf,ras;TM=M; 5.07
 452222; AW806287; Hs.21432; SEX gene; Sema,TIG,PSI,GDI; 5.07
 430300; U60805; Hs.238648; oncostatin M receptor; fn3;TM=Y;SS=M; 5.07
 408369; R38438; Hs.182575; solute carrier family 15 (H??? transporter), member 2; PTR2;TM=Y; 5.07
 422112; BE540240; Hs.111783; Lsm1 protein; Sm,BAG;SS=M; 5.06
 449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain,none; 5.06
 430024; AI808780; Hs.227730; integrin, alpha 6; integrin_A,FG-GAP;TM=Y;SS=M; 5.06
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; HSP90,HATPase_c;TM=M; 5.05
 437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; pkinase,RIO1,none; 5.05
 400296; AA305627; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran,ABC_membrane;TM=Y; 5.04
 446232; AI281848; Hs.194691; retinoic acid induced 3; 7tm_3,none; 5.04
 425262; D87119; Hs.155418; G33955 protein; pkinase;SS=M; 5.04
 414703; BE243877; Hs.76941; ATPase, Na? transporting, beta 3 polypeptide; Na_K-ATPase;TM=Y;SS=M; 5.03
 434808; AF155108; Hs.256150; Homo sapiens, Similar to RIKEN cDNA 2810027O19 gene, clone MGC:14827, mRNA, complete cds; none;TM=M; 5.03
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member 21; death,TNFR_c6;TM=Y;SS=M; 5.03
 449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; none,none; 5.03
 448913; AA194422; Hs.22564; myosin VI; rm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFILS,AT_hook,SAM;TM=M; 5.02
 413441; AI929374; Hs.75367; Src-like-adaptor; SH2,SH3;TM=M; 5.02
 427618; NM_000760; Hs.2175; colony stimulating factor 3 receptor (granulocyte); fn3;TM=M;SS=M; 5.02
 417666; AI345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4;TM=M; 5.02
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); CDK5_activator,none; 5.01
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; ras,arf,TK;SS=M; 5.01
 426285; U20620; Hs.343581; karyopherin alpha 1 (importin alpha 5); Armadillo_seg,IBB;TM=M; 5.01
 421233; AA209534; Hs.284243; tetraspan NET-6 protein; transmembrane4;TM=Y;SS=M; 5.01
 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; SH2,STAT,STAT_bind,STAT_prot,none; 5.00
 425345; AU077297; Hs.155894; protein tyrosine phosphatase, non-receptor type 1; Y_phosphatase,DSPc;TM=M;SS=M; 5.00
 446946; AI878932; Hs.317; topoisomerase (DNA) I; Topoisomerase_I,Topoisomerase_I_N,RnaAD,Hanta_nucleocap;TM=M; 4.99
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); TPR,PDZ,WW,Guanylate_kin;TM=M; 4.98
 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor); 7tm_1;TM=Y;SS=M; 4.98
 400792; AA635062; ; Homo sapiens mRNA; cDNA DKFZp434O0515 (from clone DKFZp434O0515); zf-C3HC4,CARD,BIR;TM=M; 4.98
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related oncogene homolog; SH2,SH3,pkinase;TM=M; 4.98
 427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); vwa,integrin_A,FG-GAP;TM=Y;SS=M; 4.98
 442080; AW444761; Hs.44565; ESTs; ank; 4.97
 454042; H22570; ; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 4.97
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 4.96
 416276; U41060; Hs.79136; LIV-1 protein, estrogen regulated; Peptidase_C4,Osteopontin,Zip;TM=Y;SS=M; 4.96
 408847; AW290997; Hs.30348; ESTs; pkinase,ig,none; 4.96
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 4.95
 450737; AW007152; Hs.203330; ESTs; trypsin,ldl_recept_a,none; 4.95
 443354; AW970672; Hs.9247; protein kinase, AMP-activated, alpha 1 catalytic subunit; pkinase,RIO1;TM=M; 4.94

- 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese, DSPc, Y_phosphatase; TM=M;; 4.94
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, ig, FAD_Synth, ldh, C, pkinase; SS=M; 4.94
 434206; AW136973; Hs.180479; ESTs, Weakly similar to S69890 mitogen inducible gene mig-2 [H.sapiens]; PH; TM=M;; 4.93
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); 7tm_1, 7tm_2; TM=Y; SS=M; 4.93
 5 408716; A1567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein, partial cds; UvrD-helicase, RNB, Runt; TM=M;; 4.93
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg, UQ_con, none; 4.92
 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; Ets, SAM_PNT; TM=M;; 4.92
 414570; Y00285; Hs.76473; insulin-like growth factor 2 receptor; fn2, CIMR; TM=M; SS=M; 4.92
 10 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; ig; TM=Y; SS=M; 4.92
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; DEAD, helicase_C, CARD; TM=M;; 4.91
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); ig, ITAM, Zn_clus; TM=Y; SS=M; 4.91
 404289; ; NM_002944; Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA; fn3, pkinase, DUF139; TM=Y; SS=M; 4.90
 428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1; Nramp; TM=Y;; 4.90
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none; TM=M; SS=Y; 4.89
 15 432179; X75208; Hs.2913; EphB3; EPH_lbd, fn3, pkinase, SAM; TM=Y; SS=M; 4.89
 401083; ; NM_016582; Homo sapiens peptide transporter 3 (LOC51296), mRNA. VERSION NM_016579.1 GI; PTR2; TM=Y; SS=M; 4.89
 402211; AA811738; ; KIAA0430 gene product; ion_trans, K_tetra; TM=Y;; 4.88
 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polypeptide 4; pkinase, pkinase_C; TM=M;; 4.87
 431810; X67155; Hs.270845; kinesin-like 5 (mitotic kinesin-like protein 1); kinesin; TM=M;; 4.86
 20 425295; AA431366; Hs.37251; ESTs; pkinase, none; 4.86
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; DNA_ligase;; 4.86
 419168; A1336132; Hs.33718; Homo sapiens cDNA FLJ12641 fis, clone NT2RM4001953; none, none; 4.86
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequence; K_tetra, DUF51, none; 4.86
 25 425465; L18964; Hs.1904; protein kinase C, iota; pkinase, DAG_PE-bind, pkinase_C, OPR; TM=M;; 4.86
 410293; AK000047; Hs.61960; hypothetical protein; K_tetra; TM=M;; 4.86
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; C1q, Collagen; SS=M; 4.85
 445903; A1347487; Hs.132781; class I cytokine receptor; fn3; TM=Y;; 4.85
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a ligand); 7tm_1; TM=Y; SS=M; 4.85
 30 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); vva, integrin_A, FG-GAP; TM=Y; SS=M; 4.84
 445143; U29171; Hs.75852; casein kinase 1, delta; zf-C3HC4, Filamin, zf-B_box, NHL, pkinase, zf-MIZ; TM=M;; 4.82
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG; TM=M;; 4.81
 427857; AL133017; Hs.2210; hypothetical protein FLJ22865; myosin_head, IQ, zf-MYND; TM=M; SS=M; 4.81
 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); aldedh, aakinase; TM=M;; 4.81
 35 414280; BE410768; Hs.75873; zyxin; LIM, ig, pkinase; TM=M; SS=M; 4.81
 424570; AA343306; Hs.133511; ESTs; SH3, ank, none; 4.80
 451144; AW955103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase_c, none; 4.80
 402705; AA214618; ; activator of S phase kinase; AhpC-TSA; TM=M; SS=M; 4.80
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M;; 4.80
 40 419972; AL041465; Hs.182982; golgin-67; none, none; 4.80
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C, none; 4.80
 413476; U25849; Hs.75393; acid phosphatase 1, soluble; LMWPC; TM=M; SS=M; 4.80
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, receptor for (CD32); ig; TM=Y;; 4.79
 402233; ; NM_030760; Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 8 (EDG8), mRNA; 7tm_1; TM=Y; SS=M; 4.79
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; NusG; SS=M; 4.79
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; pkB; TM=M;; 4.79
 405370; ; NM_005569; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA; pkinase, LIM, PDZ; SS=M; 4.79
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1 (TWIK-1); ion_trans; TM=Y; SS=M; 4.78
 429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen, COLFI, TSPN, laminin_G, CorA; SS=M; 4.78
 50 424415; NM_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase; TM=M;; 4.78
 433133; AB027249; Hs.104741; PDZ-binding kinase; T-cell originated protein kinase; pkinase; TM=M;; 4.78
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); none; TM=M; SS=Y; 4.78
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; ig, abhydrolase; 4.78
 55 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2; TM=Y; SS=M; 4.78
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase; SS=M; 4.77
 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (from clone DKFZp586P2321); none; NA; NA; 4.77
 446196; A1744888; Hs.149470; ESTs; zf-C3HC4, Sulfate_transp, STAS; 4.77
 429305; AF095727; Hs.287832; myelin protein zero-like 1; ig, transmembrane4; TM=Y; SS=M; 4.77
 60 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chloride transporters), member 7; none; TM=Y;; 4.77
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); Armadillo_seg, IBB, DEAD, helicase_C, Sec63, DDT, PHD, bromodomain; TM=M;; 4.77
 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; DSPC; TM=M;; 4.77
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702; GDI, 7tm_1, none; 4.76
 447207; AA442233; Hs.17731; hypothetical protein FLJ12892; none; TM=M;; 4.76
 400846; ; sortilin-related receptor, L(DLR class) A repeats-containing (SORL1); EGF, fn3, Idl_recept_a, Idl_recept_b, granulin, BNR; TM=Y; SS=M; 4.76
 65 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1, OATP_C; TM=Y;; 4.75
 406809; AF000574; Hs.22405; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2; ig, Gemini_mov; TM=M; SS=M; 4.75
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE; TM=M;; 4.75
 444042; NM_004915; Hs.10237; ATP-binding cassette, sub-family G (WHITE), member 1; ABC_tran, PRK, GBP; TM=Y;; 4.74
 70 410406; A1969703; Hs.1466; glycerol kinase; FGGY, FGGY_C; TM=M;; 4.73
 411653; AF070578; Hs.71168; Homo sapiens clone 24674 mRNA sequence; none; NA; NA; 4.73
 437667; BE616412; Hs.286218; junctional adhesion molecule 1; none, HLH; 4.73
 417781; BE279380; Hs.82563; KIAA0153 protein; TTL, Acyl_transf; 4.73
 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin, Idl_recept_a, none; 4.73
 75 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr virus) receptor 2; sushi; TM=Y; SS=M; 4.73
 418255; AW135405; Hs.37251; ESTs; pkinase, none; 4.73
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; SDF; TM=Y; SS=M; 4.73
 406906; Z25424; ; gb: H.sapiens protein-serine/threonine kinase gene, complete CDS.; none, none; 4.73
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; Metallophos; TM=M;; 4.72
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; SS=M; 4.72
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; NDK, PH, oxysterol_BP; SS=M; 4.71
 426136; AW957239; ; gb: EST369309 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence; PP2C, none; 4.71
 446203; Z47553; Hs.14286; flavin containing monooxygenase 5; FMO-like, pyr_redox; TM=Y; SS=M; 4.71
 80 451295; A1557212; Hs.17132; ESTs, Moderately similar to 154374 gene NF2 protein [H.sapiens]; pkinase, DAG_PE-bind, pkinase_C, OPR, none; 4.71

- 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran,ABC_membrane;TM=Y;; 4.70
- 424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; ldh,ldh_C,SH3,pkinase,UBA;TM=M;; 4.70
- 427206; NM_004586; Hs.173965; ribosomal protein S6 kinase, 90kD, polypeptide 3; none,none; 4.70
- 421662; NM_014141; Hs.106552; cell recognition molecule Caspr2; EGF,F5_F8_type_C,laminin_G,Sulfate_transp,STAS,7tm_3,xan_ur_permease;TM=Y;SS=M; 4.70
- 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); UQ_con;TM=M;; 4.70
- 405484; ; C3002124; gij12737280[ref]XP_006682.2| keratin 18 [Homo sapiens][6633; none;SS=M; 4.70
- 401345; M83738; ; protein tyrosine phosphatase, non-receptor type 9; none;TM=M;; 4.70
- 416602; NM_006159; Hs.79389; nel (chicken)-like 2; EGF,ywc,TSPN;SS=Y; 4.69
- 412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 4.69
- 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC;none; 4.69
- 432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M;; 4.69
- 400843; ; NM_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA;; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.68
- 433409; AI278802; Hs.25661; ESTs; pkinase,pkinase; 4.68
- 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 4.68
- 430259; BE550182; Hs.127826; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 4.68
- 425761; AW664214; Hs.196729; ESTs; SH3,Ribosomal_S3Ae; 4.68
- 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone COL04544; pkinase,Furin-like,Recep_L_domain;none; 4.68
- 419493; AF001212; Hs.90744; proteasome (prosome, macropain) 26S subunit, non-ATPase, 11; CDK5_activator,PCI;none; 4.67
- 425966; NM_001761; Hs.1973; cyclin F; cyclin,F-box,cyclin_C;TM=M;; 4.67
- 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 4.67
- 453476; AI640500; Hs.24633; SAM domain, SH3 domain and nuclear localisation signals, 1; SH3,SAM;SS=M; 4.67
- 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; MARCKS;SS=M; 4.67
- 424635; AA402687; Hs.115455; Homo sapiens cDNA FLJ14259 fis, clone PLACE1001076; pkinase,Furin-like,Recep_L_domain;none; 4.66
- 446051; BE048061; Hs.37054; ephrin-A3; Ephrin,A_deamin,dsm,z-alpha; 4.66
- 436729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.66
- 408204; AA454501; Hs.43666; protein tyrosine phosphatase type IVA, member 3; Y_phosphatase;TM=M;; 4.66
- 435542; AA687376; ; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF;none; 4.66
- 429682; NM_006306; Hs.211602; SMC1 (structural maintenance of chromosomes 1, yeast)-like 1; ABC_tran,SMC_N,SMC_C,KID;TM=M;; 4.66
- 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4;TM=Y;SS=M; 4.66
- 418736; T18979; Hs.87908; Snf2-related CBP activator protein; helicase_C,AT_hook,SNF2_N;TM=M;; 4.65
- 415117; AF120499; Hs.78016; polynucleotide kinase 3'-phosphatase; Viral_helicase1;TM=M;; 4.65
- 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA;SS=M; 4.65
- 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;; 4.64
- 429263; AA019004; Hs.198396; ATP-binding cassette, sub-family A (ABC1), member 4; ABC_tran,SRP54;TM=Y;SS=M; 4.64
- 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M;; 4.63
- 435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none;TM=M;; 4.63
- 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor); TIMP,pkinase,DAG_PE-bind,RBD; 4.63
- 413436; AF238083; Hs.68061; sphingosine kinase 1; DAGKc;TM=M;; 4.63
- 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; ehfand,ldl_recept_a;SS=M; 4.62
- 442590; AI002686; Hs.130313; ESTs; none,Y_phosphatase,Band_41,connexin; 4.62
- 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium binding domain; ehfand;SS=M; 4.62
- 423740; Y07701; Hs.293007; aminopeptidase puromycin sensitive; Peptidase_M1,Armado_seg; 4.61
- 429300; AB011108; Hs.198891; serine/threonine-protein kinase PRP4 homolog; pkinase;TM=M;; 4.60
- 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 4.60
- 412942; AL120344; Hs.75074; mitogen-activated protein kinase-activated protein kinase 2; pkinase;TM=M;; 4.60
- 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPc; 4.59
- 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); EGF,lectin_c,sushi;TM=M;SS=M; 4.59
- 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 4.59
- 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,WW,RhoGAP;SS=M; 4.58
- 447312; AI434345; Hs.36908; activating transcription factor 1; rrm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIIS,AT_hook,SAM;TM=M;; 4.58
- 435254; AW194689; Hs.30778; ESTs; pkinase,Bacterial_PQQ;none; 4.58
- 426925; NM_001196; Hs.316889; Homo sapiens cDNA: FLJ22373 fis, clone HRC06741; Esterase,enolase,Peptidase_S9;TM=M;; 4.58
- 421685; AF189723; Hs.106778; ATPase, Ca transporting, type 2C, member 1; Cation_ATPase_C,Cation_ATPase_N,E1-E2_ATPase,Hydrolase,XPG_N;TM=Y;; 4.58
- 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; fn3,ig,Y_phosphatase,MAM;TM=Y;SS=M; 4.58
- 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rrm,PAP_assoc;TM=Y;SS=M; 4.57
- 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT2RM4000200; none,none; 4.57
- 409581; U66243; Hs.55039; mitogen-activated protein kinase 12; pkinase;SS=M; 4.57
- 423184; NM_004428; Hs.1624; ephrin-A1; Ephrin;TM=M;SS=M; 4.56
- 443920; AL037764; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; none,FMO-like; 4.56
- 422627; BE336857; Hs.118787; transforming growth factor, beta-induced, 68kD; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 4.56
- 418869; AW516565; ; gb:qx01d05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone 3' similar to contains Alu repetitive element;contains element MER11 repetitive element ;, mRNA sequence; none,RasGAP,WW,IQ; 4.56
- 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus receptor; SPX,EXS;TM=Y;; 4.56
- 437157; BE048860; Hs.120655; ESTs; IRK;none; 4.55
- 422769; AA938905; Hs.120017; olfactory receptor, family 7, subfamily E, member 38 pseudogene; none,none; 4.55
- 457918; AL359590; Hs.162604; hypothetical protein DKFZp762M186; PLDc;TM=M;; 4.55
- 434467; BE552368; Hs.231853; Homo sapiens cDNA FLJ13445 fis, clone PLACE1002962; 7tm_1,none; 4.55
- 421140; AA298741; Hs.102135; signal sequence receptor, delta (translocon-associated protein delta); none;TM=Y;SS=M; 4.55
- 406364; ; Target Exon; hexapep;TM=M;; 4.55
- 434682; AA827165; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; ig;none; 4.54
- 438939; H21012; Hs.287657; Homo sapiens cDNA: FLJ21291 fis, clone COL01963; F5_F8_type_C,pkinase,Ets;none; 4.54
- 433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; EF_TS,UBA;; 4.54
- 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;SS=M; 4.54
- 408956; AK001868; Hs.49344; hypothetical protein FLJ11006; ion_trans;TM=Y;; 4.54
- 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related); SH3;TM=M;; 4.53
- 410226; AI831958; Hs.61053; hypothetical protein; SH3,TPR;TM=M;; 4.53
- 422753; AI928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); Sm;SS=M; 4.52
- 418355; L42563; Hs.1165; ATPase, H7 transporting, nongastric, alpha polypeptide; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase;TM=Y;; 4.52
- 400261; ; Eos Control; ig,MHC_IL_beta;TM=Y;SS=M; 4.52
- 444633; AF111713; Hs.286218; junctional adhesion molecule 1; ig;TM=Y;SS=M; 4.52
- 422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo sapiens cDNA, mRNA sequence; Sec7,PH,ANF_receptor,lig_chan,WD40,IRK; 4.52

- 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none,none; 4.51
 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;; 4.51
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin;TM=M;; 4.51
 5 457906; AW975939; Hs.153290; Homo sapiens cDNA FLJ14318 fis, clone PLACE3000402; none,pkinase; 4.51
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 4.51
 429690; AW956329; Hs.23721; ESTs; none,sugar_tr,Ribosomal_S25; 4.50
 424618; L29472; Hs.1802; major histocompatibility complex, class II, DO beta; ig,MHC_II_beta;TM=Y;SS=M; 4.50
 444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 4.50
 10 405490; ; NM_031414;Homo sapiens serine/threonine kinase 31 (STK31), transcript variant 1, mRNA.; pkinase,TUDOR;TM=M;; 4.50
 424494; U78575; Hs.149256; phosphatidylinositol-4-phosphate 5-kinase, type I, alpha; PIP5K;SS=M; 4.50
 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C,G-alpha,arf;TM=M;SS=M; 4.50
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22_Claudin,none; 4.50
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; SH2,Y_phosphatase,DSPc;TM=M;; 4.50
 15 429556; AW139399; Hs.98988; ESTs; none;TM=M;; 4.50
 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y;; 4.49
 425209; AL049761; Hs.155140; casein kinase 2, alpha 1 polypeptide; pkinase,ABC1;TM=M;; 4.49
 425695; NM_005401; Hs.159238; protein tyrosine phosphatase, non-receptor type 14; Y_phosphatase,Band_41,DSPc;TM=M;; 4.49
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M;; 4.49
 20 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPc;SS=M; 4.48
 400755; AA635062; ; Homo sapiens mRNA; cDNA DKFZp43400515 (from clone DKFZp43400515); zf-C3HC4,CARD,BIR;TM=M;; 4.48
 425566; AW162943; Hs.250618; UL16 binding protein 2; ldl_recept_a,PKD,MHC_I;TM=M;SS=Y; 4.48
 410151; X15723; Hs.59242; paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein); Peptidase_S8,P;TM=Y;SS=M; 4.48
 423536; L22075; Hs.1666; guanine nucleotide binding protein (G protein), alpha 13; UCR_hinge,G-alpha,arf;TM=M;; 4.48
 25 424711; NM_005795; Hs.152175; calcitonin receptor-like; 7tm_2,HRM;TM=Y;SS=M; 4.48
 427878; C05766; Hs.181022; CGI-07 protein; none,zf-C2H2; 4.48
 443991; NM_002250; Hs.10082; potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 4.48
 422605; H16646; Hs.118666; hypothetical protein PP591; PAPS_reduct,MoCF_biosynth; 4.47
 410583; AW770280; Hs.36258; ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]; SH3,PDZ,Guanylate_kin,none; 4.47
 30 434419; AL046060; Hs.296938; dual specificity phosphatase 7; DSPc;TM=M;; 4.47
 410032; BE065985; ; gb:RC3-BT0319-120200-014-a09 BT0319 Homo sapiens cDNA, mRNA sequence; abhydrolase_2,none; 4.46
 423078; M35198; Hs.123125; integrin, beta 6; integrin_B,EGF_pp-binding;TM=Y;SS=M; 4.46
 400263; ; Eos Control; GTP_EFTU,EGF_C,GTP_EFTU_D2,serpin;TM=M;; 4.46
 441406; Z45957; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase;TM=M;; 4.45
 35 434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; none;TM=M;; 4.45
 413227; M79082; ; ESTs; none,none; 4.45
 441321; H17182; Hs.7771; B-cell associated protein; Band_7;TM=M;; 4.45
 457194; H20669; Hs.35406; ESTs, Highly similar to unnamed protein product [H.sapiens]; none,pkinase,PBD; 4.45
 414745; AA160511; Hs.5326; amino acid system N transporter 2; porcupine; none,none; 4.45
 40 404276; ; NM_002944;Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA.; fn3,pkinase,DUF139;TM=Y;SS=M; 4.45
 426966; AL493134; ; sclerostin; DAN;TM=M;SS=M; 4.45
 408873; AL046017; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none,none; 4.44
 426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFZp586B0220 (from clone DKFZp586B0220); pkinase,none; 4.44
 432798; AA565309; Hs.194015; ESTs; integrin_B,Sema,PSI,TIG,none; 4.44
 45 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 4.44
 417886; AA214584; ; ESTs; SPRY,7tm_3,ANF_receptor,none; 4.43
 452098; AI858183; ; gb:wl46a12.x1 NCL_CGAP_Ut1 Homo sapiens cDNA clone 3' similar to contains Alu repetitive element,, mRNA sequence; SH3,none; 4.43
 426874; N67325; Hs.347487; ESTs; SH3,TonB_boxC,none; 4.43
 422714; AB018335; Hs.119387; KIAA0792 gene product; DUF221;TM=Y;SS=M; 4.42
 50 410741; Z11695; Hs.324473; mitogen-activated protein kinase 1; pkinase,none; 4.42
 432193; AA372264; Hs.273193; hypothetical protein FLJ10706; pkinase;TM=M;; 4.41
 409506; NM_006153; Hs.54589; NCK adaptor protein 1; SH2,SH3;TM=M;; 4.41
 429390; AB040942; Hs.201500; KIAA1509 protein; none;TM=M;; 4.41
 421859; AA356620; Hs.108947; KIAA0050 gene product; ank,PH,ArfGAP;SS=M; 4.41
 55 451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none,none; 4.41
 421748; NM_014718; Hs.107809; KIAA0726 gene product; cadherin;TM=Y;; 4.40
 410416; BE410072; Hs.63304; protein phosphatase methyltransferase-1; none;TM=M;; 4.40
 450457; AA367701; Hs.6639; KIAA1624 protein; none;TM=M;SS=M; 4.40
 433029; NM_014322; Hs.279926; opsin 3 (encephalopsin); 7tm_1,Monoxygenase;TM=Y;SS=M; 4.40
 60 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase;TM=M;; 4.40
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm_1;TM=Y;SS=M; 4.40
 440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; SPRY,BAG,UPF0001; 4.40
 451154; AA015879; Hs.33536; ESTs; TIMP,none; 4.40
 433895; AI287912; Hs.3628; mitogen-activated protein kinase kinase kinase kinase 4; pkinase,zf-C4,CNH,ERM;TM=M;; 4.40
 422034; AC006486; Hs.333069; Ets2 repressor factor; Ets;TM=M;; 4.39
 65 444009; AI380792; Hs.135104; ESTs; TNFR_c6,TIL,none; 4.39
 420020; BE295866; Hs.94382; adenosine kinase; pfkB;SS=M; 4.39
 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, complete cds; none;TM=Y;SS=M; 4.39
 417655; AA780791; Hs.14014; hypothetical protein FLJ14813; pkinase,pkinase_C;TM=M;; 4.39
 402915; ; ENSP00000202587; Bicarbonate transporter-related protein BTR1.; HCO3_cotransp;TM=Y;; 4.39
 70 453199; AI336266; Hs.32353; mitogen-activated protein kinase kinase kinase 4; pkinase;TM=M;; 4.38
 416033; NM_012201; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR;TM=Y;SS=M; 4.38
 453672; U73531; Hs.34526; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 4.38
 437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365O12.1 [H.sapiens]; GPS,7tm_2;TM=Y;; 4.38
 420039; NM_004605; Hs.94581; sulfotransferase family, cytosolic, 2B, member 1; Sulfotransfer;SS=M; 4.38
 75 412834; R77123; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone LNG00414; 7tm_1,none; 4.38
 452203; X57522; ; transporter 1, ATP-binding cassette, sub-family B (MDR/TAP); ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 4.37
 425317; AW205118; Hs.210546; interleukin 21 receptor; none;TM=Y;SS=M; 4.37
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 4.37
 80 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fis, clone Y79AA1001384, highly similar to Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA; none,none; 4.37
 434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M;; 4.37
 412596; AA161219; Hs.799; diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor); EGF;TM=Y;SS=M; 4.36
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; fn3;SS=M; 4.36

- 432987; AI864771; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none; TM=Y; SS=M; 4.36
- 436943; AA773838; Hs.5353; caspase 10, apoptosis-related cysteine protease; ICE_p10, ICE_p20, DED; TM=M; 4.36
- 457897; AI356125; Hs.345168; ESTs, Weakly similar to HXA2_HUMAN HOMEBOX PROTEIN HOX-A2 [H.sapiens]; homeobox; NA; NA; 4.36
- 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); Sema, kinase, TIG, PSI; none; 4.36
- 5 413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidylinositol-specific); SH2, SH3, C2, PH, PI-PLC-Y, PI-PLC-X, PDGF; SS=M; 4.35
- 408101; AW968504; Hs.123073; CDC2-related protein kinase 7; none; none; 4.35
- 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); Man-6-P_recep; TM=M; SS=M; 4.35
- 10 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; aldo_ket_red; none; 4.35
- 438937; AW952654; Hs.244624; ESTs; EPH_lbd, kinase, fn3, SAM; none; 4.35
- 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; none; lectin_c; 4.35
- 436540; BE397032; Hs.14468; hypothetical protein MGC14226; rrm, 7tm_1, SNF; TM=M; 4.34
- 435267; N23797; Hs.110114; ESTs; none; Syja_N, Exo_endo_phos; 4.34
- 405616; ; Target Exon; none; SH3, BAR; 4.34
- 15 432141; BE410964; Hs.272736; nuclear receptor binding protein; kinase; TM=M; 4.33
- 417927; R73095; Hs.24122; ESTs; none; kinase; 4.33
- 429849; U33053; Hs.2499; protein kinase C-like 1; kinase, kinase_C, HR1; TM=M; 4.33
- 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2; TM=Y; 4.33
- 453863; X02544; Hs.572; orosomucoid 1; lipocalin, aldehyd, ubiquitin, IRK; SS=M; 4.33
- 20 400847; ; NM_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA; EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.33
- 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT, FATC, PI3_PI4_kinase; TM=M; 4.33
- 413858; NM_001610; Hs.75589; acid phosphatase 2, lysosomal; acid_phosphat; TM=Y; SS=M; 4.33
- 442539; AL119506; Hs.58220; Homo sapiens cDNA: FLJ23005 fis, clone LNG00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP, adenylate kinase; 4.33
- 25 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; IMP4; TM=M; 4.32
- 436703; AW880614; Hs.146381; RNA binding motif protein, X chromosome; rrm, SH3, PH, CH, RhoGEF; 4.32
- 414899; AW975433; Hs.36288; ESTs; kinase, SH2, SH3; none; 4.32
- 444895; AI674383; Hs.22891; solute carrier family 7 (cationic amino acid transporter, y system), member 8; ASC, death, TNFR_c6; 4.31
- 30 415135; AW673559; Hs.78040; KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1; ER_lumen_recept; none; 4.31
- 444070; NM_015367; Hs.10267; MLI1 protein; Bcl-2; TM=Y; 4.31
- 422611; AA158177; Hs.118722; fucosyltransferase 8 (alpha (1,6) fucosyltransferase); SH3, K-box; TM=M; SS=Y; 4.31
- 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; bromodomain; TM=M; 4.30
- 440983; M20681; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; sugar_tr; TM=Y; SS=M; 4.30
- 35 414080; AA135257; Hs.47783; B aggressive lymphoma gene; A1p; TM=M; 4.30
- 415072; BE253687; Hs.77876; Homo sapiens, clone IMAGE:3461982, mRNA, partial cds; Metallophos, Armadillo_seg; TM=M; 4.30
- 442994; AI026718; Hs.16954; ESTs; ank, kinase, death, Ribosomal_S14; 4.30
- 432328; AI572739; Hs.195471; 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3; PGAM, 6PF2K; TM=M; 4.29
- 439490; AW249197; Hs.100043; ESTs, Weakly similar to A46302 PTB-associated splicing factor, long form [H.sapiens]; none; TM=M; 4.29
- 40 422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (from clone DKFZp761E212); none; Na_H_Exchange; 4.29
- 415214; AI445236; Hs.125124; EphB2; fn3, kinase, SAM, EPH_lbd; TM=Y; SS=M; 4.29
- 430316; NM_000875; Hs.239176; insulin-like growth factor 1 receptor; fn3, Furin-like, kinase, Recep_L_domain; TM=M; SS=M; 4.29
- 429099; BE439952; Hs.196177; phosphorylase kinase, gamma 2 (testis); kinase, Bac_DNA_binding; TM=M; 4.29
- 425843; BE313280; Hs.159627; death associated protein 3; myb_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; 4.28
- 45 437603; AW979259; Hs.293673; ESTs; death; none; 4.28
- 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triphosphate pyrophosphatase); Ham1p_like; TM=M; 4.28
- 424512; X53002; Hs.149846; integrin, beta 5; integrin_B, EGF; TM=Y; SS=M; 4.28
- 442980; AA857025; Hs.8878; kinesin-like 1; kinesin, Luteo_ORF3, DUF164; TM=M; 4.28
- 420166; AW732276; Hs.95583; transmembrane 4 superfamily member (tetraspan NET-7); transmembrane4; TM=Y; SS=M; 4.27
- 50 409582; R27430; Hs.271565; ESTs; none; Neur_chan_LBD, Neur_chan_memb; 4.27
- 439096; AA830185; ; ESTs; ras; none; 4.27
- 414561; AI064813; Hs.195155; Homo sapiens amino acid transport system N2 (SN2) mRNA, complete cds; Aa_trans; TM=Y; 4.27
- 411835; U29343; Hs.72550; hyaluronan-mediated motility receptor (RHAMM); bZIP; SS=M; 4.27
- 428781; AF164799; Hs.193384; putative 28 kDa protein; kinase, DAG_PE-bind, kinase_C, OPR; SS=M; 4.27
- 55 430603; AA148164; Hs.247280; HBV associated factor; zf-C3HC4, zf-RanBP, kinase; 4.27
- 415149; X12451; Hs.78056; cathepsin L; Peptidase_C1; SS=M; 4.26
- 444838; AV651680; Hs.208558; ESTs; integrin_A, FG-GAP; none; 4.26
- 402328; ; Target Exon; kinase; TM=M; 4.26
- 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none; none; 4.26
- 420942; H03514; Hs.15589; ESTs; none; kinase; 4.26
- 60 453902; BE502341; Hs.3402; ESTs; none; none; 4.26
- 425505; AL036458; ; gb:DKFZp564D2062_r1 564 (synonym: htrb2) Homo sapiens cDNA clone DKFZp564D2062 5', mRNA sequence; arf, G-alpha; none; 4.26
- 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor 3A; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 4.26
- 432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met-related tyrosine kinase); kinase, Sema, PSI, TIG, A4_EXTRA; TM=M; SS=M; 4.26
- 65 417007; AF224741; Hs.80768; chloride channel 7; CBS, voltage_CLC; TM=Y; 4.26
- 447960; AW954377; Hs.26412; ring finger protein 26; zf-C3HC4; TM=Y; SS=M; 4.26
- 442300; AI765908; Hs.129166; ESTs; none; SS=M; 4.25
- 421856; NM_016447; Hs.108931; MAGUK protein p57; Protein Associated with Lins 2; SH3, PDZ, Guanylate_kin, L27; TM=M; 4.25
- 452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PLACE1010076; kinase, Activin_recp; none; 4.25
- 70 422451; AA310753; Hs.42491; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; PDZ, SH2, STAT, STAT_bind, STAT_prot; none; 4.25
- 453955; AW579207; Hs.304666; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; fn3, ig, MAM; none; 4.25
- 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substrate; SH3; TM=M; 4.25
- 419133; U46116; Hs.89627; protein tyrosine phosphatase, receptor type, G; fn3, Y_phosphatase, carb_anhydrase, DSPc; TM=Y; SS=M; 4.25
- 419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; aa_permeases; TM=Y; SS=M; 4.25
- 75 415198; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M; 4.24
- 416440; AI823912; Hs.79335; Homo sapiens, Similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1, clone MGC:15280, mRNA, complete cds; SWIB; TM=M; 4.24
- 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothetical protein [H.sapiens]; none, spectrin, SH3, PH, CH; 4.24
- 449444; AW818436; Hs.23590; solute carrier family 16 (monocarboxylic acid transporters), member 4; none; TM=Y; SS=M; 4.24
- 80 433848; AF095719; Hs.93764; carboxypeptidase A4; Zn_carbOpept, Propep_M14; SS=M; 4.24
- 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glucose transporter), member 10; sugar_tr; TM=Y; SS=M; 4.24
- 412681; AW983655; Hs.172004; titin; fn3, ig, SGXXSG, kinase; TM=M; 4.24
- 424653; AW977534; Hs.151469; calcium/calmodulin-dependent serine protein kinase (MAGUK family); none; none; 4.24
- 421066; AU076725; Hs.101408; branched chain aminotransferase 2, mitochondrial; aminotran_4; 4.23

- 428338; AF147765; Hs.232093; ESTs; fn2,CIMR;TM=M;SS=M; 4.23
 443329; BE262943; Hs.9234; hypothetical protein MGC1936; none;TM=Y;SS=M; 4.23
 432314; AA533447; Hs.312989; ESTs; Xlink;none; 4.23
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 4.23
 5 454166; AW993356; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 4.23
 442596; AI457102; Hs.347970; Human glucose transporter pseudogene; none;none; 4.23
 442549; AI751601; Hs.8375; TNF receptor-associated factor 4; MATH,zf-TRAF,zf-C3HC4;SS=M; 4.22
 424154; AF026004; Hs.141660; chloride channel 2; voltage_CLC,CBS,EPO_TPO,PC_rep; 4.22
 433419; AI830342; Hs.211272; ESTs; transmembrane4;none; 4.22
 10 421921; H83363; Hs.6820; translocase of inner mitochondrial membrane 10 (yeast) homolog; zf-Tim10_DDP,efhand,CH,spectrin,serpin;TM=M;; 4.22
 445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK;none; 4.22
 424812; AF059252; Hs.153299; DOM-3 (C. elegans) homolog Z; none;TM=M; 4.22
 410668; BE379794; Hs.65403; hypothetical protein; death,TNFR_c6;TM=Y;SS=M; 4.22
 15 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic acid transporters), member 6; none;none; 4.22
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;; 4.21
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; none;none; 4.21
 400208; ; Eos Control; FCH,RhoGAP,SH3;TM=M; 4.21
 405369; ; NM_005569; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA.; pkinase,LIM,PDZ;SS=M; 4.21
 20 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2;TM=M; 4.21
 441208; AI339704; Hs.150401; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ion_trans,RYDR_JTPR,MIR;none; 4.21
 427217; AA399272; Hs.144341; ESTs; ANP,GHMP_kinases;none; 4.21
 400845; ; NM_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA.; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.21
 25 422667; H25642; ; ESTs; FMO-like,FMO-like; 4.21
 450056; BE047394; Hs.8208; ESTs, Weakly similar to S71512 hypothetical protein T2 - mouse [M.musculus]; ABC_tran,ABC_membrane,ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.20
 448950; AF288687; Hs.9275; CGI-152 protein; E1-E2_ATPase,Hydrolase;TM=Y;; 4.20
 30 408634; AW407254; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none;none; 4.20
 422335; AA375957; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none;none; 4.20
 426754; NM_014264; Hs.172052; serine/threonine kinase 18; pkinase;TM=M; 4.20
 435810; BE349853; Hs.2785; keratin 17; zf-Tim10_DDP,SH2,SH3,pkinase,PH,BTK,Ribosomal_L44; 4.20
 446143; BE245342; Hs.306079; sec61 homolog; NUDIX,secY,E1_dehydrog,transkel_pyr;TM=Y;SS=M; 4.20
 35 426626; AI124572; Hs.323879; inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma; zf-C2H2;TM=M;; 4.20
 403716; ; Target Exon; Adap_comp_sub,PDZ,DEP,DIX,Dishevelled,hexapep,W2,ABC_tran; 4.19
 415749; BE262529; Hs.78771; phosphoglycerate kinase 1; PGK;none; 4.19
 434599; AB002313; Hs.3989; plexin B2; PSI,Sema,TIG;NA;NA; 4.19
 412600; L28824; Hs.74101; spleen tyrosine kinase; SH2,pkinase; 4.19
 416738; N29218; Hs.40290; ESTs; ABC_tran,ABC_membrane;none; 4.19
 40 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; DEAD,helicase_C,PRK,AIP3;TM=M;; 4.19
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none;none; 4.19
 407305; AA715284; ; gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens cDNA clone similar to contains Alu repetitive element, mRNA sequence; pkinase,integrin_B,Sema,PSI,TIG;none; 4.18
 45 452880; AA029332; Hs.87549; ESTs; none,integrin_B; 4.18
 428245; AF151048; Hs.183180; anaphase promoting complex subunit 11 (yeast APC11 homolog); none;SS=M; 4.18
 421964; X73079; Hs.288579; polymeric immunoglobulin receptor; ig,Cobalamin_bind;TM=M;SS=M; 4.18
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M; 4.18
 421790; AW896201; Hs.22654; sodium channel, voltage-gated, type I, alpha polypeptide; ion_trans,IQ,PEP-utilizers_C;TM=Y;; 4.18
 50 429668; AA626142; Hs.179991; ESTs, Weakly similar to S28942 protein kinase C [H.sapiens]; none;none; 4.18
 443068; AI188710; ; ESTs; Endonuclease,pkinase,Activin_recpt;none; 4.18
 418827; BE327311; Hs.47166; HT021; none;TM=M;; 4.18
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine protease; ICE_p10,ICE_p20,DED;TM=M; 4.18
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M; 4.18
 55 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; none;none; 4.18
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ;SS=M; 4.18
 413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like 1; SH2,SAM,Exo_endo_phos;SS=M; 4.18
 424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,WD40,IRK;TM=M; 4.17
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none;none; 4.17
 60 431544; AK000770; Hs.299329; Homo sapiens cDNA FLJ20763 fis, clone COL09911; none;none; 4.17
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; CBS,IMPDH_C,IMPDH_N,NPD;TM=M;; 4.17
 452012; AA307703; Hs.279766; kinesin family member 4A; kinesin,DNA_topoisolV,K-box;TM=M; 4.17
 425606; U52112; Hs.158331; renin-binding protein; none; 4.16
 416817; AA398045; Hs.104679; ESTs; Furin-like,pkinase,Recep_L_domain,fn3;none; 4.16
 65 402447; ; C1000201.gij204416[gb]AAA02627.1| (L05195) fructose transporter [Rattus norvegicus] gjl44; none;TM=Y;SS=M; 4.16
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; Euk_porin;TM=M;SS=M; 4.15
 426395; BE151985; Hs.5722; hypothetical protein FLJ23316; pkinase;none; 4.15
 404140; ; NM_006510; Homo sapiens ret finger protein (RFP), transcript variant alpha, mRNA.; zf-C3HC4,SPRY,zf-B_box;SS=M; 4.15
 432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate synthase 2; APS_kinase,ATP-sulfurylase;TM=M; 4.15
 70 405516; ; ENSP00000200457; Thyroid receptor interacting protein 6 (TRIP6) (OPA-interacting protein 1) (Zyxin related protein 1) (ZRP-1); LIM;TM=M;; 4.15
 448390; AL035414; Hs.21068; hypothetical protein; FGGY_C;TM=M; 4.15
 435732; AF229178; Hs.123136; leucine rich repeat and death domain containing protein; none;none; 4.15
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol_BP,pkinase;TM=M; 4.15
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor, pi; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 4.14
 75 424339; BE257148; Hs.145416; endoglycan; none;TM=Y;SS=M; 4.14
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog; ig,pkinase;TM=Y;SS=M; 4.14
 440524; R71264; Hs.11098; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF;none; 4.14
 436115; AW512033; Hs.102004; ESTs; pkinase;none; 4.14
 447050; NM_016314; Hs.17200; STAM-like protein containing SH3 and ITAM domains 2; SH3,VHS,UIM;SS=M; 4.14
 80 418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 4.14
 420727; H75701; Hs.99886; complement component 4-binding protein, beta; sushi;SS=M; 4.14
 433075; NM_002959; ; sortilin 1; Exo_endo_phos,Atrophin-1,BNR,Kelch;TM=M; 4.14
 422783; AA598956; Hs.120439; ethanolamine kinase; Choline_kinase;TM=Y; 4.14
 410726; AI623859; Hs.15936; ESTs; pkinase,pro_isomerase;none; 4.14

417903; NM_002342; Hs.1116; lymphotoxin beta receptor (TNFR superfamily, member 3); TNFR_c6; TM=M; SS=M; 4.14
 428307; W27393; Hs.183648; protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1; SAM,SH3,HS1_rep; 4.14
 442434; AA995787; Hs.129583; ESTs; IRK; none; 4.13
 438361; AA805666; Hs.146217; Homo sapiens cDNA: FLJ23077 fis, clone LNG05840; pkinase, pkinase_C, none; 4.13
 445580; AF167572; Hs.12912; skb1 (S. pombe) homolog; none; SS=M; 4.13
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; ehand, kazal, arf, ras, 7tm_1; TM=M; 4.13
 400252; ; NM_004651; Homo sapiens ubiquitin specific protease 11 (USP11), mRNA. substrate 1 (PTPNS1), mRNA; UCH-1, UCH-2; TM=M; 4.13
 446641; AL049229; Hs.15787; Homo sapiens mRNA; cDNA DKFp564O1016 (from clone DKFp564O1016); none, pkinase, PBD; 4.13
 400209; ; NM_001666; Homo sapiens Rho GTPase activating protein 4 (ARHGAP4), mRNA. VERSION NM_006083.2 GI; FCH, RhoGAP, SH3; TM=M; 4.13
 429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm, BAG; SS=M; 4.13
 411826; AW947946; Hs.26706; CGI-121 protein; none, DSPc; 4.13
 423189; M59371; Hs.171596; EphA2; fn3, pkinase, SAM, EPH_1b; TM=Y; SS=M; 4.12
 413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; integrin_B, Glyco_hydro_56; SS=M; 4.12
 414874; D26351; Hs.77515; inositol 1,4,5-triphosphate receptor, type 3; ion_trans, MIR, RYDR, ITPR; TM=Y; 4.12
 432047; NM_016247; Hs.272380; interphotoreceptor matrix proteoglycan 200; EGF, SEA; TM=Y; SS=M; 4.12
 451820; AW058357; Hs.199248; ESTs; 7tm_1; TM=Y; SS=M; 4.12
 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; zf-C2H2, BTB, K_tetra, WD40, Syntaxin; 4.12
 424539; L02911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK-2); pkinase, Activin_rec; TM=M; SS=M; 4.12
 405110; ; C7000199.gil12643960[sp]Q9Y6T7[KDGB_HUMAN DIACYLGLYCEROL KINASE, BETA (DIGLYCERIDE KINASE); none, none; 4.12
 441026; AW179058; Hs.99858; ribosomal protein L7a; pkinase, LRR, LRRCT, Ribosomal_L7Ae, none; 4.11
 443142; A1696513; Hs.108705; protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform; HEAT, Vitellogenin_N, HEAT_PBS; SS=M; 4.11
 450505; NM_004572; Hs.25051; plakophilin 2; Armadillo_seg; TM=M; 4.11
 459601; AL044470; Hs.270604; ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; none, SH3, PGAM, UBA; 4.10
 417300; A1765227; Hs.55610; solute carrier family 30 (zinc transporter), member 1; Cation_efflux; TM=Y; SS=M; 4.10
 427315; A179949; Hs.175563; Homo sapiens mRNA; cDNA DKFp564N0763 (from clone DKFp564N0763); none, spectrin, SH3, PH, CH; 4.10
 416239; AL038450; Hs.48948; ESTs; E1-E2_ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase, none; 4.10
 429311; AF080157; Hs.198998; conserved helix-loop-helix ubiquitous kinase; pkinase, none; 4.10
 412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); Exo_endo_phos, Atrophin-1, BNR, Kelch; TM=M; 4.10
 418420; AW604405; Hs.324874; hypothetical protein MGC3079; Phosphodiesterase; TM=Y; 4.10
 434396; AA632270; Hs.162851; Homo sapiens cDNA FLJ14317 fis, clone PLACE3000401; pkinase, none; 4.10
 454438; AA224053; Hs.172405; cell division cycle 27; SPRY, 7tm_3, ANF_receptor; 4.10
 439578; AW263124; Hs.315111; nuclear receptor co-repressor/HDAC3 complex subunit; WD40; TM=M; 4.10
 451995; A1827431; Hs.224645; ESTs, Weakly similar to IF16_HUMAN GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 [H.sapiens]; none, PAAD_DAPIN, HIN; 4.10
 420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TIT3 complex); ITAM; TM=M; SS=M; 4.10
 442942; AW167087; Hs.131562; ESTs; pkinase, none; 4.09
 428187; A1687303; Hs.285529; G protein-coupled receptor 49; 7tm_1, none; 4.09
 418838; AW385224; Hs.351198; ecdonucleotide pyrophosphatase/phosphodiesterase 5 (putative function); Phosphodiesterase; TM=Y; SS=M; 4.09
 416445; AL043004; Hs.79337; KIAA0135 protein; pkinase, PAS; TM=M; 4.08
 427001; NM_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2; pkinase; TM=M; 4.08
 403608; ; C3001199.gil7494834[pilr]T15308 hypothetical protein B0286.2 - Caenorhabditis elegans [41]; 7tm_1, 7tm_2, GPS, WIF; TM=Y; SS=M; 4.08
 427177; AB006537; Hs.173880; interleukin 1 receptor accessory protein; ig, TIR; TM=Y; SS=M; 4.08
 401241; AB028989; ; mitogen-activated protein kinase 8 interacting protein 3; Cys_knot, TGF-beta, vwa, vwc, vwd, TIL, DUF139; SS=M; 4.07
 444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligase Rsp5; potential epithelial sodium channel regulator; WWW, HECT, RNA_pol_A, none; 4.07
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 4.06
 426006; R49031; Hs.22627; ESTs; pkinase, TBC; 4.06
 434521; NM_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg, IBB; TM=M; 4.06
 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not available 7496841) [C.elegans]; 7tm_1, none; 4.05
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN, HIN; SS=M; 4.05
 413109; AW389845; Hs.110855; ESTs; PHO4, none; 4.05
 426457; AW894667; Hs.169965; chimerin (chimaerin) 1; DAG_PE-bind, RhoGAP, SH2; TM=M; 4.05
 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase, TrkA-N, 2-Hacid_DH_C; TM=M; 4.04
 429747; M87507; Hs.2490; caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase); CARD, ICE_p10, ICE_p20; SS=M; 4.04
 444378; R41339; Hs.12569; ESTs; ig, pkinase, LRR, LRRNT, LRRCT, none; 4.04
 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; none; TM=Y; SS=M; 4.04
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone LNG00414; 7tm_1, none; 4.04
 413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-related family, member 3; none, START; 4.04
 418540; A1821597; Hs.90877; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ank, CAP_GLY, 7tm_1; 4.03
 442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; rrm, IRK; SS=M; 4.02
 448659; AF191838; Hs.21712; TANK-binding kinase 1; pkinase; TM=M; 4.02
 412935; BE267045; Hs.75064; tubulin-specific chaperone c; none; 4.02
 414844; AA296874; Hs.77494; deoxyguanosine kinase; dNK; 4.02
 445817; NM_003642; Hs.13340; histone acetyltransferase 1; none; TM=M; 4.02
 426728; NM_007118; Hs.171957; triple functional domain (PTPRF interacting); SH3, ig, pkinase, PH, spectrin, RhoGEF; TM=M; 4.02
 420676; A1434780; Hs.4248; vav 2 oncogene; RhoGEF, PH, CH, SH2, SH3, DAG_PE-bind, none; 4.02
 405102; ; C15001220.gil4469558[gb]AAD21311.1 [AF126008] breast cancer nuclear receptor-binding auxi; DAG_PE-bind, PH, RhoGEF, DC1; SS=M; 4.02
 439964; A1732902; Hs.124652; Homo sapiens cDNA FLJ12376 fis, clone MAMMA1002494; pkinase, none; 4.01
 429680; AL035754; Hs.2474; toll-like receptor 1; LRR, LRRCT, TIR; TM=M; SS=M; 4.01
 453891; AB037751; Hs.36353; Homo sapiens mRNA full length insert cDNA clone EUOIMAGE 1035904; none, none; 4.01
 426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR motif, Y isoform [H.sapiens]; Kunitz_BPTI, Kunitz_BPTI, 7tm_2, HRM; 3.99
 424232; AB015982; Hs.143460; protein kinase C, nu; pkinase, DAG_PE-bind, PH; TM=M; 3.99
 408308; AL033377; Hs.44197; hypothetical protein DKFp564D0462; none, none; 3.98
 449517; AW500106; Hs.23643; serine/threonine protein kinase MASK; pkinase; TM=M; 3.98
 404185; ; Target Exon; sugar_tr; TM=Y; SS=M; 3.98
 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; none; TM=M; 3.98
 429638; A1916662; Hs.211577; kinectin 1 (kinesin receptor); bZIP, Tropomyosin, spectrin, LBP_BPI_CETP, B56, M; TM=Y; SS=M; 3.97
 417386; AL037228; Hs.82043; D123 gene product; NUDIX, secY, E1_dehydrog, transket_pyr; TM=Y; SS=M; 3.97
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; MORN, sugar_tr; TM=Y; SS=M; 3.96
 417183; R52089; Hs.172717; ESTs; pkinase, LRRCT, ig, LRR, LRRNT, none; 3.95
 439176; A1446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; none; TM=M; 3.94
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M; 3.94
 422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, subfamily J, member 2; IRK; TM=Y; 3.94

- 450746; D82673; Hs.278589; general transcription factor II, i; none,SH3,PX; 3.94
 418516; NM_006218; Hs.85701; phosphoinositide-3-kinase, catalytic, alpha polypeptide; PI3_PI4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B,none; 3.94
 414217; A1309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone LNG09846; none,NA,NA; 3.93
 416537; T99086; Hs.144904; nuclear receptor co-repressor 1; myb_DNA-binding,RNA_pol_A,none; 3.93
 450747; A1064821; Hs.318535; ESTs, Highly similar to 1818357A EWS gene [H.sapiens]; rrm,zf-RanBP,GAS2; 3.93
 444825; AW167613; ; mitogen-activated protein kinase kinase kinase 8; pkinase;TM=M;; 3.93
 408354; A1382803; Hs.159235; ESTs; none,none; 3.93
 453945; NM_005171; Hs.36908; activating transcription factor 1; rrm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M;; 3.93
 428532; AF157326; Hs.184786; TBP-interacting protein; Armadillo_seg,VHS,HEAT;TM=M;; 3.92
 413967; AW204431; Hs.117853; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Armadillo_seg,IBB,PHD,DDT,none; 3.91
 415906; A1751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fis, clone HRC02860; Ephrin,none; 3.91
 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none,none; 3.91
 440255; A1932285; Hs.160569; ESTs; none,pkinase; 3.90
 421077; AK000061; Hs.101590; hypothetical protein; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M;; 3.90
 433211; H11850; Hs.12808; MARK; pkinase,UBA,KA1;SS=M; 3.90
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M;; 3.90
 419609; U46415; Hs.270379; gb:HSU46415 Human pancreatic cancer cell line Patu 8988t Homo sapiens cDNA clone xs476, mRNA sequence; PWWP,none; 3.90
 433198; AA992841; Hs.27263; KIAA1458 protein; none,none; 3.89
 407721; Y12735; Hs.38018; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3; pkinase;TM=M;; 3.89
 427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none;TM=M;; 3.89
 453035; AW581943; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; none,none; 3.89
 446329; NM_013272; Hs.14805; solute carrier family 21 (organic anion transporter), member 11; kazal,OATP_N,OATP_C;TM=Y;SS=M; 3.89
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone;TM=M;; 3.88
 432074; AA525248; Hs.149723; ESTs; Y_phosphatase,none; 3.88
 435143; R12375; Hs.194600; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 3.87
 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese,none; 3.87
 428474; AB023182; Hs.184523; KIAA0965 protein; pkinase;TM=M;; 3.87
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT2RP2002066, highly similar to Rattus norvegicus transmembrane receptor Unc5H2 mRNA; death,ZU5;SS=M; 3.86
 415457; AW081710; Hs.7369; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; MORN,sugar_tr;TM=Y;SS=M; 3.86
 447061; D86964; Hs.17211; dedicator of cyto-kinesis 2; SH3;TM=M;; 3.86
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M;; 3.86
 451961; NM_003800; Hs.27345; RNA guanylyltransferase and 5'-phosphatase; mRNA_cap_enzyme,DSPc,DNA_ligase,mRNA_cap_C;TM=M;; 3.86
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-receptor type 2; Y_phosphatase;TM=Y;; 3.86
 446874; AW968304; Hs.56156; ESTs; none,RGS; 3.85
 418630; A1351311; Hs.251946; poly(A)-binding protein, cytoplasmic 1-like; pkinase,none; 3.85
 416140; A1918035; Hs.301198; roundabout (axon guidance receptor, Drosophila) homolog 1; none,none; 3.85
 425474; Z48054; Hs.158084; peroxisome receptor 1; TPR;TM=M;; 3.85
 413073; AL038165; Hs.75187; translocase of outer mitochondrial membrane 20 (yeast) homolog; MAS20,zf-A20,VPS9;TM=M;SS=M; 3.85
 411770; NM_014278; Hs.71992; heat shock protein (hsp110 family); HSP70;TM=M;; 3.84
 428782; X12830; Hs.193400; interleukin 6 receptor; fn3,ig;TM=Y;SS=M; 3.84
 450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig;TM=Y;SS=M; 3.84
 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine protease; CARD,ICE_p10,ICE_p20;SS=M; 3.83
 440332; A1218517; Hs.188051; ESTs; fn3,pkinase,SAM,EPH_lbd,none; 3.83
 445803; AV655264; Hs.4283; ESTs; pkinase,RGS,PH,myosin_head,Myosin_tail; 3.83
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH;TM=M;; 3.83
 414991; C17898; ; gb:C17898 Human placenta cDNA (Tfujiiwara) Homo sapiens cDNA clone GEN-554E10 5', mRNA sequence; Zip,none; 3.83
 423067; AA321355; Hs.285401; colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage); fn3;TM=Y;SS=M; 3.82
 419088; A1538323; Hs.52620; integrin, beta 8; integrin_B,none; 3.82
 411704; A1499220; Hs.71573; hypothetical protein FLJ10074; pkinase;TM=M;; 3.82
 459346; AW510557; Hs.258016; EST; none;TM=M;; 3.82
 445330; R52656; Hs.21691; ESTs; 7tm_1,none; 3.82
 451452; BE560065; Hs.26433; dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminophosphotransferase 1 (GlcNAc-1-P transferase); Glycos_transf_4;TM=Y;SS=M; 3.81
 405545; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.81
 448165; NM_005591; Hs.20555; meiotic recombination (S. cerevisiae) 11 homolog B; Metallophos,Ribosomal_L15e;SS=M; 3.81
 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; ig;TM=Y;SS=M; 3.80
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate transporter), member 1; PHO4,LIM;TM=M;; 3.80
 421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo_seg;SS=M; 3.80
 438581; AW977766; Hs.292133; ESTs, Moderately similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; pkinase,RIO1,none; 3.79
 439199; R40373; Hs.26299; ESTs; ion_trans,none; 3.78
 450931; N25156; Hs.25648; tumor necrosis factor receptor superfamily, member 5; TNFR_c6;TM=Y;SS=M; 3.78
 417691; AU076610; Hs.82399; low density lipoprotein receptor defect C complementing; none;SS=M; 3.78
 430355; NM_006219; Hs.239818; phosphoinositide-3-kinase, catalytic, beta polypeptide; PI3_PI4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B;TM=M;; 3.78
 448119; H38587; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y;; 3.78
 442013; AA506476; Hs.10600; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSS, GSSs and CpG islands. Contains the NIFS gene for cysteine desulfurase, two genes for novel proteins and the gene for the splicing factor CC1.3 with a second isoform (CC1.; none,none; 3.77
 425481; AW978162; Hs.18571; ESTs; none,Oxysterol_BP; 3.77
 411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA1330 protein [H.sapiens]; RNA_pol_A,ig,MHCK_EF2_kinase;SS=M; 3.77
 426866; U02330; Hs.172816; neuregulin 1; Peptidase_M49,EGF,ig,Neuregulin;TM=M;; 3.77
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 3.77
 434398; AA121098; Hs.3838; serum-inducible kinase; pkinase,POLO_box;TM=M;; 3.77
 415485; AW272990; Hs.18571; ESTs; none,Oxysterol_BP; 3.76
 453226; AA641926; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase_c,none; 3.76
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M;; 3.76
 424842; AA034127; Hs.153487; signal transducing adaptor molecule (SH3 domain and ITAM motif) 1; SH3,VHS,UIM;TM=M;; 3.75
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M;; 3.75
 419952; AK000967; Hs.93872; KIAA1682 protein; none;TM=M;; 3.75
 425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;; 3.75
 431696; AA259068; Hs.267819; protein phosphatase 1, regulatory (inhibitor) subunit 2; none;SS=M; 3.75

444184; T87841; Hs.282990; Human DNA sequence from clone RP1-28H20 on chromosome 20q13.1. Contains part of a gene for a novel protein similar to membrane transport proteins, the 5' end of a novel gene, ESTs, STSs, GSSs and three CpG islands; pkinase,RIO1,APH,KOW;TM=M; 3.75

405411; ; ENSP00000252213:SODIUM BICARBONATE COTRANSPORTER; none;TM=Y;SS=M; 3.75

405602; ; Target Exon; pkinase;SS=M; 3.75

429355; AW973253; Hs.292689; ESTs; pkinase,bZIP,Armadoillo_seg,none; 3.75

430153; AW968128; Hs.336679; ESTs; pkinase,none; 3.74

414180; AI863304; Hs.120905; Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391; PI3_Pi4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B,none; 3.74

432236; AA531132; ; gb:nj47h06.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone, mRNA sequence; pkinase,none; 3.74

433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds; none,spectrin,SH3,PH,CH; 3.74

426485; NM_006207; Hs.170040; platelet-derived growth factor receptor-like; ig;SS=M; 3.74

408414; AI114688; Hs.17998; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; fn3,ig;TM=Y;SS=M; 3.73

409793; AI825463; Hs.147996; protein kinase, X-linked; pkinase,pkinase_C;TM=M; 3.73

412456; T32689; Hs.7859; ESTs; BAG,none; 3.73

407894; AJ278313; Hs.41143; phosphoinositide-specific phospholipase C-beta 1; C2,PI-PLC-Y,PI-PLC-X;TM=M; 3.73

442229; AI885776; Hs.8164; Mulibrey nanism; MATH,DENN,GRAM,zf-B_box,dDENN,uDENN;SS=M; 3.73

450161; AI088196; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA sequence; ig,pkinase,none; 3.72

408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc;TM=M; 3.72

417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofillin_ADF;SS=M; 3.72

403391; ; C3001164*.gil1730196[sp]P50573[GAR3_RAT GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-3 SUBUNIT PRE; none;TM=Y; 3.72

417527; AA203524; ; gb:zx56e10.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone 5', mRNA sequence; SH3;SS=M; 3.71

428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase); pkinase;TM=M; 3.71

428180; AI129767; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; G-alpha,arf;TM=M; 3.71

422127; AW504286; Hs.112049; SET binding factor 1; dDENN,DENN,GRAM,PH;SS=M; 3.70

430570; AI417881; Hs.292464; ESTs; 7Im_2,Fz,Frizzled,none; 3.70

452561; AI692181; Hs.49169; KIAA1634 protein; TPR,PDZ,WW,Guanylate_kin;TM=M; 3.69

432336; NM_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm,pkinase;TM=M; 3.69

419945; AW290975; Hs.118923; ESTs; SH3,PDZ,Guanylate_kin,transferrin; 3.69

426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3,PDZ,Guanylate_kin;TM=M; 3.68

436534; AA721628; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; ig;TM=Y;SS=M; 3.68

407202; NS8172; Hs.109370; ESTs; F5_F8_type_C,pkinase,Ets,none; 3.67

420297; AI628272; Hs.88323; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; pkinase,TUDOR,none; 3.67

417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase;TM=M; 3.67

425304; AA463844; Hs.31339; fibroblast growth factor 11; FGF,Neur_chan_LBD,Neur_chan_memb,none; 3.67

418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 3.67

419511; AA429750; Hs.75113; general transcription factor IIA; Glypican,none; 3.66

424315; AW614850; Hs.193384; putative 28 kDa protein; none,none; 3.66

413076; U10564; Hs.75188; weel (S. pombe) homolog; pkinase;TM=M; 3.66

425838; NM_014071; Hs.159613; nuclear receptor coactivator RAP250; peroxisome proliferator-activated receptor interacting protein; thyroid hormone receptor binding protein; none;TM=M; 3.65

446983; AA157484; Hs.97199; complement component C1q receptor; EGF,lectin_c,Tissue_fac,Xlink,TIL;TM=Y;SS=M; 3.65

434350; AL042940; Hs.93872; KIAA1682 protein; none,none; 3.65

457317; AA683016; Hs.12210; hypothetical protein FLJ13732 similar to tensin; SH2;TM=M; 3.65

434416; AA805903; Hs.59498; cell division cycle 2-like 5 (cholinesterase-related cell division controller); pkinase,none; 3.65

410174; AA306007; Hs.59461; DKFZP434C245 protein; none,DSPc; 3.65

423598; BE247600; Hs.155538; ESTs; 7Im_1;TM=Y;SS=M; 3.65

440861; BE244115; Hs.7482; KIAA0682 gene product; rrm,Guanylate_kin;TM=M; 3.64

454954; AW993013; Hs.49169; KIAA1634 protein; TPR,PDZ,WW,Guanylate_kin;TM=M; 3.64

430250; NM_016929; Hs.283021; chloride intracellular channel 5; none;TM=M; 3.64

450587; AI828854; Hs.258538; striatin, calmodulin-binding protein; pkinase,WD40;TM=Y; 3.64

424893; AW295112; Hs.153648; Homo sapiens cDNA FLJ13303 fis, clone OVARC1001372, highly similar to Homo sapiens liprin-alpha4 mRNA; SAM;SS=M; 3.64

425645; AA361027; ; gb:EST70242 T-cell lymphoma Homo sapiens cDNA 5' end, mRNA sequence; HMG_box,DNA_mis_repair,HATPase_c,none; 3.64

417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,Integrin_B;SS=M; 3.63

415292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M; 3.63

412314; AA825247; Hs.250899; heat shock factor binding protein 1; 7Im_1;TM=Y;SS=M; 3.63

418303; AA215701; Hs.186541; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; eIF5_eIF2B,W2,pkinase,UBA,KA1; 3.63

452716; AI914925; Hs.222240; ESTs; SH2,STAT,STAT_bind,STAT_prot,none; 3.63

403869; ; NM_004520*.Homo sapiens kinesin heavy chain member 2 (KIF2), mRNA. member 3 (KCNQ3), mRNA; kinesin;TM=M; 3.63

450377; AB033091; Hs.74313; KIAA1265 protein; Zip;TM=M;SS=M; 3.63

417793; AW405434; Hs.82575; small nuclear ribonucleoprotein polypeptide B"; rrm;TM=M; 3.63

404942; U30825; ; splicing factor, arginine/serine-rich 9; CD36;TM=Y;SS=M; 3.63

429554; NM_012275; Hs.207224; interleukin 1, delta; IL1;TM=M; 3.63

417871; AA521368; Hs.24252; ESTs; IBB,Armadoillo_seg,none; 3.62

437672; AW748265; Hs.5741; flavohemoprotein b5"; hema_1,NAD_binding,lipoxygenase,FAD_binding_6;TM=M; 3.62

438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; lipoxygenase,PLAT,none; 3.62

447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C;TM=M;SS=M; 3.61

407961; AW672939; Hs.41694; origin recognition complex, subunit 2 (yeast homolog)-like; none,pkinase,pro_isomerase; 3.61

428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1; SH2,SH3,pkinase;SS=M; 3.61

455808; BE011437; ; gb:CM4-BN0220-080500-170-f03 BN0220 Homo sapiens cDNA, mRNA sequence; none,CDK5_activator; 3.61

407748; AL079409; Hs.38176; KIAA0606 protein; SCN Circadian Oscillatory Protein (SCOP); PP2C,LRR,PH;TM=M; 3.60

421474; U76362; Hs.104637; solute carrier family 1 (glutamate transporter), member 7; SDF;TM=Y;SS=M; 3.60

449987; AW079749; Hs.184719; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ABC_tran,ABC_membrane,ion_trans; 3.60

403142; ; NM_002706*.Homo sapiens protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform (PPM1B), mRNA; PP2C;TM=M; 3.60

400844; ; NM_003105*.Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 3.59

450152; AI138635; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA sequence; ig,pkinase,none; 3.59

429782; NM_005754; Hs.220689; Ras-GTPase-activating protein SH3-domain-binding protein; rrm,NTF2;TM=M; 3.59

436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none;SS=M; 3.59

437400; AB011542; Hs.5599; EGF-like-domain, multiple 5; TNFR_c6,laminin_EGF;TM=Y; 3.58

426797; AW936258; Hs.342849; ADP-ribosylation factor-like 5; arf,Ca_channel_B,SH3; 3.58

431170; AW971246; Hs.291022; ESTs; LRR,CARD,none; 3.58

434542; AA769310; Hs.61260; hypothetical protein FLJ13164; PH,Oxysterol_BP;TM=M;SS=M; 3.58

- 420181; A1380089; Hs.158951; ESTs; none,ig, pkinase,LRR,LRRCT; 3.57
 450572; A1700863; Hs.202494; Homo sapiens cDNA FLJ13245 fis, clone OVARC1000681; Na_sulph_symp,none; 3.57
 433618; AA602539; Hs.345494; ESTs; G-alpha,A_deaminase; 3.57
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; pkinase,none; 3.57
 418512; AW498974; ; diacylglycerol kinase, zeta (104kD); ras,none; 3.57
 451752; AB032997; Hs.26966; KIAA1171 protein; ATP-synt_C,TBC;TM=Y;SS=M; 3.57
 417129; A1381800; Hs.300684; calcitonin gene-related peptide-receptor component protein; none,none; 3.57
 449474; AA019344; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing); ThiF,UBACT, pkinase,UCH-2,UCH-1,rrm,zf-C2H2,zf-RanBP,G-patch; 3.57
 412124; H43378; Hs.288550; Homo sapiens cDNA: FLJ23156 fis, clone LNG09609; none,none; 3.56
 435021; AA922192; Hs.54709; ESTs; EPH_Lbd, pkinase,fn3,SAM,none; 3.56
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit, alpha type, 4; proteasome;TM=M; 3.56
 437387; A1198874; Hs.28847; AD026 protein; none,7tm_1,WD40; 3.56
 422583; AA410506; Hs.27973; KIAA0874 protein; ank,G-alpha;TM=M; 3.55
 452102; U04343; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none;TM=Y;SS=M; 3.56
 420112; NM_005109; Hs.95220; oxidative-stress responsive 1; pkinase;TM=M; 3.55
 437639; AA827712; Hs.291880; ESTs; SH3,none; 3.55
 457500; NM_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm, pkinase;TM=M; 3.55
 415660; A1909007; Hs.78563; ubiquitin-conjugating enzyme E2G 1 (homologous to C. elegans UBC7); UQ_con;TM=M; 3.55
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD;TM=M; 3.55
 428727; AF078847; Hs.191356; general transcription factor IIH, polypeptide 2 (44kD subunit); PHO4,LIM;TM=M; 3.55
 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase, pkinase_C,HR1;TM=M; 3.55
 408683; R58665; Hs.46847; TRAF and TNF receptor-associated protein; Exo_endo_phos;TM=M; 3.55
 412350; A1659306; Hs.73826; protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte); Y_phosphatase,Band_41,PDZ;TM=M; 3.55
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 3.55
 427283; AL119799; Hs.174185; ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin); Sulfatase,Somatomedin_B,Phosphodiesterase,Endonuclease;TM=M;SS=Y; 3.55
 414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14_17,none; 3.55
 424848; A1263231; Hs.327090; EST; SH3,PDZ,Guanylate_kin,none; 3.54
 402704; ; C1001099; gi|6005896|ref|NP_009101.1| testis-specific protein kinase 2 [Homo sapiens] gil4; none,none; 3.54
 444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; aa_permeases;TM=Y;SS=M; 3.54
 429687; A1675749; Hs.211608; nucleoporin 153kD; zf-RanBP, integrin_B;TM=M; 3.53
 413879; AA132961; Hs.212533; Homo sapiens cDNA: FLJ22572 fis, clone HSI02313; none,none; 3.53
 431045; AW968560; Hs.301957; nudix (nucleoside diphosphate linked moiety X)-type motif 5; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 3.53
 423855; AA331761; Hs.254859; ESTs; none, pkinase,UQ_con,vwa,FG-GAP, integrin_A; 3.53
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin,bZIP;TM=M; 3.52
 410686; A1733735; Hs.114905; IRE1, S. cerevisiae, homolog of; pkinase,Bacterial_PQ;TM=M;SS=M; 3.52
 449810; AB008681; Hs.23994; activin A receptor, type IIB; pkinase,Activin_recpt;TM=Y;SS=M; 3.52
 418755; Y14443; Hs.88219; zinc finger protein 200; zf-C2H2,zf-BED;TM=M; 3.52
 448804; AW512213; Hs.342849; ADP-ribosylation factor-like 5; arf,Ca_channel_B,SH3; 3.52
 438507; AA809052; Hs.182018; ESTs; none,none; 3.52
 456559; A1336273; Hs.102548; glucocorticoid receptor DNA binding factor 1; none,PAS; 3.51
 410054; AL120050; Hs.58220; Homo sapiens cDNA: FLJ23005 fis, clone LNG00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP,adenylatekinase; 3.51
 422321; AA906427; Hs.181035; hypothetical protein MGC11296; none;TM=M; 3.51
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2,PH;TM=M; 3.50
 407393; AB038237; ; gb:Homo sapiens mRNA for G protein-coupled receptor C5L2, complete cds.; 7tm_1;TM=Y;SS=M; 3.50
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine protease; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 3.50
 420673; AB008112; Hs.99847; peroxisome biogenesis factor 1; AAA,APS_kinase;TM=M;SS=M; 3.49
 424663; NM_002351; Hs.151544; SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome); SH2;TM=M; 3.49
 429327; AA283981; Hs.199248; prostaglandin E receptor 4 (subtype EP4); 7tm_1;TM=Y;SS=M; 3.49
 400178; ; Eos Control; none,Somatomedin_B; 3.49
 439549; AW937885; Hs.137314; ESTs; SH2,none; 3.49
 436345; AA873008; Hs.121572; ESTs; CARD,BIR,zf-C3HC4,CARD,BIR,zf-C3HC4; 3.49
 427658; H61387; Hs.30868; nogo receptor; LRR,LRRNT, LRRCT;SS=M; 3.48
 402833; ; C1002508; gi|6691937|emb|CAB65797.1| (AL096770) bA150A6.2 (novel 7 transmembrane receptor; none,none; 3.48
 442363; A1337304; Hs.23120; PIST; fn3, pkinase,PDZ,DUF139;TM=Y;SS=M; 3.48
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; none;TM=M; 3.47
 417971; Y08991; Hs.83050; phosphoinositide-3-kinase, regulatory subunit 4, p150; pkinase,WD40,HEAT;SS=M; 3.47
 432169; Y00971; Hs.2910; phosphoribosyl pyrophosphate synthetase 2; Pribosylran; 3.47
 447425; A1963747; Hs.18573; acylphosphatase 1, erythrocyte (common) type; Acylphosphatase;SS=M; 3.47
 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 3.46
 401851; ; NM_002401; Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP3K3), mRNA; pkinase;SS=M; 3.46
 407877; AW016811; Hs.234478; Homo sapiens cDNA: FLJ22648 fis, clone HSI07329; pkinase, pkinase_C,none; 3.45
 432279; NM5104; Hs.274260; ATP-binding cassette, sub-family C (CFTR/MRP), member 6; ABC_tran,ABC_membrane,none; 3.45
 437103; AW139408; Hs.152940; ESTs; Choline_kinase,none; 3.45
 420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339, mRNA, complete cds; 7tm_1;TM=Y;SS=M; 3.44
 422209; AF005210; Hs.113222; chemokine (C-C motif) receptor 8; 7tm_1,7tm_2;TM=Y;SS=M; 3.44
 410781; A1375672; Hs.165028; ESTs; pkinase,laminin_Nterm,laminin_EGF,cyclin,F-box,cyclin_C,serpin,ATP-synt_C; 3.44
 437296; AA350994; Hs.20281; KIAA1700; Rhodanese,DSF;TM=M; 3.43
 419855; A1935182; Hs.144139; ESTs; zf-C3HC4,UBA,Cbl_N,Cbl_N3,zf-C3HC4,UBA,Cbl_N,Cbl_N2,Cbl_N3; 3.43
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2; Fz,NTR;SS=M; 3.43
 428483; A1908539; Hs.184592; KIAA0344 gene product; none,none; 3.43
 445119; AF035121; Hs.12337; kinase insert domain receptor (a type III receptor tyrosine kinase); ig, pkinase;TM=Y;SS=M; 3.42
 454468; A1590319; Hs.19122; eukaryotic translation initiation factor 4E-like 3; none,Neur_chan_LBD,Neur_chan_membr,IF4E; 3.42
 410386; W26187; Hs.3327; Homo sapiens cDNA: FLJ22219 fis, clone HRC01637; pkinase,Guanylate_kin,PDZ,SH3,L27,none; 3.42
 422907; A1879263; Hs.77273; Human glucose transporter pseudogene; none,none; 3.42
 449816; A1701457; Hs.38694; ESTs; SET,BAH,PK,PK_C; 3.42
 440074; AA863045; Hs.10669; ESTs, Weakly similar to T00050 hypothetical protein KIAA0400 [H.sapiens]; SH3,ank,tubulin-binding,ArfGap,PH;TM=M;SS=M; 3.42
 425475; W56339; Hs.107057; ESTs; pkinase,none; 3.42
 401242; AB028989; ; mitogen-activated protein kinase 8 interacting protein 3; Cys_knot,TGF-beta,vwa, vwc,vwd,TIL,DUF139;SS=M; 3.41
 429276; AF056085; Hs.198612; G protein-coupled receptor 51; 7tm_3,ANF_receptor,bZIP;TM=Y; 3.41
 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, type I, 107kD; none,none; 3.41
 410908; AA121686; Hs.10592; ESTs; GTP_EFTU,GTP_EFTU_D3,GTP_EFTU_D2,none; 3.41

- 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor type, E; Y_phosphatase:none; 3.40
 447898; AW969638; Hs.112318; 6.2 kd protein; none:none; 3.40
 450402; BE218027; Hs.89969; ESTs; SH3:none; 3.40
 441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB:none; 3.40
 408546; W49512; Hs.46348; bradykinin receptor B1; 7tm_1;TM=Y;SS=M; 3.40
 410927; T77635; ; gb:yc91h06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone 5', mRNA sequence; none:none; 3.40
 409646; AW161391; Hs.709; deoxycytidine kinase; dNK;SS=M; 3.39
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone COL04162; Sulfate_transp,STAS,HMG_box; 3.39
 449343; A1151418; ; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); none:none; 3.39
 450511; R07423; Hs.85092; thyroid hormone receptor interactor 11; Myosin_tail,EGF; 3.39
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M; 3.38
 418428; Y12490; Hs.85092; thyroid hormone receptor interactor 11; bZIP,kinesin,GTP_cyclohydrol,M;TM=M; 3.37
 422369; AF005216; Hs.115541; Janus kinase 2 (a protein tyrosine kinase); SH2,pkinase;TM=M; 3.37
 456451; A1761180; Hs.94211; rcd1 (required for cell differentiation, S.pombe) homolog 1; none;TM=M; 3.37
 438543; AA810141; Hs.192182; ESTs; SH2,pkinase:none; 3.37
 401943; NM_012434; ; solute carrier family 17 (anion/sugar transporter), member 5; none;TM=M; 3.36
 415276; U88666; Hs.78353; SFRS protein kinase 2; pkinase;TM=M; 3.36
 447881; BE620886; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; pkinase,pkinase; 3.35
 434533; AA639257; Hs.292549; ESTs; SH3,PDZ,Guanylate_kin:none; 3.35
 432639; AW973785; ; gb:EST385886 MAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence; none,IRK; 3.35
 410678; BE540516; Hs.293732; hypothetical protein MGC3195; Armadillo_seg;TM=M;SS=Y; 3.35
 402807; ; ENSP00000235229:SEMB; integrin_B,Sema,PSI;TM=Y; 3.35
 420189; AW296380; Hs.95821; osteoclast stimulating factor 1; SH3,ank; 3.34
 437389; AL359587; Hs.271586; hypothetical protein DKFZp762M115; secY,E1_dehydrog,transket_pyr:none; 3.34
 453423; NM_002647; Hs.32971; phosphoinositide-3-kinase, class 3; PI3_Pi4_kinase,PI3Ka,PI3K_C2;TM=M; 3.34
 414270; L20852; Hs.347527; solute carrier family 20 (phosphate transporter), member 2; Enterotoxin_A,PHO4;TM=Y;SS=M; 3.33
 417479; A1057052; ; ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]; LRR,CARD:none; 3.33
 424946; M64572; Hs.153932; protein tyrosine phosphatase, non-receptor type 3; Band_41,PDZ,Y_phosphatase:none; 3.33
 452681; AF153330; Hs.30246; solute carrier family 19 (thiamine transporter), member 2; Folate_carrier;TM=Y;SS=M; 3.33
 426477; AA379464; ; gb:EST92386 Skin tumor I Homo sapiens cDNA 5' end, mRNA sequence; DUF6,MATH,BTB; 3.33
 438283; A1458931; Hs.37282; ESTs; none,transmembrane4; 3.33
 421327; AA837295; Hs.188802; ESTs; none,IMP4,Y_phosphatase; 3.33
 432481; AW451645; Hs.151504; Homo sapiens cDNA FLJ11973 fis, clone HEMBB1001221; laminin_G,Collagen,COLFI,CorA,TSPN:none; 3.33
 452682; AA456193; Hs.9071; progesterone membrane binding protein; homeobox:none; 3.32
 428997; AF065391; Hs.194718; zinc finger protein 265; zf-RanBP;TM=M; 3.32
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M; 3.31
 443601; A1078554; Hs.15682; ESTs; ank,pkinase,death,Ribosomal_S14; 3.31
 430597; AF062006; Hs.285529; G protein-coupled receptor 49; 7tm_1,LRR,LRRNT;TM=Y;SS=M; 3.31
 419912; AF249745; Hs.6066; Rho guanine nucleotide exchange factor (GEF) 4; SH3,PH,RhoGEF;TM=M; 3.31
 400380; NM_018485; Hs.283079; G protein-coupled receptor C5L2; 7tm_1;TM=Y;SS=M; 3.31
 415983; A1436798; Hs.117078; Homo sapiens cDNA: FLJ23028 fis, clone LNG01852, highly similar to HSU08023 Human cellular proto-oncogene (c-mer) mRNA; fn3,ig,pkinase;TM=Y;SS=M; 3.31
 441054; AA913591; Hs.126480; ESTs; none,7tm_1; 3.31
 418342; BE002723; ; leptin receptor; ICE_p20,DED,ICE_p10,ICE_p20,DED; 3.31
 446128; AW836779; Hs.113029; ribosomal protein S25; none,7tm_1; 3.31
 425086; AW957571; Hs.12319; Homo sapiens cDNA FLJ12774 fis, clone NT2RP2001663, moderately similar to ENOLASE (EC 4.2.1.11); none,Guanylate_kin,PDZ,SH3; 3.31
 425725; NM_012243; Hs.159322; solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3; DUF6;TM=Y;SS=M; 3.30
 422608; AW160644; Hs.118695; potassium voltage-gated channel, subfamily G, member 1; ion_trans,K_tetra;TM=Y; 3.30
 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M; 3.30
 433656; AW974941; Hs.292385; ESTs, Weakly similar to T78885 serine/threonine-specific protein kinase [H.sapiens]; pkinase,ABC1:none; 3.30
 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic) inhibitor alpha; PKI;SS=M; 3.30
 402603; ; ENSP00000251206:KIAA0778 PROTEIN (FRAGMENT).; none;TM=Y; 3.30
 418801; AA228366; Hs.115122; ESTs; integrin_A,FG-GAP:none; 3.30
 400275; ; NM_006513: Homo sapiens seryl-IRNA synthetase (SARS), mRNA. (SAM68), mRNA.; tRNA-synt_2b,Seryl_IRNA_N;TM=M; 3.29
 440286; U29599; Hs.7138; cholinergic receptor, muscarinic 3; 7tm_1;TM=Y; 3.29
 409101; NM_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; G-alpha:none; 3.29
 432736; AA788898; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 3.29
 408738; NM_014785; Hs.47313; KIAA0258 gene product; none;TM=M; 3.29
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955; Aa_trans:none; 3.29
 405328; ; NM_005391: Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3), mRNA.; HATPase_c;SS=M; 3.28
 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit 6; none:none; 3.28
 408756; AA524743; Hs.44883; ESTs; Armadillo_seg,IBB,DEAD,helicase_C,Sec63,DDT,PHD,bromodomain;TM=M; 3.28
 415474; NM_014252; Hs.78457; solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15; mito_carr;TM=M; 3.28
 417805; U38545; Hs.82587; phospholipase D1, phosphatidylcholine-specific; PH,PLDc,PX;TM=M; 3.28
 410254; BE004131; Hs.318510; Homo sapiens cDNA FLJ13682 fis, clone PLACE2000015, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15; etfhand:none; 3.28
 443968; AA287702; Hs.10031; KIAA0955 protein; CARD;TM=M;SS=M; 3.28
 438899; AF085833; Hs.135624; ESTs; none,PI3_Pi4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B; 3.27
 415663; AW296841; Hs.313332; ESTs; UQ_con,Neur_chan_LBD,Neur_chan_memb; 3.27
 414087; W19712; ; gb:zb36403.r1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone 5', mRNA sequence; pkinase:none; 3.27
 442833; AA328153; Hs.88201; ESTs, Weakly similar to A Chain A, Crystal Structure Of The Human Acyl Protein Thioesterase 1 At 1.5 A Resolution [H.sapiens]; abhydrolase_2;TM=M; 3.27
 444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none;TM=Y;SS=M; 3.26
 432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis repressor with CARD domain); CARD;TM=M; 3.26
 458943; AW249181; Hs.19954; ESTs, Weakly similar to T19873 hypothetical protein C41C4.2 - Caenorhabditis elegans [C.elegans]; none,pkinase,RGS; 3.26
 411974; AW880414; Hs.84264; acidic protein rich in leucines; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,asp; 3.26
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbonate cotransporter, member 4; HCO3_cotransp;TM=Y; 3.26
 423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 3.25
 442643; U82756; Hs.3991; PRP4/STK/WD splicing factor; WD40;SS=M; 3.25
 417525; R93355; Hs.192991; ESTs, Weakly similar to ALUB_HUMAN !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]; SH3,ig,pkinase,PH,spectrin,RhoGEF;SS=M; 3.25
 412283; BE069084; ; gb:QV3-BT0379-140100-059-g12 BT0379 Homo sapiens cDNA, mRNA sequence; ion_trans,RYDR,ITPR,MIR:none; 3.25
 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 3.25
 400352; AF227133; ; taste receptor, type 2, member 7; none;TM=Y;SS=M; 3.25

- 402974; ; ; Target Exon; Y_phosphatase, GnRH, hormone5, hormone4; 3.25
 407644; D16815; Hs.37288; nuclear receptor subfamily 1, group D, member 2; hormone_rec, zf-C4; TM=M; SS=M; 3.25
 421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; helicase_C; SS=M; 3.25
 438022; AW517524; Hs.135201; NOD2 protein; LRR, CARD, GTP_CDC, Viral_helicase1; TM=M; 3.24
 449964; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase; TM=M; 3.24
 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; EGF_sushi, trypsin, CUB, ABC_tran, ABC_membrane; SS=M; 3.24
 427319; AW631495; Hs.27135; B-cell receptor-associated protein BAP29; filament; TM=Y; SS=M; 3.24
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RRN3;
 aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_PI4_kinase, FAT, FATC, BoIA, RUN; TM=M; 3.24
 411887; AW182924; Hs.128790; ESTs; pkinase; TM=M; 3.24
 430180; AA331406; Hs.75456; A kinase (PRKA) anchor protein 10; RGS; SS=M; 3.24
 410267; AW978005; Hs.12600; N-ethylmaleimide-sensitive factor attachment protein, beta; none, NTF2; 3.23
 410240; AL157424; Hs.61289; synaptotagmin 2; Exo_endo_phos, Syja_N, rrm, Gram-ve_porins; TM=M; 3.23
 434510; AF143885; Hs.18190; EST; SH3, FCH, none; 3.22
 422592; BE081857; Hs.94211; rcd1 (required for cell differentiation, S.pombe) homolog 1; none, PI-PLC-X, PH, PI-PLC-Y, C2; 3.22
 439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none, none; 3.22
 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase, DCX; TM=M; 3.22
 409245; AA361037; Hs.288036; IRNA isopentenylpyrophosphate transferase; Armadillo_seg; TM=M; 3.22
 458946; AA009716; Hs.42311; ESTs; none, DSPc, Y_phosphatase; 3.22
 409048; H59990; Hs.37699; ESTs; Armadillo_seg, IBB, none; 3.22
 420357; U94333; Hs.97199; complement component C1q receptor; EGF, lectin_c, Tissue_fac, Xlink, TIL; TM=Y; SS=M; 3.22
 426230; AA367019; Hs.241395; protease, serine, 1 (trypsin 1); trypsin, toxin_4; SS=M; 3.21
 411352; NM_002890; Hs.758; RAS p21 protein activator (GTPase activating protein) 1; SH2, SH3, C2, PH, RasGAP; TM=M; SS=M; 3.21
 438333; R39382; Hs.25283; cyclin-dependent kinase 8; pkinase, none; 3.20
 414202; BE275653; Hs.270379; transmembrane 6 superfamily member 1; 7tm_5, none; 3.20
 429651; D79248; Hs.279870; ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; MgtE, none; 3.20
 400987; ; C11000939; gi11464993[ref] NP_065260.1 gene for odorant receptor MOR83 [Mus musculus] glif; none; TM=Y; SS=M; 3.20
 413760; Z25101; Hs.25127; Homo sapiens mRNA for KIAA1725 protein, partial cds; none, ank, ArfGAP; 3.20
 408468; AI909712; Hs.93837; phosphatidylinositol transfer protein, membrane-associated; PX, PH, PLDc, PH, PLDc, PX; 3.20
 409463; AI458165; Hs.17296; hypothetical protein MGC2376; K_tetra; TM=M; 3.20
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none; TM=M; 3.19
 423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbonate cotransporter, member 7; HCO3_cotransp; TM=Y; SS=M; 3.19
 407753; AL045916; Hs.293419; ESTs; Ephrin, none; 3.19
 419355; AA428520; Hs.90061; progesterone binding protein; heme_1; TM=Y; SS=M; 3.19
 454128; AL031259; Hs.41639; programmed cell death 2; zf-MYND; TM=M; 3.19
 421202; AF193339; Hs.102506; eukaryotic translation initiation factor 2-alpha kinase 3; pkinase; TM=Y; SS=M; 3.19
 446360; N42553; Hs.267914; homolog of mouse transient receptor potential-phospholipase C-interacting kinase CHAK; hypothetical protein FLJ20117;
 ion_trans, MHCK_EF2_kinase; TM=M; 3.18
 458882; R34993; Hs.226666; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; CRAL_TRIO, PKI; 3.18
 424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; pkinase, TBC; 3.18
 444745; AF117754; Hs.11861; thyroid hormone receptor-associated protein, 240 kDa subunit; none; TM=M; 3.18
 426399; AA652588; Hs.301348; Homo sapiens cDNA FLJ13271 fis, clone OVARC1001000; SH3, HS1_rep, none; 3.18
 425836; AW955696; Hs.90960; ESTs; Cbl_N, Cbl_N2, Cbl_N3, UBA, zf-C3HC4, none; 3.18
 403335; ; NM_021815; Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA.; SSF; TM=Y; SS=M; 3.17
 428788; AF082283; Hs.193516; B-cell CLL/lymphoma 10; CARD; TM=M; 3.17
 429558; AI391454; Hs.207251; nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein; none; SS=M; 3.17
 440248; AA876138; Hs.153136; ESTs; SH2, none; 3.17
 423706; U95218; Hs.131924; G protein-coupled receptor 65; 7tm_1; TM=Y; SS=M; 3.17
 429752; H52348; Hs.36636; ESTs; pkinase, pkinase; 3.17
 446163; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 fis, clone PLACE1010270; none, NA; NA; 3.17
 456773; AI038192; Hs.129764; EGF-like repeats and discoidin I-like domains 3; rrm, SH3, myosin_head, IQ, MyTH4, EGF, F5_F8_type_C, Band_41; TM=M; 3.17
 434392; AW983709; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone HRC12631; pkinase, none; 3.16
 435972; W95088; Hs.114198; ESTs; pkinase, OPR, none; 3.16
 441401; AI824338; Hs.126891; ESTs; Tissue_fac; TM=M; SS=M; 3.16
 410497; AL157648; Hs.157078; Homo sapiens cDNA FLJ12793 fis, clone NT2RP2002033; none, none; 3.16
 401113; H25530; ; solute carrier family 22 (organic cation transporter), member 1-like; none; SS=M; 3.16
 424833; NM_003894; Hs.153405; period (Drosophila) homolog 2; PAS; SS=M; 3.15
 453880; AI803166; Hs.28462; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; HSP70, none; 3.15
 435391; AA704588; Hs.58934; ESTs; PIP5K, none; 3.15
 428065; AI634046; Hs.157313; ESTs; ICE_p20, DED, ICE_p10, ICE_p20, DED; 3.15
 452688; AA721140; Hs.49930; ESTs, Weakly similar to putative p150 [H.sapiens]; SH3, none; 3.15
 426839; M74782; Hs.172689; interleukin 3 receptor, alpha (low affinity); none; TM=M; SS=M; 3.15
 421247; BE391727; Hs.102910; general transcription factor IIH, polypeptide 4 (52kD subunit); none; TM=M; 3.14
 440249; AI246590; Hs.249175; ESTs; TatD_DNase, pkinase, death, none; 3.14
 409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG; TM=M; 3.13
 446135; AW130288; Hs.170318; hypothetical protein FLJ10147; hormone_rec, zf-C4; SS=M; 3.13
 400440; X83957; Hs.83970; nebulin; SH3, Nebulin; 3.12
 409099; AK000725; Hs.50579; hypothetical protein FLJ20718; Armadillo_seg; TM=M; 3.12
 434237; AF119908; Hs.235516; hypothetical protein PRO22955; none; SS=M; 3.12
 428179; AI127772; Hs.279696; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; pkinase, PX, pkinase_C; SS=M; 3.12
 422824; NM_012108; Hs.121128; BCR downstream signaling 1; SH2, PH; TM=M; 3.11
 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B14E12, mRNA sequence; 7tm_1, zf-C3HC4, In3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 3.11
 435411; AW444619; Hs.138211; ESTs; none, pkinase; 3.11
 424852; AI222779; Hs.144848; ESTs; adenylatekinase, SH2, pkinase, none; 3.11
 441970; AW959918; Hs.155160; ESTs; rrm, zf-C2H2; 3.11
 433370; AI470523; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran, ABC_membrane; TM=Y; 3.11
 413285; BE078405; ; gb:QV2-BT0617-080300-071-g03 BT0617 Homo sapiens cDNA, mRNA sequence; GCV_T; SS=M; 3.10
 429458; BE161832; Hs.292689; ESTs; pkinase, bZIP, Armadillo_seg, none; 3.10
 401185; ; NM_021625; Homo sapiens vanilloid receptor-related osmotically activated channel; OTRPC4 protein (OTRPC4), mRNA.; ank, ion_trans; TM=Y; 3.10
 404537; Z25884; ; chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant); none; TM=Y; 3.10
 417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone HEP03834; voltage_CLC, CBS, none; 3.09
 450792; AA400323; Hs.183041; ESTs; none, ABC_tran; 3.09

- 420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP,7tm_1; 3.09
 444040; AF204231; Hs.182982; golgin-67; SH3,C2,PH,RhoGEF,ehand;TM=M;; 3.09
 416990; AF124145; Hs.80731; autocrine motility factor receptor; zf-C3HC4,CUE;TM=Y;; 3.09
 442215; AI703172; Hs.129005; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; none,none; 3.09
 424187; AA338561; Hs.17287; ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK,none; 3.09
 426623; AA382826; Hs.132793; ESTs; none;TM=M;; 3.08
 419577; L36531; Hs.91296; integrin, alpha 8; integrin_A,FG-GAP;TM=Y;; 3.08
 426618; AL036456; Hs.171374; smg GDS-ASSOCIATED PROTEIN; Armadillo_seg;TM=M;; 3.08
 445133; AW157646; Hs.153506; ESTs; ehand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AIP3;TM=M;; 3.08
 423681; AB023215; Hs.131525; Homo sapiens mRNA; cDNA DKFZp434E199 (from clone DKFZp434E199); partial cds; TTL;TM=M;; 3.08
 428730; AA625947; Hs.25750; ESTs; HECT,none; 3.08
 427976; AW977808; Hs.80545; mitogen-activated protein kinase 8 interacting protein 2; Ribosomal_L37e,pkinase; 3.08
 412448; L12964; Hs.73895; tumor necrosis factor receptor superfamily, member 9; TNFR_c6;TM=Y;SS=M; 3.08
 416814; AW192307; Hs.80042; dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylglucosyltransferase; Alg6_Alg8,7tm_1;TM=Y;SS=M; 3.08
 427395; AW298741; Hs.97861; ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens]; none,aldedh,aakinas; 3.08
 436267; AW450938; Hs.180115; ESTs; none,PFK; 3.07
 422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic acid transporters), member 6; sugar_tr;TM=Y;SS=M; 3.07
 439238; N47305; Hs.46668; ESTs; 7tm_1;TM=Y;SS=M; 3.07
 458760; AL498631; Hs.111334; ferritin, light polypeptide; cystatin,ferritin,histone,HCO3_cotransp,SH3,RhoGAP,xan_ur_permease,FCH;SS=M; 3.07
 424236; AW058114; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase;TM=M;; 3.06
 427286; AW732802; Hs.2132; epidermal growth factor receptor pathway substrate 8; SH3,TonB_boxC;TM=M;; 3.06
 423878; AI907090; Hs.52891; hypothetical protein PRO1853; cystatin,ferritin,histone,HCO3_cotransp,SH3,RhoGAP,xan_ur_permease,FCH;SS=M; 3.06
 419270; NM_005232; Hs.89839; EphA1; fn3,pkinase,SAM,EPH_lbd;TM=M;SS=M; 3.06
 450407; NM_000810; Hs.24969; gamma-aminobutyric acid (GABA) A receptor, alpha 5; Neur_chan_LBD,Neur_chan_memb;TM=Y;; 3.06
 456249; AI206144; Hs.82508; HRIHFB2206 protein; none;SS=M; 3.06
 441560; F13386; Hs.7888; Homo sapiens clone 23736 mRNA sequence; pkinase,Recep_L_domain,Furin-like,YLP,none; 3.05
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;SS=M; 3.05
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); pyr_redox;TM=M;; 3.05
 425390; AI092634; Hs.156114; protein tyrosine phosphatase, non-receptor type substrate 1; ig;TM=Y;SS=M; 3.04
 409705; M37762; Hs.56023; brain-derived neurotrophic factor; NGF;SS=M; 3.04
 413962; AA331563; Hs.24678; sphingosine-1-phosphatase; PAP2;TM=Y;; 3.04
 426578; R23027; ; gb:yh27e07.r1 Soares placenta Nb2HP Homo sapiens cDNA clone 5', mRNA sequence; pkinase,none; 3.04
 438005; BE151746; ; gb:PM1-HT0305-061299-003-a06 HT0305 Homo sapiens cDNA, mRNA sequence; pkinase,UBA,KA1,none; 3.04
 438316; AA789249; Hs.80042; gb:aj27g08.s1 Soares testis_NHT Homo sapiens cDNA clone 1391582 3', mRNA sequence; none,none; 3.04
 452850; H23230; Hs.22481; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; CBS,voltage_CLC,none; 3.03
 405266; ; ; Target Exon; arf,G-alpha;SS=M; 3.03
 402615; ; ; C1003844*.gil6912550[ref][NP_036483.1] olfactory receptor, family 10, subfamily J, member 1; none;TM=Y;SS=M; 3.03
 422803; W28669; Hs.139041; ESTs; transmembrane4,none; 3.02
 439325; AF086139; Hs.150423; cyclin-dependent kinase 9 (CDC2-related kinase); pkinase,Mur_ligase,Mur_ligase_C; 3.02
 416389; AA180072; Hs.149846; integrin, beta 5; integrin_B,none; 3.02
 418836; AI655499; Hs.161712; ESTs; pkinase,Activin_recpt,PDZ,ZU5,death; 3.02
 438996; AW748336; Hs.110613; KIAA0421 protein; none;TM=M;; 3.02
 422676; D28481; Hs.1570; histamine receptor H1; 7tm_1;TM=Y;SS=M; 3.02
 450267; AW505538; Hs.243620; ESTs; pkinase,none; 3.01
 400566; ; ; Target Exon; none;TM=Y;; 3.01
 407816; AW500857; Hs.40137; anaphase-promoting complex 1; meiotic checkpoint regulator; PI-PLC-X,C2,SH2,PH,SH3,PI-PLC-Y,PAN,none; 3.01
 429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase); Y_phosphatase,Band_41,PDZ;SS=M; 3.01
 417067; AJ001417; Hs.81086; solute carrier family 22 (extraneuronal monoamine transporter), member 3; sugar_tr;TM=Y;SS=M; 3.00
 403212; ; NM_019595;Homo sapiens intersectin 2 (ITSN2), mRNA. (CHRNA9), mRNA.; SH3,ehand,C2,PH,RhoGEF;TM=M;; 3.00
 410141; R07775; Hs.287657; Homo sapiens cDNA: FLJ21291 fis, clone COL01963; F5_F8_type_C,pkinase,Ets,none; 3.00
 421059; AI654133; Hs.30212; thyroid receptor interacting protein 15; none,none; 3.00
 452335; AW188944; Hs.61272; ESTs; none,IRK; 2.99
 437644; AA748575; Hs.136748; lectin-like NK cell receptor; lectin_c;TM=Y;SS=M; 2.99
 435876; AW612586; Hs.160271; G protein-coupled receptor 48; 7tm_1,LRR,LRRNT;TM=Y;SS=M; 2.99
 429177; AA447527; Hs.207429; ESTs; 7tm_1,none; 2.99
 449289; BE466067; Hs.225660; ESTs; 3Beta_HSD,pkinase; 2.99
 454701; AW854930; ; gb:PM0-CT0263-201099-003-f06 CT0263 Homo sapiens cDNA, mRNA sequence; SH2,STAT,STAT_bind,STAT_prot,none; 2.99
 409995; AW960597; Hs.129206; ESTs; pkinase,none; 2.98
 446860; AV660685; Hs.282953; ESTs; none,PP2C; 2.98
 438684; AA830105; Hs.194976; SH2 domain-containing phosphatase anchor protein 1; ig;TM=Y;SS=M; 2.98
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;; 2.98
 403290; ; ; C10001011*.gil4758212[ref][NP_004411.1] dual specificity phosphatase 8 [Homo sapiens] gil601; none;TM=M;; 2.97
 433556; W56321; Hs.111460; calcium/calmodulin-dependent protein kinase (CaM kinase) II delta; pkinase,none; 2.97
 421990; T31811; Hs.110480; DC12 protein; GKAP,DUF159;TM=M;; 2.97
 428315; AA688152; Hs.98505; ESTs; pkinase,none; 2.97
 411140; AW819463; ; gb:RC5-ST0293-061299-031-C07 ST0293 Homo sapiens cDNA, mRNA sequence; Choline_kinase,Carn_acyltransf,Sulfatase,Carn_acyltransf; 2.97
 453998; H47802; Hs.7557; FK506-binding protein 5; none,none; 2.97
 401342; ; ; Target Exon; none,none; 2.97
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); dNK,none; 2.96
 410976; R36207; Hs.25092; hypothetical protein MGC10744; none;TM=M;SS=M; 2.96
 431074; BE072772; Hs.153279; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; none,serpin; 2.96
 443829; AI087954; Hs.23348; S-phase kinase-associated protein 2 (p45); F-box,none; 2.96
 400356; AF227137; ; taste receptor, type 2, member 13; none;TM=Y;SS=M; 2.95
 422559; AW247696; Hs.155839; hypothetical protein MGC12934; adh_zinc,PGK,Semialdehyde_dh;SS=M; 2.95
 423482; BE280172; Hs.129228; galactokinase 2; GHMP_kinases;TM=M;; 2.95
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 2.95
 414581; AA256213; Hs.72010; ESTs; none,Carn_acyltransf,Choline_kinase,SCO1-SenC,Glycos_transf_3,Glycos_trans_3N; 2.95
 453058; AW612293; Hs.288684; Homo sapiens cDNA FLJ11750 fis, clone HEMBA1005568; SH2,SH3,C2,PH,RasGAP,none; 2.95
 430556; AW967807; Hs.13797; ESTs; HECT,none; 2.94
 400471; ; ; Target Exon; none;TM=M;; 2.94
 419459; AW291128; Hs.278422; DKFZP586G1122 protein; Metallophos,7tm_1; 2.94
 407013; U35637; ; gb:Human nebulin mRNA, partial cds; SH3,Nebulin; 2.94
 421476; AW953805; Hs.21887; ESTs; Piwi,PAZ,Piwi; 2.94

- 426806; T19228; Hs.172572; hypothetical protein FLJ20093; ank,pkinase,UPF0073;SS=M; 2.94
 405588; ; NM_000299*:Homo sapiens plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) (PKP1), mRNA.; Armadillo_seg;TM=M;; 2.94
 443614; AV655386; Hs.7645; fibrinogen, B beta polypeptide; none,none; 2.94
 416737; AF154335; Hs.79691; LIM domain protein; LIM,PDZ;TM=M;; 2.93
 5 428522; R10184; Hs.191987; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; none,ArlGap,PH,TNFR_c6; 2.93
 447818; W79940; Hs.21906; Homo sapiens clone 24670 mRNA sequence; none,pkinase; 2.93
 432925; AA878324; ; ESTs; none,none; 2.93
 10 443670; AW178935; Hs.238707; ESTs; RmaAD,DENN,dDENN,uDENN;TM=M;; 2.93
 447555; A1391662; Hs.160963; Homo sapiens, clone MGC:12318, mRNA, complete cds; none;TM=M;; 2.93
 435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; none;TM=M;; 2.93
 417670; R07785; ; gb:ylf15c06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 5' similar to contains Alu repetitive element;contains MSR1 repetitive element ;, mRNA sequence; XYPPX,ABC_membrane,ABC_tran; 2.93
 15 424148; BE242274; Hs.1741; integrin, beta 7; integrin_B,EGF,metalthio,PSI;TM=Y;SS=M; 2.92
 439090; H65724; Hs.347158; gb:yr76a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 5', mRNA sequence; pkinase,none; 2.92
 408048; NM_007203; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemm;TM=M; 2.92
 428796; AU076734; Hs.193665; solute carrier family 28 (sodium-coupled nucleoside transporter), member 2; Nucleoside_tra2,BPD_transp_2;TM=Y;; 2.92
 415272; AA164215; Hs.203186; ESTs; none,Exo_endo_phos,BNR,Atrophin-1,B56,pkinase,ig,TPR; 2.92
 20 424775; AB014540; Hs.153026; SWAP-70 protein; efhand,PH,Neuregulin;TM=M;; 2.92
 439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 2.92
 441680; AW444598; Hs.7940; RAP1, GTP-GDP dissociation stimulator 1; Armadillo_seg;TM=M;; 2.91
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1; Somatomedin_B,Endonuclease,Phosphodiester;TM=Y;SS=M; 2.91
 400398; AF137396; Hs.283879; ubiquitin 3; 7tm_1,Abl;TM=Y;SS=M; 2.91
 25 435592; A1830490; Hs.1466; glycerol kinase; FGGY,FGGY_C;TM=M;; 2.90
 400539; ; Target Exon; none;TM=M;; 2.90
 403743; ; C1002604.gi|8393668|ref|NP_058989.1| kinase interacting with leukemia-associated gene (st; none;TM=M;; 2.90
 418913; BE046745; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Y_phosphatase,IMP4,none; 2.90
 428169; A1928984; Hs.182793; golgi phosphoprotein 2; photoRC,UPF0118;TM=Y;; 2.90
 403912; ; C5000394.gi|12737280|ref|XP_006682.2| keratin 18 [Homo sapiens]||6633; none;TM=M;; 2.89
 30 431868; BE246400; Hs.285176; acetyl-Coenzyme A transporter; none;TM=Y;; 2.89
 421558; AB011125; Hs.105749; KIAA0553 protein; none;TM=M;; 2.89
 444100; AA383343; Hs.22116; CDC14 (cell division cycle 14, S. cerevisiae) homolog B; Y_phosphatase,DSPC;TM=M;; 2.89
 47437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupled, 2; 7tm_1,SH2;TM=Y;SS=M; 2.89
 35 431512; BE270734; Hs.2795; lactate dehydrogenase A; Idh,Idh_C,SH3,pkinase,UBA;TM=M;; 2.89
 446601; A1312783; Hs.155772; Homo sapiens thymic stromal co-transporter mRNA, complete cds; sugar_tr;TM=Y;; 2.89
 420747; BE294407; Hs.99910; phosphofructokinase, platelet; PFK;TM=M;; 2.88
 449459; BE546846; Hs.195048; ESTs; ank,ras,PH,ArlGap,HCO3_cotransp; 2.88
 405099; ; Target Exon; C2,PI-PLC-Y,PI-PLC-X;TM=M;; 2.88
 445890; AF055019; Hs.21906; Homo sapiens clone 24670 mRNA sequence; pkinase,pkinase; 2.88
 40 401445; ; NM_021161*:Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA.; ion_trans;TM=Y;SS=M; 2.87
 405480; ; Target Exon; none,none; 2.87
 400189; ; Eos Control; LRR,PPTA;TM=M;; 2.87
 45 450125; AA005418; Hs.158186; ESTs; CIDE-N,7tm_1,none; 2.87
 432056; AB040973; Hs.272385; G protein-coupled receptor 72; 7tm_1;TM=Y;SS=M; 2.86
 423619; T48691; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm_1,7tm_2;TM=Y;SS=M; 2.86
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; xan_ur_permease,RA; 2.86
 420035; F26725; Hs.187908; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; HATPase_c,MOZ_SAS,zf-C2H2; 2.86
 425480; AB023198; Hs.158135; KIAA0981 protein; PIP5K;SS=M; 2.86
 50 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc finger protein, ESTs, STSs, GSSs and a putative CpG; none;TM=M;; 2.86
 444595; AL121094; Hs.83572; hypothetical protein MGC14433; Y_phosphatase,SH2,Y_phosphatase,SH2; 2.85
 411331; AW837178; ; gb:QV1-LT0037-070300-100-d11 LT0037 Homo sapiens cDNA, mRNA sequence; SH2,none; 2.85
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; none,none; 2.85
 55 440617; AA894880; Hs.181181; ESTs; none,none; 2.85
 454071; A1041793; Hs.42502; ESTs; 7tm_1,none; 2.85
 411040; AF007393; Hs.177574; protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor); HLH;TM=M;; 2.85
 402183; ; NM_004491*:Homo sapiens glucocorticoid receptor DNA binding factor 1 (GRLF1), mRNA.; none;SS=M; 2.85
 428753; AW939252; Hs.192927; hypothetical protein FLJ20251; none;TM=M;; 2.84
 60 417070; Z19077; Hs.172004; titin; fn3,ig,SGXXSG,pkinase;TM=M;; 2.84
 458456; A1122709; Hs.153609; ESTs; bZIP,Armadillo_seg,rrm,NTF2,none; 2.84
 421226; AL096748; Hs.102708; DKFZP434A043 protein; Armadillo_seg,integrin_B,PSI,TIG;TM=M;SS=M; 2.84
 436733; BE327477; Hs.166941; ESTs; 7tm_3,oxidored_q5_N,Presenilin,PWI; 2.84
 427161; A1024595; Hs.97508; a disintegrin and metalloproteinase domain 6; ig;TM=Y;SS=M; 2.84
 65 419462; AF071076; Hs.112255; nucleoporin 98kD; DEAD,helicase_C,Nucleoporin_FG,homeobox;SS=M; 2.83
 413658; AA055369; Hs.75456; A kinase (PRKA) anchor protein 10; none,none; 2.83
 400749; ; NM_003105*:Homo sapiens sorilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA.; EGF,fn3,Idl_recept_a,Idl_recept_b,granulin,BNR;TM=Y;SS=M; 2.83
 447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; TB2_DP1_HVA22;TM=Y;SS=M; 2.83
 70 413243; AA769266; Hs.193657; ESTs; pkinase,zf-C4,ERM,CNH,none; 2.83
 423690; AA329648; Hs.23804; ESTs, Weakly similar to PN0099 son3 protein [H.sapiens]; ion_trans,IQ,none; 2.82
 447993; AW139525; Hs.170362; ESTs; none,none; 2.82
 423061; A1290473; Hs.44807; ESTs; integrin_B,Sema,PSI,TIG,none; 2.82
 440619; AW408586; Hs.91052; ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; abhydrolase_2,none; 2.82
 75 423497; U92642; Hs.129701; G protein-coupled receptor 45; 7tm_1;TM=Y;SS=M; 2.81
 446126; AW085909; Hs.10177; pleckstrin homology domain interacting protein; none,none; 2.81
 452488; N74921; Hs.184389; ESTs; none;TM=M;; 2.80
 449515; A1653378; Hs.302012; ESTs; ion_trans;TM=Y;SS=M; 2.79
 80 443881; R64512; Hs.237146; hypothetical protein FLJ12752; none,none; 2.79
 449636; A1656608; Hs.281328; ESTs, Weakly similar to T00378 KIAA0641 protein [H.sapiens]; pkinase,hormone3;TM=Y;SS=M; 2.78
 424348; AB020523; Hs.266258; endonuclease G-like 1; Endonuclease;TM=M;SS=M; 2.78
 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase,PLAT;TM=M;; 2.78
 442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; MIF,sugar_tr,none; 2.78

- 450010; AW293801; Hs.255052; ESTs; ARID,7tm_1; 2.78
 452813; U54727; Hs.191445; ESTs; pkinase,Activin_recpt,none; 2.78
 418177; N44967; ; ESTs; pkinase,none; 2.78
 408014; AA723782; Hs.41749; protein kinase, cGMP-dependent, type II; cNMP_binding,pkinase;SS=M; 2.77
 448362; AA641767; Hs.21015; hypothetical protein DKFZp564L0864 similar to HIAT1; sugar_tr;TM=Y;SS=M; 2.77
 423994; X01057; Hs.1724; interleukin 2 receptor, alpha; sushi;TM=Y;SS=M; 2.77
 427342; AL110150; Hs.176680; Homo sapiens mRNA; cDNA DKFZp586D0724 (from clone DKFZp586D0724); none;NA;NA; 2.76
 447574; AF162666; Hs.18895; tousel-like kinase 1; pkinase;TM=M; 2.76
 442681; A1809182; Hs.130907; ESTs; transketolase,E1_dehydrog,transket_pyr,transketolase_C,pkinase; 2.75
 433637; AW024214; Hs.102307; ESTs; Na_sulph_symp,aa_permeases;TM=Y;SS=M; 2.75
 458997; AW937420; Hs.69662; ESTs; SH3,RhoGAP,FCH;TM=M; 2.75
 432284; AA532807; Hs.105822; ESTs; pkinase,none; 2.74
 406139; ; Target Exon; ig,Tub;TM=Y;SS=M; 2.74
 439518; W76326; ; gb:zd6d04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone 5' similar to contains Alu repetitive element; mRNA sequence; Armadillo_seg,none; 2.74
 428536; A1143139; Hs.2288; visinin-like 1; efhand;SS=M; 2.73
 400211; ; NM_003899; Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. VERSION NM_003897.1 GI; SH3,PH,RhoGEF,Terpene_synt;TM=M; 2.73
 402129; ; Target Exon; SH2,Peptidase_C9;TM=M; 2.73
 424238; AA337401; Hs.137635; ESTs; none;TM=M;SS=M; 2.73
 433834; AA620742; Hs.130786; ESTs; SPX,EXS;TM=Y; 2.73
 409339; AB020686; Hs.54037; ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function); Sulfatase,Phosphodiester;TM=M;SS=M; 2.73
 408163; AW779842; Hs.258217; ESTs; 7tm_1,zf-B_box,zf-C3HC4,7tm_1,zf-B_box,zf-C3HC4; 2.73
 422358; AL133030; Hs.115429; Homo sapiens mRNA for KIAA1666 protein, partial cds; SH3;TM=M; 2.73
 426409; AA594207; ; gb:nn29e01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone 3', mRNA sequence; pkinase,Fibrillarin,none; 2.72
 400645; ; Target Exon; lig_chan,SBP_bac_3,ANF_receptor,none; 2.72
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; adenylatekinase,none; 2.71
 442572; A1001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 2.71
 409317; U20165; Hs.53250; bone morphogenetic protein receptor, type II (BMPR2); pkinase,Activin_recpt;TM=M;SS=M; 2.71
 403201; ; Target Exon; none; 2.71
 459357; AW848421; ; gb:IL3-CT0214-150200-075-B11 CT0214 Homo sapiens cDNA, mRNA sequence; ABC_tran,ABC_membrane,ion_trans; 2.70
 439935; S75105; Hs.8358; glutamate receptor, ionotropic, kainate 2; ANF_receptor,lig_chan,none; 2.70
 414924; C06267; Hs.44247; ESTs; none,none; 2.69
 421008; BE259378; Hs.103147; hypothetical protein FLJ21347; DUF255; 2.69
 449951; AA004982; Hs.120904; ESTs; DED,Calsequestrin; 2.69
 411226; AW833022; ; gb:RC3-TT0005-191099-012-d04 TT0005 Homo sapiens cDNA, mRNA sequence; pkinase,none; 2.68
 417625; U59305; Hs.44708; Ser-Thr protein kinase related to the myotonic dystrophy protein kinase; pkinase,bZIP,G-gamma,K-box,pkinase_C;SS=M; 2.68
 408051; A1623351; Hs.172148; ESTs; PH,RhoGAP,none; 2.68
 412521; AW753481; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 2.68
 413922; A1535895; Hs.221024; ESTs; ion_trans,RYDR_ITPR,MiR,UDPGT; 2.68
 432188; A1362952; Hs.2928; solute carrier family 7 (cationic amino acid transporter, y system), member 1; aa_permeases;TM=Y;SS=M; 2.67
 415516; F11411; ; gb:HSC2WF081 normalized infant brain cDNA Homo sapiens cDNA clone c-2wf08, mRNA sequence; ion_trans,none; 2.67
 419749; X73608; Hs.93029; sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican); kazal,thyroglobulin_1;SS=M; 2.66
 416095; AW014327; Hs.221951; ESTs; Weakly similar to I38022 hypothetical protein [H.sapiens]; ig,zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3,none; 2.66
 403609; ; C3001199:gil7494834[pil]T15308 hypothetical protein B0286.2 - Caenorhabditis elegans[41]; 7tm_1,7tm_2,GPS,WIF;TM=Y;SS=M; 2.66
 458213; AL047521; Hs.12210; hypothetical protein FLJ13732 similar to tensin; pkinase,none; 2.66
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.66
 435410; AL135067; Hs.117182; ESTs; none,pkinase,RBD,DAG_PE-bind; 2.66
 437838; A1307229; Hs.184304; ESTs; CARD,ICE_p20,ICE_p10,HIT,voltage_CLC,CBS,HCCA_isomerase; 2.66
 430293; A1416988; Hs.238272; inositol 1,4,5-trisphosphate receptor, type 2; ion_trans,RYDR_ITPR,MiR,none; 2.65
 433090; A1720050; ; immortalization-upregulated protein; none;SS=M; 2.65
 432103; T15803; Hs.272458; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); Metallophos;TM=M; 2.65
 435852; H72303; Hs.36011; ESTs; pkinase,none; 2.64
 433327; A1674779; Hs.126744; ESTs; none,7tm_1; 2.64
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; none,FMO-like; 2.64
 432251; AW972983; Hs.232165; polycythemia rubra vera 1; cell surface receptor; none;TM=M;SS=M; 2.63
 446963; A1862668; Hs.176333; ESTs; OMPdecase,Pribosyltran,pkinase,RhoGEF,PH; 2.63
 444821; AA053564; Hs.12040; STE20-like kinase; pkinase;TM=M; 2.63
 436206; AK001451; ; CD2-associated protein; none,none; 2.63
 434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic receptor; death,Kunitz_BPTI;TM=Y;SS=M; 2.63
 439039; A1656707; Hs.48713; ESTs; pkinase,none; 2.63
 449656; AA002008; Hs.188633; ESTs; PIP5K,none; 2.63
 429341; X73874; Hs.2393; phosphorylase kinase, alpha 1 (muscle); none;TM=M; 2.62
 445174; AV652850; Hs.172004; titin; fn3,ig,SGXXSG,none; 2.62
 424950; AA602917; Hs.156974; ESTs; none,CDP-OH_P_transf; 2.62
 438141; AW946871; ; gb:RC2-ET0022-080500-012-d02 ET0022 Homo sapiens cDNA, mRNA sequence; SH2,STAT,STAT_bind,STAT_prot,none; 2.61
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, complete cds; pkinase,TBC,Rhodanese;TM=M; 2.61
 409264; NM_014937; Hs.52463; KIAA0966 protein; Sjia_N;TM=M; 2.60
 458438; A1141520; Hs.151464; ESTs; Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]; pkinase,none; 2.60
 400719; ; NM_004055; Homo sapiens calpain 5 (CAPN5), mRNA. VERSION NM_004335.2 GI; C2,Peptidase_C2,Calpain_III;TM=M; 2.60
 427318; AF186081; Hs.175783; zinc transporter; Zip;TM=Y;SS=M; 2.59
 426086; T94907; Hs.188572; ESTs; PH,Et,CH,spectrin,Ca_channel_B,none; 2.59
 430105; X70297; Hs.2540; cholinergic receptor, nicotinic, alpha polypeptide 7; Neur_chan_LBD,Neur_chan_membr,pkinase;TM=Y;SS=M; 2.58
 411495; AP000693; Hs.70359; KIAA0136 protein; HATPase_c,bZIP;TM=M; 2.58
 438167; R28363; Hs.24286; ESTs; none;TM=Y;SS=M; 2.58
 418749; N75147; Hs.22488; ESTs; none,zf-C2H2,KRAB,pkinase; 2.58
 454289; AL137554; Hs.49927; protein kinase NYD-SP15; dCMP_cyt_deam;TM=M; 2.58
 443605; H06865; Hs.134131; ESTs; efhand,ion_trans,none; 2.57
 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 2.57
 403088; ; NM_003319; Homo sapiens titin (TTN), mRNA. mRNA; ; fn3,ig,SGXXSG;TM=M; 2.57
 409190; AU076536; Hs.50984; sarcoma amplified sequence; transmembrane4;TM=Y;SS=M; 2.57
 426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 fis, clone HRC04468; ig;TM=Y;SS=M; 2.56
 403328; ; Target Exon; Glyco_hydro_35;TM=M; 2.56

- 426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo_seg,HEAT_PBS;; 2.56
 428695; A1355647; Hs.189999; purinergic receptor (family A group 5); 7tm_1,TM=Y;SS=M; 2.54
 419285; D31887; Hs.89968; KIAA0062 protein; Zip;TM=Y;SS=M; 2.54
 415740; N80486; Hs.39911; Homo sapiens mRNA for FLJ00089 protein, partial cds; CBM_21;TM=M;; 2.53
 403305; NM_006825;; transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment; pkinase;TM=Y;SS=M; 2.53
 443804; AL135352; Hs.255883; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Peptidase_M18,Peptidase_M18,Y_phosphatase; 2.53
 450425; H06607; Hs.6099; ESTs; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,none; 2.51
 401702;; NM_001171;Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 6 (ABCC6), mRNA.; ABC_tran,ABC_membrane;TM=Y;SS=M; 2.50
 439463; W69304;; gb:zd46f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone 5', mRNA sequence; fn3,Y_phosphatase,none; 2.50
 425975; AB011082; Hs.165559; organic cationic transporter-like 4; sugar_tr;TM=Y;; 2.50
 443259; AW090601; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1,none; 2.50
 400777;; NM_007325;Homo sapiens glutamate receptor, ionotropic, AMPA 3 (GRIA3), transcript variant flp, mRNA.; lig_chan,SBP_bac_3,ANF_receptor;TM=M;SS=Y; 2.49
 426044; AA502490; Hs.170290; ESTs; none,none; 2.48
 454564; AW807573;; gb:MR1-ST0088-021299-004-g01 ST0088 Homo sapiens cDNA, mRNA sequence; pkinase,none; 2.48
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; KH-domain,TUDOR;TM=M;SS=M; 2.47
 426481; AW963941;; gb:EST376014 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence; Y_phosphatase,Band_41,DSpc,none; 2.46
 426005; AA377499;; gb:EST90341 Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence; tubulin,FKBP,COX6B,7tm_1,tubulin_C;SS=M; 2.46
 424879; AA348013; Hs.273385; ESTs; arf,G-alpha,none; 2.46
 415156; X84908; Hs.78060; phosphorylase kinase, beta; none;TM=M;; 2.46
 416508; R39769;; ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; SH3,PDZ,Guanylate_kin,ZU5,none; 2.46
 408087; AW150645;; gb:xcg54f07.x1 NCL_CGAP_Ut4 Homo sapiens cDNA clone 3', mRNA sequence; XYPPX,ABC_membrane,ABC_tran; 2.46
 433434; AA588429;; gb:nc22b03.s1 NCL_CGAP_Pr22 Homo sapiens cDNA clone 3', mRNA sequence; pkinase,DNA_mis_repair,HATPase_c; 2.45
 446768; AV660305; Hs.110286; ESTs; ICE_p20,DED,ICE_p10,ICE_p20,DED; 2.45
 437158; AW090198;; KIAA1150 protein; none;NA;NA; 2.45
 430177; AW969233; Hs.302746; MSTP028 protein; K_tetra,none; 2.45
 422270; AF114494; Hs.114062; protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a; none;TM=Y;; 2.45
 430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; Y_phosphatase,Adaptin_N,Y_phosphatase; 2.44
 446569; AW248031; Hs.155839; hypothetical protein MGC12934; adh_zinc,PGK,Semialdehyde_dh;SS=M; 2.44
 411902; AW875344;; gb:RC1-PT0009-220300-013-f06 PT0009 Homo sapiens cDNA, mRNA sequence; none,pkinase,ank; 2.43
 430057; AW450303; Hs.2534; bone morphogenetic protein receptor, type IA (BMPRI1A) (ALK-3); Activin_rec,pkinase;TM=Y;SS=M; 2.43
 446338; AL289121; Hs.206978; ESTs; none,SH3; 2.42
 426221; AB007881; Hs.110613; KIAA0421 protein; none,Ribosomal_S8; 2.42
 446796; AI652497; Hs.110103; RNA polymerase I transcription factor RRN3; none,none; 2.41
 428360; H10291; Hs.30974; ESTs; pkinase,PBD,none; 2.40
 428379; X06026; Hs.2259; CD3G antigen, gamma polypeptide (TIT3 complex); ITAM;TM=Y;SS=M; 2.40
 432488; AA551010; Hs.216640; ESTs; Na_sulph_symp,none; 2.40
 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, yeast, homolog)-like; none,Ribosomal_S13,Galactosyl_T,Zip,adh_short,zf-C3HC4; 2.40
 448595; AB014544; Hs.21572; KIAA0644 gene product; LRR,LRRCT;TM=Y;SS=M; 2.40
 428283; AI430906; Hs.323079; Homo sapiens mRNA; cDNA DKFZp564P116 (from clone DKFZp564P116); Y_phosphatase,fn3,lg,none; 2.39
 432460; H12912; Hs.274691; adenylate kinase 3; adenylatekinase,none; 2.38
 429549; AI333013; Hs.250505; retinoic acid receptor, alpha; none,zf-C3HC4,BRCT,lig_chan; 2.38
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; Phosphodiester,Somatostatin_B,Endonuclease,none; 2.36
 417473; M55268; Hs.82201; casein kinase 2, alpha prime polypeptide; pkinase,ABC1;TM=M;; 2.35
 453186; AK001708; Hs.32271; hypothetical protein FLJ10846; TK,DUF300;TM=Y;SS=M; 2.33
 447276; AL049795; Hs.17987; hypothetical protein MGC1203; none;TM=M;; 2.33
 445310; AL242490; Hs.153290; Homo sapiens cDNA FLJ14318 fis, clone PLACE3000402; none,pkinase; 2.31
 432942; AF083955; Hs.279852; G protein-coupled receptor; 7tm_1,globin;TM=Y;SS=M; 2.30
 434693; AW976001; Hs.337603; ESTs; none,none; 2.26
 452034; F12234; Hs.75893; ankyrin 3, node of Ranvier (ankyrin G); ZU5,death,none; 2.25
 423732; AF058056; Hs.132183; solute carrier family 16 (monocarboxylic acid transporters), member 7; sugar_tr;TM=Y;SS=M; 2.25
 404956;; C1003210*gi|6912582|ref|NP_036524.1| peflin [Homo sapiens] gi|6009487|dbj|BAA84922.1| (AB; none,PI3_P14_kinase,PI3K_C2,PI3K_rbd,PX,PI3Ka,C2; 2.24
 452183; NM_006594; Hs.28298; adaptor-related protein complex 4, beta 1 subunit; Adaptin_N,Y_phosphatase; 2.23
 420529; D25259; Hs.319844; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; pkinase,DAG_PE-bind,RBD,ras,DC1,GFP;TM=M;; 2.21
 408808; BE074219; Hs.17230; hypothetical protein FLJ22087; Armadillo_seg;TM=M;SS=M; 2.21
 451932; AA360954; Hs.27268; Homo sapiens cDNA: FLJ21933 fis, clone HEP04337; SH3,PH,RhoGEF;TM=M;; 2.21
 432008; AW296791; Hs.193170; hypothetical protein FLJ21687; LIM,Synaptophysin,ion_trans,KOW; 2.20
 455840; BE145897;; gb:MR0-HT0208-221299-204-b07 HT0208 Homo sapiens cDNA, mRNA sequence; PI3_P14_kinase,PI3Ka,PI3_P14_kinase,PI3Ka; 2.19
 429238; NM_002849; Hs.198288; protein tyrosine phosphatase, receptor type, R; Y_phosphatase;TM=Y;SS=M; 2.19
 430975; AA490055;; gb:ab05b09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 3', mRNA sequence; adenylatekinase,Thymidylate_kin;TM=M;; 2.17
 407174; T79938; Hs.77062; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5; ig,none; 2.16
 450921; AA098790; Hs.146245; ESTs, Moderately similar to T17242 hypothetical protein DKFZp586B1417.1 [H.sapiens]; none;NA;NA; 2.15
 427209; H06509; Hs.92423; KIAA1566 protein; pkinase;TM=M;; 2.14
 401917; AL050149;; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_prot,ion_trans,PAC,PAS,none; 2.12
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; adenylatekinase,none; 2.07
 439520; W76548; Hs.336621; ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ion_trans,none; 2.06
 410439; R35943; Hs.63758; transferrin receptor 2; PA;TM=Y;; 2.05
 448696; AI564769; Hs.173070; EST, Weakly similar to ZN42_HUMAN ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1) [H.sapiens]; none,zf-C2H2; 2.04
 449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K_tetra,ion_trans,none; 2.04
 453496; AA442103; Hs.33084; solute carrier family 2 (facilitated glucose/fructose transporter), member 5; sugar_tr;TM=Y;SS=M; 2.02
 443952; AI149106; Hs.143530; ESTs; pkinase,none; 2.02
 437589; AA761322; Hs.269662; ESTs; SH2,SH3,C2,PH,RasGAP,none; 2.02
 422637; AA399024; Hs.118836; myoglobin; globin;TM=M;; 2.01
 450253; AL133047; Hs.24715; Homo sapiens mRNA; cDNA DKFZp434D0215 (from clone DKFZp434D0215); partial cds; SH3;TM=M;; 1.97
 401984;; C17000146*gi|2143629|pir|J|A57156 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I; pkinase;; 1.96
 453464; AI884911; Hs.32989; receptor (calcitonin) activity modifying protein 1; none;TM=Y;; 1.95
 417733; AL048678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown protein; none;NA;NA; 1.94
 411450; H49619; Hs.127301; ESTs; pkinase,none; 1.82
 406303;; C16000922*gi|7499103|pir|T20903 hypothetical protein F14F4.3b - Caenorhabditis elegans gi; ABC_tran,GTP_EFTU,PRK,ABC_membrane;TM=Y;; 1.80
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor type, M; fn3,lg,Y_phosphatase,MAM;TM=Y;SS=M; 1.74

425280; U31519; Hs.1872; phosphoenolpyruvate carboxykinase 1 (soluble); PEPCK;TM=M;; 1.65
 425958; AW163271; Hs.301839; intracellular antigen detected by monoclonal antibody Ki-1; intracellular hyaluronan-binding protein; Y_phosphatase,DSPC;TM=M;; 1.63
 432563; NM_013261; Hs.198468; peroxisome proliferative activated receptor, gamma, coactivator 1; rrm;TM=M;; 1.51

TABLE 49B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586 AW978432 AA830185 N67023 R80000 AL036458 AA358606 AW962990 X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 AI910663 BF905778 BG251264 AL562106 AI890538 AW769258 AI590391 AI913055 AW083235 AI078474 AI925022 AW504628 AW129725 BE466589 AW002786 AW591760 AI968816 AW006268 AW593787 BG236814 AW769893 AW407608 AW075982 AI248207 AI762509 AI812070 AI249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245 BI014177 AL519126 BE675314 AW806520 BI870778 BF879549 BF714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893 BE798121 R09703 BI013066 AI758223 AW469334 BF940841 AW080348 AI270363 AI055892 BE464168 BF431797 BE350144 BF448739 AI693409 BF432999 D62848 AA398070 AI383375 AW611490 AA715338 AA715284 AA715344 AV752763 AI032142 N30308 N22181 H95390 AW675632 X98248 NM_002959 AU127082 AU143346 BE327147 AI168442 AA426361 BF056336 AA418378 AI470560 AI365213 BI032745 BI032986 AA969895 AA233278 AW291971 AA418326 AI198417 AI337018 BI032747 AA888000 AU099083 AU129681 AL036861 AA418275 BF887436 BF767448 AA232975 BI094065 BI859449 AL079651 BF877391 AW902319 BF878798 BG281450 AA418268 BG770672 BE890328 BI520437 BE387505 AW375004 BI020046 BI033747 BF800905 BF869732 N99710 BF905459 BE715637 BE746496 BF918537 BF751392 BF751390 BF369123 BG949840 AA984366 H85743 AW593418 AI990196 T92267 AA018359 H38111 BM050097 BF692315 AW805907 AI547305 AA631091 BF845219 BG949806 T92310 BE277220 X44839 NM_004651 BC000350 BI458316 AU117940 BG759024 BG749694 BE799505 BG831537 AI816335 AA325352 AL547005 AW157038 AI859331 AI816186 AU150786 AL043549 AW162880 AU159233 AI143169 T03478 BE727648 AA764725 BE206603 AI369814 AI984369 AW157545 BE221486 H99016 AU159025 AI074496 AI494516 BE245950 AA704385 AA280862 AI479595 AI369776 BE671398 T05538 AA682249 BI677303 BE645335 AI359434 H92868 D52599 D53609 D54715 T06015 BE222174 AI954706 D53218 D53787 R69889 W86896 AI497670 R70771 BF309414 BE620147 BG910597 AW964968 BE836120 AL579715 H56512 D55956 BI044097 AL555239 BF220278 AA081991 AI819544 AW001573 AW131600 AI858764 D52367 W22034 BG818979 BG024561 BE702779 BI458863 BI910399 BG707755 BF348284 H10055 BI086315 BE620574 H41088 BG119517 W23267 W21941 AA328817 X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 AI910663 BF905778 BG251264 AL562106 AI890538 AW769258 AI590391 AI913055 AW083235 AI078474 AI925022 AW504628 AW129725 BE466589 AW002786 AW591760 AI968816 AW006268 AW593787 BG236814 AW769893 AW407608 AW075982 AI248207 AI762509 AI812070 AI249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245 BI014177 AL519126 BE675314 AW806520 BI870778 BF879549 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893 BE798121 R09703 BI013066 AV659361 BE075267 BF743302 AL549208 AI950002 AI224961 AI471552 AI356537 AA768943 AA677028 AI358509 AI147596 AI208057 AI042009 AA156840 AA156603 AA151281 AA151341 N73171 AL540476 AI950893 BG960775 AL573355 D78831 C17898 D78863 AW747857 BI062758 AW629481 AA837630 AA557850 AA531132 AW973966 AW747856 AA203524 W88451 BE539344 AA361027 BF328781 BE011406 BE011437 BE011402 BE011395 BE011428 BE011421 BE011407 BM046773 AA224297 T33786 T08951 T09274 T08592 T30936 AA350905 NM_018485 AB038237 U69668 AA448366 X63105 BC016514 BE694436 AI655840 AW235355 BG427984 AA612862 AA448223 BM145813 BM194565 AI870824 BE973573 BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687 BF908518 BF907890 R11490 AL536642 BF109180 AA953881 AI783716 BE622908 AI621005 AW148784 AI690114 AW275000 AI765790 BF222859 AW167268 AI990460 AW300443 AA779660 AI620568 BF115024 BE504703 AW628332 AI922851 BE006636 AU158376 AI168279 AA809916 AI469757 AA830828 AA830388 N64324 AI049683 AA970275 BF477364 BG261301 AI326388 AU150565 AU158374 AA687967 N58510 AI650450 AL549572 BF349280 BF349269 BM463016 AW836798 AL120958 AW836891 AW385525 BE175733 BE175727 BE175723 BF092430 BI061782 AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW847833 AL536643 AW366516 AW391532 BE934857 BF925057 AW438446 R86246 AW179270 BE087782 BE832144 AW956025 AW956024 BE550261 BF747649 BF802668 AA369961 AV747207 AW973072 BE467756 N51927 AA531539 AW241296 AI797097 BI492823 AW021896 F10837 BE715542 BE715487 AW087443 AA533638 R51354 AW131541 R51852 N53741 R39257 T77635 BF955795 BF331656 F13236 AW810749 AK055378 BE896063 AV722833 BI032095 BF952019 BG547204 AI151418 W03542 W60401 AI346936 AA862855 W60310 N72501 BF963436 C04881 H90060 AA001203 AI863984 AI932612 AI499771 AI187944 AA501896 AA714924 H00689 AA918680 AA573996 AA521308 AW182868 BF996707 AA908959 AI628880 AW173363 AW65845 AA130178 AI818267 AI653663 AI828924 AA746655 AI951984 AI635625 AI093113 AI377976 AI624029 AI418242 R76291 W92652 AI207798 AV706224 AA742467 AA641806 W61229 AA130170 AA160170 H85007 W72474 W61163 H97873 AL047509 R76567 AA812071 H81599 AA021275 H85004 H85894 BG537537 BF830518 W76228 W46673 Z43839 R78710 C01747 H00789 BI036345 W92828 BE150445 AW380821 AW173095 H85630 H81598 H86032 R84855 R13223 AA774992 AW973785 H60163 AA557608 AI057052 AI241633 T89416 AA379611 AA379464 AA379463 BG025680 AW890852 BE002723 BE763824
10	413227 426966	25501_86 349_1	
15	417886 452098 452203	1031334_1 161393_1 2630_1	
20			
25	439096 425505 400208	1241997_1 1228213_1 16640_1	
30			
35	422667 407305 443068 433075	224778_1 2466680_1 18695_17 78_6	
40			
45	400252	2656_2	
50	400209	16640_1	
55	444825	19904_1	
60	414991 432236 417527 425645 455608 418512 407393 400178	1785136_1 1001131_1 2431831_1 1283068_1 1478902_1 12225_6 6807_1 840_4	
65			
70	410927	3618_2	
75	449343	14470_1	
80	432639 417479 426477 418342	1237887_1 2356588_1 1296538_1 295203_2	

400275	18707_1	NM_006513 BC009390 X91257 BC000716 BM450041 BI771139 AV710955 AU120415 AU141179 AU121081 BE409287 AU141397 AU122238 BI256788 BE386217 AU143368 AU133780 AU139704 BG531086 BE268235 BE545230 AU143414 AV761720 AU129842 AU143343 BE270064 BG473378 BE298813 BI772360 BE617354 AU140124 BE277005 BG746716 BE814960 AW161287 AV762084 BG898985 AW674875 AA313975 AV749916 AA374328 BM011248 AU098465 AW238888 BG940091 BG284599 AW410037 AA378483 D49914 AL573323 AL549819 AL572282 AL572871 AL568117 AL571945 AL547790 AL581217 AL514659 AL573926 AL540816 AW410038 BI262249 BG284713 AL659394 AI093582 AW965846 AA652206 AI686014 AA654357 AU146982 AW273447 AW157715 AW574750 BG683509 AW887824 AI818522 AA703770 BE542873 AA515504 AU154982 AA831254 AA828521 AI088602 AA854654 AA190869 BF062816 AA464944 BG261335 AI003584 BG402820 AA932098 W68695 AW182900 W37334 AI073864 C17924 C18528 AI299318 BF154399 BG319570 BF764242 BF764209 AI620320 T06029 BF447193 F29285 AL548949 BI333775 BE743602 BE618230 BE268139 BF036434 BE562718 BG774381 AA659833 AA297649 AA010945 BG105512 BE269205 T32623 BG015679 AL518518 AL517118 AL538396 AI049861 AL581976 AV752041 W26586 BE181609 AI963016 BG057603 AI720256 AA844560 AA055570 BE619606 C17428 AI042174 N93945 N69743 BF795208 AW057940 BI091399 AW975179 AA909936 H28712 W65445 AL515439 W37117 H66514 T85377 W37369 W19712 BE247277 L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138 AW936035 AW935951 AW935789 AW935881 AW936018 AW935892 BE069084 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445 BE078405 BE078404 BE168534 AV742719 R23027 R63874 AA381749 BG542693 D63271 T94955 AA877494 BF697879 BG984482 AW854930 AW854941 AW814115 AW814431 AW814190 BF325887 BF325890 BF985536 AW819463 AW819514 AW819617 AW819618 AW819609 U35637 AA192323 AA194508 BG011583 F25712 AL596820 BE185376 AA878324 AI619686 AI014377 T85948 R07785 T86972 Y08200 NM_004581 BC003093 BE733834 BI753321 BG773890 BF091906 BI917541 AI023762 AA587230 BF435086 AI264262 AI687392 AI810536 AW589886 AI244419 AA749261 AA535435 AW205689 AI765770 AI765431 C02465 AW305347 AI818456 AA322111 AW381845 AW381829 AV749407 AA811636 AU159893 AA603065 AA652542 AI468678 R49616 AW381863 BE389867 BE182387 BF087771 AA527551 AA134051 AA831504 AA134052 AI871759 AW089048 BI913532 AA367709 BG828155 BF093014 AW837178 T77002 F13038 AK056654 AJ420421 AI127111 AA705921 AA749298 AA776967 AI343768 AW070583 AA766587 AA804876 AA460658 AA394137 W72279 AW071467 AI343843 AA393817 AW769379 AA861873 AA715043 AW512448 AI452856 AI819873 T17354 AW779778 BF477620 AI783605 AI624523 AA261906 AA514931 BI964124 AW576481 AI864544 AA490863 AA860972 BI963076 AI632879 AA291985 AA255873 BI966876 BI963833 Z38970 BI495302 BI495301 AI784395 AU185472 AA652150 AA652026 D20449 BI088167 BI260636 BE869946 AI935271 BI792882 AI762915 AI809275 AI813351 BF447139 AI052069 AI057127 AA398950 AA291984 AA292934 AA262543 BF760287 R46455 R72980 H90786 BE698016 AW959314 BI031449 AL574617 AA776284 AA393770 BM455617 BI602104 BI793150 N36710 H59529 BI005937 BI600748 BF085914 BF085907 BF835429 BF835210 BF085926 AA226136 BF836829 BF836606 BM007373 AI369807 BF085930 W25119 BI252884 BI001270 BE549079 BF238403 R56934 AF086341 W76326 W72300 NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030 AW964027 AA377709 AW848421 T71427 T62567 AW833022 AW833054 H20760 R15237 Z43915 BF372479 F11411 AB038318 BC008888 BE905346 BE301941 AA705936 AW014954 BE378742 AI720050 BE395327 BG951204 AK001451 AU151098 AW515640 AW439618 AI671555 AW304963 AA565885 AI829434 AW590882 AI889234 AW117522 AA847824 AI636224 AA883540 AA169387 AW771571 AI130803 BF438773 AA088710 AI972691 AI972638 AI762358 AI473907 AI925905 AA502277 BG943806 BG218468 AA194853 AU128875 AA306025 BG986896 AA778849 AW946871 AW946782 AW946955 AF086283 W69200 W69304 AW807573 AW807572 AW963941 AA379825 AW963944 AA379564 NM_054014 X52220 BC005147 BI551326 AI393601 AW592611 AA608921 AA731598 W96331 AW590007 AI076813 AI022644 AA158365 AI699321 AI146747 AW296894 H85337 AA017692 AA354519 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TABLE 49C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
5				
10	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	401027	7230983	Minus	70407-70554,71060-71160
	400991	8096825	Plus	159197-159320
	406137	9166422	Minus	30487-31058
	404083	9944029	Minus	16650-17082
15	404440	7528051	Plus	80430-81581
	400792	7382433	Plus	134339-134593
	404289	2769644	Plus	15049-15286,30267-30457
	401083	3242744	Plus	33192-33360
	402211	7689783	Minus	67414-68229
20	402705	8782736	Plus	89961-90114,90773-90895,91131-91261
	402233	7690102	Plus	90281-91477
	405370	2078469	Minus	38980-39111
	400846	9188605	Plus	39310-39474
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
25	401345	9926424	Plus	148042-148392
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
	406364	9256114	Minus	50715-50833
	405490	7705240	Plus	20683-20850
	400755	8119083	Minus	120084-120889
30	404276	9885189	Plus	127624-127856
	402915	7406502	Minus	140-276
	405616	5649378	Minus	2782-3308
	400847	9188605	Plus	44643-44835
	402328	4464283	Minus	13758-13922,14558-14752
35	405369	2078469	Minus	34183-34357,35686-35751
	400845	9188605	Plus	34428-34612
	403716	7239669	Plus	86899-87122
	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
	404140	9843520	Plus	37761-38147
40	405516	9454624	Plus	112707-112876,113676-113854
	405110	8096888	Minus	118940-119100
	403608	8308266	Minus	121321-121476
	401241	4827300	Minus	30503-30844,31056-31248
	405102	8076881	Minus	120922-121296
45	404185	4572584	Minus	129171-129327
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405411	3451356	Minus	17503-17778,18021-18290
	405602	4753260	Plus	44647-44778
	403391	9438337	Plus	42410-42544,83317-83540,86840-86922,8797
50	403869	7280046	Minus	34379-34583
	404942	7382153	Plus	92095-92252
	403142	9444521	Plus	89286-90131
	400844	9188605	Plus	24746-24872,25035-25204
	402704	8782736	Plus	37368-37493
55	402833	8918545	Plus	26987-27778
	401851	7770425	Minus	146443-146664,147794-147971,148351-14848
	401242	4827300	Minus	32616-32863
	401943	4914397	Plus	65925-66371
	402807	6456148	Minus	101542-101660,103476-103656
60	402603	9909396	Minus	141663-141852
	405328	3253114	Plus	21399-21583
	402974	9663349	Plus	124035-124321
	400987	8086488	Minus	22052-22185
	403335	8568884	Plus	112307-112524,114074-114703
65	401113	9966541	Minus	19419-19959
	401185	9625304	Minus	177393-177691
	404537	8247909	Minus	188775-189573
	405266	4156171	Minus	63337-63552
	402615	9926801	Plus	131390-132157
70	400566	9884730	Plus	64486-64714
	403212	7630897	Minus	156037-156210
	403290	8083176	Plus	19288-20076
	401342	9908882	Plus	3096-3242
	400471	9931670	Minus	105629-105760
75	405588	5002511	Plus	46180-46366
	400539	7574902	Plus	8559-8721
	403743	7652003	Minus	136463-136646
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	405099	8074292	Minus	114365-114514,128635-128831
80	401445	8218584	Minus	93700-93886
	405480	2766593	Plus	33325-33659
	402183	7658390	Minus	100618-104298
	400749	7331445	Minus	9162-9293
	406139	9166768	Minus	72397-72602

402129	7704953	Minus	166156-166365
400645	8117693	Minus	58471-58716
403201	9958297	Minus	109782-109934
403609	8308266	Minus	125974-126320
400719	8118911	Minus	44579-44656,45294-45487,46449-46641
403088	8954241	Plus	169894-170193,170504-170806
403328	8469086	Minus	120428-120703
403305	8099945	Plus	114632-114805
401702	1871197	Minus	68182-68325
400777	8131663	Plus	70745-71121
404956	7387343	Plus	55883-56203
401917	9502466	Plus	25054-25229
401984	4454511	Plus	103825-104024
406303	8575868	Plus	173622-173786

Table 50A lists about 414 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 85th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 51A lists about 518 genes up-regulated in seminomatous testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" seminomatous testicular cancer level was set to the 85th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 52A lists about 673 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal adult tissues was greater than or equal to 6. The "average" testicular cancer level was set to the 75th percentile amongst testicular cancers. The "average" normal adult testicular tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 53A lists about 735 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal adult tissues was greater than or equal to 3. The "average" testicular cancer level was set to the 95th percentile amongst testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 54A lists about 476 testis-specific genes downregulated in testicular cancer (non-seminomatous and seminomatous). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio (R1) of normal testis to normal adult tissues was greater than or equal to 3. R1 was calculated as the mean number of interquartile range values over the median normal adult body tissue expression among normal testicular samples. The ratio (R2) of "average" normal testis to "average" testicular cancer among these genes was greater than or equal to 2. The "average" normal testis level was set to the 50th percentile amongst normal testis. The "average" normal testicular cancer level was set to the 95th percentile amongst testicular cancer samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 55A lists about 586 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 95th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult testicular tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 56A lists about 812 genes up-regulated in seminomatous testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" seminomatous testicular cancer level was set to the 50th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 50A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues

Pkey	ExAccn	UniGene	Unigene Title	R1
432666	AW204069		ESTs, Weakly similar to unnamed protein	74.60
432730	AI066520	Hs.131358	ESTs	50.55
450581	AF081513	Hs.25195	TGF-beta 4	47.85
418696	AW959433	Hs.326290	hypothetical protein FLJ12581	44.05
423458	AI204212		ESTs	36.60
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	30.60
448981	AI968719	Hs.195387	ESTs	26.40
407710	AW022727	Hs.23616	ESTs	24.00
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	19.35
451106	BE382701	Hs.25960	N-MYC oncogene	18.85
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	18.40
420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	18.25

	424578	AK001973	Hs.150890	hypothetical protein	17.86
	418756	AA252254	Hs.226949	ESTs	17.20
	404996			Target Exon	16.15
5	447534	AW953935	Hs.288655	ESTs	15.80
	456847	AI360456	Hs.37776	ESTs	15.00
	446979	AI654443	Hs.197683	ESTs	14.80
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	14.75
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	14.70
10	449322	AI638616	Hs.196566	ESTs	14.35
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	14.20
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	12.95
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	12.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	12.55
15	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.43
	406547			Target Exon	12.35
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	12.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	11.65
	408908	BE296227	Hs.250822	serine/threonine kinase 15	11.55
20	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	11.05
	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (10.08
	426866	U02330	Hs.172816	neuregulin 1	10.05
	446791	AI632278	Hs.195922	ESTs	10.05
	433159	AB035898	Hs.150587	kinesin-like protein 2	9.85
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.95
25	427521	AW973352		ESTs	8.92
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	8.90
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.52
	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
30	408465	AW196940	Hs.253277	ESTs	8.47
	444971	AI651116	Hs.148659	ESTs	8.35
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	8.35
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	8.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.95
35	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	7.75
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	7.65
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	7.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	7.36
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	7.25
40	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.25
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	7.22
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.13
	435918	AF263538	Hs.86232	growth differentiation factor 3	7.13
	412537	AL031778		nuclear transcription factor Y, alpha	7.08
45	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	7.05
	428916	AF003001	Hs.194552	telomeric repeat binding factor (NIMA-in	6.88
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.75
	437052	AA861697	Hs.120591	ESTs	6.75
50	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.72
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.71
	457465	AW301344	Hs.122908	DNA replication factor	6.62
	442832	AW206560	Hs.253569	ESTs	6.54
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	6.30
55	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	6.30
	448588	AI970276	Hs.156905	KIAA1676	6.12
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	6.09
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	5.95
	412642	BE244598	Hs.809	hepatocyte growth factor (hepatopoietin A;	5.85
60	443068	AI188710		ESTs	5.85
	438450	AI050866	Hs.65853	nodal, mouse, homolog	5.81
	441287	AW293132	Hs.131373	ESTs	5.80
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	5.76
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
65	436902	AW247145	Hs.192729	ESTs	5.70
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
70	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	5.56
	436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCL_CGAP_Su	5.55
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	5.51
	431354	BE046956	Hs.251673	DNA (cytosine-5)-methyltransferase 3 be	5.51
	430044	AA464510	Hs.152812	ESTs	5.47
	437036	AI571514	Hs.133022	ESTs	5.45
	435663	AI023707	Hs.134273	ESTs	5.40
75	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.40
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.21
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	5.15
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	5.15
	430272	X04898	Hs.237658	apolipoprotein A-II	5.12
80	427961	AW293165	Hs.143134	ESTs	5.05
	424315	AW614850	Hs.193384	putative 28 kDa protein	5.05
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!!	5.00
	418477	AW022983		gb:df46h12.y1 Morton Fetal Cochlea Homo	5.00
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	4.95

	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.94
	443537	D13305	Hs.203	cholecystokinin B receptor	4.92
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	4.90
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
5	423642	AW452650	Hs.157148	hypothetical protein MGC13204	4.80
	449592	AI655494	Hs.195718	ESTs	4.75
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 s3	4.73
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.68
10	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	4.61
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.60
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	4.48
	402145			Target Exon	4.48
15	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	4.47
	453289	AI188161	Hs.144627	ESTs	4.45
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	4.40
	422689	AW856655		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	4.32
20	426427	M86699	Hs.169840	TTK protein kinase	4.30
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	4.20
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.18
	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (4.15
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.10
25	438188	AA779975	Hs.128859	ESTs	4.10
	435514	AW592804		ESTs	4.10
	442333	AI650877	Hs.129302	ESTs	4.05
	413627	BE182082	Hs.246973	intron of Bicaudal D homolog 1	4.00
	445140	AI650599	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
30	448038	AW015073	Hs.232026	ESTs, Weakly similar to ROS2_HUMAN 52 KD	4.00
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.95
	419423	D26488	Hs.90315	KIAA0007 protein	3.95
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	3.95
	441553	AA281219	Hs.121296	ESTs	3.95
35	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.91
	409757	NM_001898	Hs.123114	cystatin SN	3.89
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.88
	450351	BE547267	Hs.59791	hypothetical protein MGC13183	3.85
	403780			C4001759:glj133250[sp]P19474[RO52_HUMAN	3.84
40	421917	AB028943	Hs.109445	KIAA1020 protein	3.84
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	3.84
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	3.82
	410193	AJ132592	Hs.59757	zinc finger protein 281	3.80
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.80
45	415829	AW450198	Hs.163742	ESTs	3.78
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.77
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.70
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.68
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.66
50	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	3.65
	420900	AL045633	Hs.44269	ESTs	3.65
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.65
	426496	D31765	Hs.170114	KIAA0061 protein	3.60
	452461	N78223	Hs.108106	transcription factor	3.60
55	418379	AA218940	Hs.137516	fidgetin-like 1	3.50
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.48
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.45
	419384	AA490866	Hs.39429	ESTs	3.44
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	3.43
60	446293	AI420213	Hs.149722	LIM domain transcription factor LIM-1 (h	3.41
	422094	AF129535	Hs.272027	F-box only protein 5	3.40
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.40
	423198	M81933	Hs.1634	cell division cycle 25A	3.39
	424153	AA451737	Hs.141496	MAGE-like 2	3.38
65	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.37
	443715	AI583187	Hs.9700	cyclin E1	3.34
	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.34
	449571	AW016812	Hs.200266	ESTs	3.34
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.31
70	452807	AA028933	Hs.162434	ESTs	3.31
	422756	AA441787	Hs.119889	glycoprotein hormones, alpha polypeptide	3.30
	421650	AA781795	Hs.122587	ESTs	3.30
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, alp	3.28
	438494	AA908678	Hs.130183	ESTs	3.23
75	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.22
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	3.20
	427642	R40761	Hs.9834	ESTs	3.20
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.18
	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.18
80	442618	R56222	Hs.26514	ESTs	3.17
	415799	AA653718	Hs.225841	DKFZP434D193 protein	3.17
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.15
	450431	AW136797	Hs.266041	ESTs	3.13
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.12

	430835	AI240006	Hs.192326	ESTs	3.12
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.10
	417791	AW965339	Hs.111471	ESTs	3.10
5	434609	R76593		gb:yi60c11.1 Soares placenta Nb2HP Homo	3.05
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.04
	411975	AI916058	Hs.144583	ESTs	3.01
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
10	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	2.99
	440207	AI371978	Hs.128326	ESTs	2.98
	435726	BE535787	Hs.113170	ESTs	2.97
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.97
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	2.95
	435373	AW665538	Hs.117689	ESTs	2.93
15	452571	W31518	Hs.34665	ESTs	2.93
	454679	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo	2.91
	414972	BE263782	Hs.77695	KIAA0008 gene product	2.90
	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.90
	420092	AA814043	Hs.88045	ESTs	2.89
20	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	2.89
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	2.87
	422746	NM_004484	Hs.119651	glypican 3	2.87
	446258	AI283476	Hs.263478	ESTs	2.86
	444371	BE540274	Hs.239	forkhead box M1	2.86
25	409517	X90780		tropoin I, cardiac	2.85
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	2.84
	443169	AI038687	Hs.133338	ESTs	2.84
	447519	U46258	Hs.339665	ESTs	2.84
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.84
30	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.83
	416201	AA467752	Hs.195161	ESTs	2.83
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.83
	457191	AI376228		Friend leukemia virus integration 1	2.82
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	2.81
35	413646	BE155042		gb:PMO-HT0349-101299-002-E04 HT0349 Homo	2.80
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	2.75
	427719	AI393122	Hs.134726	ESTs	2.75
	451684	AF216751	Hs.26813	CDA14	2.75
	414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	2.74
40	442032	AW016786		ESTs	2.73
	437123	AL049285	Hs.302053	Homo sapiens mRNA; cDNA DKFZp564M193 (fr	2.72
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	2.72
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	2.71
	438180	AA808189	Hs.272151	ESTs	2.70
45	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.70
	423765	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.69
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	2.69
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	2.68
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.67
50	445413	AA151342	Hs.12677	CGI-147 protein	2.66
	448769	N66037	Hs.38173	ESTs	2.66
	411022	AW936378		gb:QV4-DT0021-301299-071-f05 DT0021 Homo	2.65
	423600	AI633559	Hs.310359	ESTs	2.65
	447175	AI365208	Hs.293606	ESTs	2.65
55	414151	AW976468	Hs.257245	ESTs	2.65
	448877	AI583696	Hs.253313	ESTs	2.62
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.61
	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	2.61
	449665	AI655391	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.61
60	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.60
	429228	AI553633		ESTs	2.60
	410929	H47233	Hs.30643	ESTs	2.59
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.58
	446142	AI754693	Hs.145968	ESTs	2.56
65	445093	AI207197		ESTs	2.56
	413686	AI469213	Hs.71404	ESTs	2.55
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	2.55
	420218	AW958037		ribosomal protein L4	2.55
70	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	2.55
	414312	AA155694	Hs.191060	ESTs	2.55
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synth	2.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.52
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.51
	435096	AA664977		gb:nu73b07.s1 NCI_CGAP_Alv1 Homo sapiens	2.50
75	422468	AA355210		gb:EST63589 Jurkat T-cells V Homo sapien	2.50
	449576	AW014631	Hs.225068	ESTs	2.50
	415684	D59356		sorbitol dehydrogenase	2.50
	452226	AA024898	Hs.157103	ESTs	2.50
	421451	AA291377	Hs.50831	ESTs	2.50
80	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.50
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.49
	453941	U39817	Hs.36820	Bloom syndrome	2.49
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.49
	449655	AI021987	Hs.59970	ESTs	2.49

	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.49
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	2.48
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.48
5	445363	NM_005993	Hs.12570	tubulin-specific chaperone d	2.47
	452404	AW450675	Hs.212709	ESTs	2.46
	444823	BE262989	Hs.12045	putative protein	2.46
	427675	AW138190	Hs.180248	zinc finger protein 124 (HZF-16)	2.45
	444159	AF116846	Hs.10431	dead ringer (Drosophila)-like 2 (bright	2.45
10	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	2.45
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.45
	433183	AF231338	Hs.222024	transcription factor BMAL2	2.45
	447350	AI375572		v-erb-a avian erythroblastic leukemia vi	2.45
	428728	NM_016625	Hs.191381	hypothetical protein	2.43
15	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	2.43
	410276	AI554545		angiopoietin-2	2.42
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.42
	419029	AA233397	Hs.326290	hypothetical protein FLJ12581	2.42
	437908	AI082424		ESTs	2.41
20	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.41
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	2.40
	425212	AW962253	Hs.171618	ESTs	2.39
	423787	AJ295745	Hs.236204	nuclear pore complex protein	2.38
	425601	AW629485	Hs.140720	GSK-3 binding protein FRAT2	2.38
25	449676	AW380579	Hs.209657	ESTs	2.38
	429467	NM_004477	Hs.203772	FSHD region gene 1	2.37
	453227	AW135862	Hs.243991	ESTs	2.37
	417833	AW003251	Hs.86264	hypothetical protein FLJ14549	2.36
	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.36
30	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.35
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	2.35
	410060	NM_001448	Hs.58367	glypican 4	2.35
	449138	AW294215	Hs.195631	ESTs	2.35
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.35
35	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	2.35
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.34
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	2.34
	407818	AL021938	Hs.40154	jumonji (mouse) homolog	2.34
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	2.33
40	401704			NM_021195*:Homo sapiens claudin 6 (CLDN6	2.33
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	2.32
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.32
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	2.31
	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.30
45	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.30
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	2.30
	448755	AW503807	Hs.21907	histone acetyltransferase	2.30
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	2.29
50	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	2.29
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.28
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	2.27
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.26
	401220			branched chain aminotransferase 1, cytos	2.26
55	453985	N44545	Hs.251865	ESTs	2.25
	414890	BE281095	Hs.77573	uridine phosphorylase	2.25
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.25
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	2.25
	424765	AA428211		hypothetical protein FLJ14033 similar to	2.25
60	419278	AU076799	Hs.1247	apolipoprotein A-IV	2.24
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	2.24
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	2.23
	417273	AK002209	Hs.81831	Homo sapiens cDNA FLJ11347 fis, clone PL	2.23
	449722	BE280074	Hs.23960	cyclin B1	2.22
65	443184	AI638728	Hs.131973	ESTs	2.22
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	2.21
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	2.21
	435045	BE297155	Hs.143698	ESTs	2.21
	414883	AA926960		CDC28 protein kinase 1	2.21
70	446323	AI288274	Hs.345792	ESTs	2.20
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.20
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	2.20
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor;	2.20
	418973	AA233056	Hs.191518	ESTs	2.20
75	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.20
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.20
	443748	AW206447		gb:UL-H-B11-afg-g-02-0-UL.s1 NCI_CGAP_Su	2.20
	415989	AI267700		ESTs	2.20
	400195			NM_007057*:Homo sapiens ZW10 interactor	2.20
80	428878	AA436884	Hs.48926	ESTs	2.20
	431805	NM_014053	Hs.270594	FLVCR protein	2.19
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.19
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	2.18
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.18

5	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	2.18
	413992	W26276	Hs.104557	RNA, U2 small nuclear	2.18
	412722	AI343300	Hs.15091	ESTs	2.18
	409089	NM_014781	Hs.50421	KIAA0203 gene product	2.17
	430809	AI791150	Hs.262009	ESTs, Moderately similar to I38022 hypot	2.17
	406542			C19000728*:gi12585552[sp]Q9Y2Q1[Z257_HU	2.17
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfam	2.17
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	2.17
10	425580	L11144	Hs.1907	galanin	2.16
	439398	AA284267	Hs.221504	ESTs	2.16
	452833	BE559681	Hs.30736	KIAA0124 protein	2.15
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	2.15
	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	2.15
	449410	AA001356	Hs.18159	ESTs	2.15
15	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.15
	427953	AA417944	Hs.44331	ESTs	2.15
	422281	M36803	Hs.346935	hemopexin	2.15
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.14
20	444960	AI611317	Hs.341531	ESTs	2.14
	415890	H08225	Hs.268712	ESTs	2.14
	402099			ENSP00000217725*:Laminin alpha-1 chain p	2.14
	427779	AA906997	Hs.180780	TERA protein	2.14
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	2.14
25	422170	AI791949	Hs.112432	anti-Mullerian hormone	2.14
	414161	AA136106	Hs.184852	KIAA1553 protein	2.14
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	2.13
	449810	AB008681	Hs.23994	activin A receptor, type IIB	2.11
	450663	H43540	Hs.25292	ribonuclease HI, large subunit	2.11
30	419525	T79257	Hs.1259	asialoglycoprotein receptor 2	2.11
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.10
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.10
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.10
	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr	2.09
35	418552	AF198254	Hs.86088	IGF-II mRNA-binding protein 1	2.09
	408291	AB023191	Hs.44131	KIAA0974 protein	2.09
	425474	Z48054	Hs.158084	peroxisome receptor 1	2.09
	453028	AB006532	Hs.31442	RecQ protein-like 4	2.09
	447831	AI433293	Hs.164115	ESTs	2.08
40	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.08
	429166	AB033096	Hs.197668	KIAA1270 protein	2.08
	432446	AA542845	Hs.294088	GAJ protein	2.08
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.07
	431093	AB031038	Hs.301704	eomesodermin (Xenopus laevis) homolog	2.07
45	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.07
	449569	AI656634	Hs.195389	ESTs	2.07
	429999	AI761902	Hs.99597	ESTs	2.06
	420552	AK000492	Hs.98806	hypothetical protein	2.06
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	2.05
50	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.05
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.05
	450375	AA009647		a disintegrin and metalloproteinase doma	2.05
	409066	AA062980	Hs.66960	ESTs	2.05
	425700	AF076292	Hs.159251	forkhead box H1	2.05
55	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	2.05
	409093	BE243834	Hs.50441	CGI-04 protein	2.05
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.04
	408446	AW450669	Hs.45068	hypothetical protein DKFZp434I143	2.04
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.04
60	429840	AA459699	Hs.99496	ESTs	2.03
	409717	AW452871	Hs.56043	CGI-115 protein	2.02
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.02
	448275	BE514434	Hs.20830	kinesin-like 2	2.02
	432731	R31178	Hs.287820	fibronectin 1	2.02
65	405157			NM_003213*:Homo sapiens TEA domain famil	2.02
	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	2.01
	423739	AA398155	Hs.97600	ESTs	2.01
	421310	AW630087	Hs.103315	trinucleotide repeat containing 1	2.00
	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	2.00
70	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	2.00
	407259	L02256		gb:Human Fab fragment binding syncytial	2.00

TABLE 50B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
		BG215094 BG198867 BG196332 BG208220 BG212418

	430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603
			AI352469 BE061601 BI062752 AW818206 BF887722
	427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165
5			AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
	427486	684159_1	BF510715 BE673055 BE464111 AW590620 AI637839 AA404324 AW236441 AI650952 BF056796 AA974433
	412537	14066_1	AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114
			AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364
			BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793
			AA382556 AW235763 AA927051 AI862075 BE886691 BE619282
10	443068	18695_17	AV752763 AI032142 N30308 N22181 H95390 AW675632
	436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673
	418477	4172_1	BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092
			AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
15	418378	1227421_1	AA218925 AW962081 AA354237
	422689	874209_1	AW954733 AA315006 AW856665
	435514	132288_1	AA683356 AW592804 AI150287
	439780	49082_1	AL109688 R23665 R26578
	434609	14739_1	AF147390 R76593 R76594
20	454679	174325_1	AW813110 BF771370 BF771371 AW813113 AW003381
	434414	35978_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422
			AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298
			AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175
			BF854337
25	409517	4537_1	NM_000363 X54163 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI657074 C03333 AI193911 C05024 C03193 AI950215 C05070
			C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255
			T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339
	406687	0_0	M31126
	457191	1389182_1	AI216469 AI354789 AA446136 H24336 AA446443 AI376228 R48940
30	410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
			BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
			AW840571
	413646	1525656_1	BE155042 BE155040 BE154987 BE155012
	442032	15407_1	BF223060 BF222818 AI950472 AW016786 AI207136 AI969730 BF222890 AI633857 AI968711 AA974235 AI352637
35	411022	1066666_1	AW936378 AW936544 AW813513
	429228	215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620
			AW969605 AI553633
	445093	175963_1	AI207197 BF773544 AW196462
	420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756
			AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
40	435096	125215_1	H30075 AA664977 AW975278
	422468	216674_1	AW962701 AA310998 AW962699
	415684	18695_18	BF666746 D59356 BG678312 N56640 AA166861
	447350	2267324_1	AI375572 AI480404 BF430912 T06882
45	410276	641443_1	AA083514 AI554545 AW169852 AI363822 AI633826 AI656026 AI765624 AA147545 AA147552
	437908	13268_11	AI740586 AA771806 BE500996 AW204531 AI082424 AI033879 BF093176 AA771764 D38676
	418866	245947_1	T65754 AA229658 AA229857
	424765	6857_1	AK021881 AU145974 AU145787 C16964 AA428211 AU119698 AA993264 BF999192 AW903017 AA346559 AU119446 AW581679 AA991677
			AW898165 AW386878 AW890957 Z18340
50	414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360
			AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871
			AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887
			AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407
			AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
55	443748	669881_1	BM467830 AI084433 AW206447 AI400976 AI248530 R16553
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF090208 BF090960 BF095153
			BG285837 AI720344 BF541715 AA355086 AA172236
	400195	16894_2	BM477554 BM423967 BC020979 AF067656 NM_007057 BI869291 BG468263 BG760599 BI261788 AA855060 BE257094 BF212452 BE888249
			BI259219 AW409765 BE089556 AL564377 BI258884 AW440401 AL578460 AL578434 AL556136 BG036804 AL531381 AW371767 BG610641
60			BF102552 BE294929 BF792282 BG121657 BG502285 BG777493 AL564510 AW770358 AA573448 AA564001 AA969560 AW078946 AW750065
			AL573860 AA143778 H99221 AA969210 AW103401 AW750073
	450375	16559_3	BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410
			H59605 BE157601 AA113758
65	TABLE 50C		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.	
70	Strand:	Indicates DNA strand from which exons were predicted.	
	NL_position:	Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand
	404996	6007890	Plus
	406547	7711513	Minus
75	402145	8018280	Plus
	403780	8076989	Plus
	403432	9719611	Minus
	401704	3097841	Plus
	403433	9719611	Minus
80	401220	9929324	Minus
	406542	7711499	Plus
	402099	8117697	Plus
	406137	9166422	Minus

405157 9966228 Plus 156363-156502,157573-157746

5

TABLE 51A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of seminomatous testicular cancer compared to normal adult tissues

10

Pkey	ExAccn	UnigenelD	Unigene Title	R1
418696	AW959433	Hs.326290	hypothetical protein FLJ12581	56.62
432666	AW204069		ESTs, Weakly similar to unnamed protein	49.00
432730	AI066520	Hs.131358	ESTs	37.64
426534	U58096	Hs.2051	testis specific protein, Y-linked	37.60
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	32.70
420367	AA259090	Hs.257028	ESTs	29.98
420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	26.50
437052	AA861697	Hs.120591	ESTs	26.42
407710	AW022727	Hs.23616	ESTs	23.85
420528	AF130728	Hs.98586	doublesex and mab-3 related transcriptio	23.12
424578	AK001973	Hs.150890	hypothetical protein	22.27
420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	22.06
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	20.46
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	18.44
434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	15.92
430252	AI638774	Hs.105328	testes development-related NYD-SP20	15.44
423458	AI204212		ESTs	15.28
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	15.26
427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	14.84
427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	12.98
426427	M86699	Hs.169840	TTK protein kinase	12.44
420401	AK001907	Hs.97464	hypothetical protein	12.40
406937	U14622		gb:Human transketolase-like protein gene	11.60
430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	11.55
425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	11.52
418477	AW022983		gb:df46h12.y1 Morton Fetal Cochlea Homo	10.94
434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	10.78
436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-U1.s1 NCL_CGAP_Su	10.54
437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothei	10.40
433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	10.32
421241	X91817	Hs.102866	transketolase-like 1	10.14
410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	10.02
418134	AA397769	Hs.86617	ESTs	9.76
433159	AB035898	Hs.150587	kinesin-like protein 2	9.56
433975	AA971953	Hs.122055	ESTs	9.36
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	9.30
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	9.22
431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	9.16
436899	AA764852		ESTs	8.76
426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.76
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	8.64
408908	BE296227	Hs.250822	serine/threonine kinase 15	8.50
413627	BE182082	Hs.246973	intron of Bicaudal D homolog 1	8.42
425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	8.30
415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.14
408728	AL137379	Hs.47125	hypothetical protein FLJ13912	8.14
406547			Target Exon	8.02
424153	AA451737	Hs.141496	MAGE-like 2	7.90
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.64
437421	AA917062		ESTs	7.53
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.50
419423	D26488	Hs.90315	KIAA0007 protein	7.38
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.38
431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.32
430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (7.29
436608	AA628980	Hs.192371	down syndrome critical region protein DS	7.25
435206	AI432364	Hs.160594	ESTs	7.20
414972	BE263782	Hs.77695	KIAA0008 gene product	7.12
407340	AA810168	Hs.284289	vittigo-associated protein VIT-1	7.10
426518	Z43039	Hs.170198	KIAA0009 gene product	7.10
436513	AJ278110	Hs.125507	DEAD-box protein	7.04
427521	AW973352		ESTs	6.96
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	6.92
422232	D43945	Hs.113274	transcription factor EC	6.90
420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	6.83
431041	AA490967	Hs.197955	KIAA0704 protein	6.76
427335	AA448542	Hs.251677	G antigen 7B	6.58
422797	AB033064	Hs.236463	KIAA1238 protein	6.55
418379	AA218940	Hs.137516	fidgetin-like 1	6.46

	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	6.45
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	6.44
	422665	AJ011812	Hs.119018	transcription factor NRF	6.38
5	433701	AW445023	Hs.15155	ESTs	6.34
	436909	AA907120		ESTs	6.28
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	6.27
	429228	AI553633		ESTs	6.26
	419384	AA490866	Hs.39429	ESTs	6.23
10	435514	AW592804		ESTs	6.08
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	5.90
	430835	AI240006	Hs.192326	ESTs	5.89
	438188	AA779975	Hs.128859	ESTs	5.88
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	5.80
15	408758	NM_003686	Hs.47504	exonuclease 1	5.78
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	5.70
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.67
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	5.64
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	5.58
20	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	5.58
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	5.55
	438494	AA908678	Hs.130183	ESTs	5.52
	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	5.52
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	5.48
25	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	5.45
	413623	AA825721	Hs.246973	intron of Bicaudal D homolog 1	5.36
	402145			Target Exon	5.30
	414136	AA812434		SMC2 (structural maintenance of chromoso	5.28
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	5.22
30	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	5.16
	408460	AA054726	Hs.285574	ESTs	5.14
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.12
	420900	AL045633	Hs.44269	ESTs	5.08
	426496	D31765	Hs.170114	KIAA0061 protein	5.01
35	407122	H20276	Hs.31742	ESTs	5.00
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	4.95
	402199			Target Exon	4.90
	409103	AF251237	Hs.112208	XAGE-1 protein	4.90
	416859	H43437	Hs.80305	hypothetical protein MGC14258	4.84
40	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	4.82
	410929	H47233	Hs.30643	ESTs	4.73
	417886	AA214584		ESTs	4.73
	426223	AW977812	Hs.130391	ESTs	4.72
	409421	AA199883	Hs.67624	ESTs	4.72
45	428249	AA130914	Hs.183291	zinc finger protein 268	4.71
	429999	AI761902	Hs.99597	ESTs	4.68
	431721	AB032996	Hs.268044	KIAA1170 protein	4.68
	408321	AW405882	Hs.44205	cortistatin	4.67
	419197	N48921	Hs.27441	KIAA1615 protein	4.66
50	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	4.64
	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	4.64
	427119	AW880562	Hs.272525	ESTs	4.64
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.64
55	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.64
	409066	AA062980	Hs.66960	ESTs	4.62
	416201	AA467752	Hs.195161	ESTs	4.53
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.52
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.50
60	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	4.46
	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.46
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.34
	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	4.32
	418971	AA360392	Hs.87113	ESTs	4.30
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (4.29
65	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.21
	415717	AA167270	Hs.130435	ESTs	4.18
	423198	M81933	Hs.1634	cell division cycle 25A	4.12
	433849	BE465884	Hs.280728	ESTs	4.12
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.11
70	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	4.07
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.07
	414725	AA769791		ring finger protein 21, interferon-respo	4.05
	408291	AB023191	Hs.44131	KIAA0974 protein	4.05
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.04
75	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.04
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.03
	421917	AB028943	Hs.109445	KIAA1020 protein	4.02
	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	4.02
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.01
80	436360	AI962796	Hs.156100	ESTs	4.00
	438624	AA889055	Hs.123468	ESTs	3.99
	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	3.92
	411945	AL033527	Hs.92137	L-myc-2 protein(MYCL2)	3.90
	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.90

	413833	Z15005	Hs.75573	centromere protein E (312kD)	3.90
	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.88
	438456	AA913381	Hs.20594	ESTs	3.88
5	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.87
	412537	AL031778		nuclear transcription factor Y, alpha	3.86
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.85
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	3.83
	422094	AF129535	Hs.272027	F-box only protein 5	3.82
10	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.80
	416350	AF188625	Hs.189507	phospholipase A2, group IID	3.78
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.76
	401435			C14000397*.gi 7499898 pir T33295 hypoth	3.76
	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	3.74
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	3.70
15	409089	NM_014781	Hs.50421	KIAA0203 gene product	3.70
	426067	AW664691	Hs.97053	ESTs	3.67
	415684	D59356		sorbitol dehydrogenase	3.66
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.62
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	3.62
20	427761	AA412205	Hs.140996	ESTs	3.61
	433641	AF080229		gb:Human endogenous retrovirus K clone 1	3.60
	418216	AA662240	Hs.283099	AF15q14 protein	3.59
	438180	AA808189	Hs.272151	ESTs	3.58
	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	3.56
25	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.55
	428878	AA436884	Hs.48926	ESTs	3.54
	438885	AI886558	Hs.184987	ESTs	3.53
	416445	AL043004	Hs.79337	KIAA0135 protein	3.52
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.51
30	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.49
	427298	AA400495		ESTs	3.48
	420218	AW958037		ribosomal protein L4	3.40
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	3.40
35	410420	AA224053	Hs.172405	cell division cycle 27	3.40
	432809	AA565509	Hs.131703	ESTs	3.36
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.34
	421373	AA808229	Hs.46677	ESTs	3.34
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.31
40	418830	BE513731	Hs.88959	hypothetical protein MGC4816	3.30
	431077	AI669133	Hs.115660	hypothetical protein FLJ12810	3.30
	418049	AA211467		Homo sapiens, Similar to nuclear localiz	3.26
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.22
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	3.21
45	434288	AW189075	Hs.116265	fibrillin3	3.20
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.19
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.17
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.17
	420161	AI683069	Hs.120817	ESTs	3.17
50	414618	AI204600	Hs.95978	hypothetical protein MGC10764	3.16
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.14
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.14
	423419	R55336	Hs.23539	ESTs	3.13
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.12
55	408092	NM_007057	Hs.42650	ZW10 interactor	3.12
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	3.12
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	3.12
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.12
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.11
60	420552	AK000492	Hs.98806	hypothetical protein	3.11
	402408			NM_030920*.Homo sapiens hypothetical pro	3.10
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.10
	415829	AW450198	Hs.163742	ESTs	3.09
	423739	AA398155	Hs.97600	ESTs	3.07
65	418459	R85436	Hs.268814	ESTs	3.07
	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.07
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	3.06
	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.06
	420524	AB010575	Hs.98547	amiloride-sensitive cation channel 3, te	3.06
70	433023	AW864793		thrombospondin 1	3.04
	421633	AF121860	Hs.106260	sorting nexin 10	3.04
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.04
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	3.03
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.03
75	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (3.03
	425312	AA354940	Hs.145958	ESTs	3.02
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.01
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.01
	432446	AA542845	Hs.294088	GAJ protein	3.01
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	3.00
80	436902	AW247145	Hs.192729	ESTs	3.00
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.00
	430056	X97548	Hs.228059	KRAB-associated protein 1	2.98
	427617	D42063	Hs.199179	RAN binding protein 2	2.98

	406367		NM_022357:Homo sapiens putative metallo	2.97
	418866	T65754	gb:yc11c07.s1 Stratagene lung (937210) H	2.97
	435918	AF263538	Hs.86232 growth differentiation factor 3	2.97
5	436511	AA721252	Hs.291502 ESTs	2.96
	402680		Target Exon	2.96
	414161	AA136106	Hs.184852 KIAA1553 protein	2.95
	427239	BE270447	ubiquitin carrier protein	2.95
	433683	AI817723	Hs.22678 hypothetical protein FLJ21832	2.94
10	417576	AA339449	Hs.82285 phosphoribosylglycinamide formyltransfer	2.94
	402299		Target Exon	2.92
	420697	AA827705	Hs.26605 ESTs	2.90
	427719	AI393122	Hs.134726 ESTs	2.90
	419131	AA406293	Hs.109526 ESTs	2.89
15	410048	W76467	Hs.343874 proline oxidase homolog	2.89
	427314	AB033024	Hs.175475 KIAA1198 protein	2.89
	424315	AW614850	Hs.193384 putative 28 kDa protein	2.88
	430335	D80007	Hs.239499 KIAA0185 protein	2.87
	410361	BE391804	Hs.62661 guanylate binding protein 1, interferon-	2.87
20	413686	AI469213	Hs.71404 ESTs	2.87
	429183	AB014604	Hs.197955 KIAA0704 protein	2.86
	430292	AK000634	Hs.238270 hypothetical protein FLJ20627	2.86
	422726	U11690	Hs.1572 faciogenital dysplasia (Aarskog-Scott sy	2.86
	437834	AA769294	gb:nz36g03.s1 NCL_CGAP_GCB1 Homo sapiens	2.86
25	435159	AA668879	Hs.116649 ESTs	2.84
	428361	NM_015905	Hs.183858 transcriptional intermediary factor 1	2.84
	430388	AA356923	Hs.240770 nuclear cap binding protein subunit 2, 2	2.84
	434070	AF116652	Hs.270087 hypothetical protein PRO0813	2.83
	429323	NM_001649	Hs.2391 apical protein, Xenopus laevis-like	2.83
30	433247	AB040948	Hs.142856 KIAA1515 protein	2.82
	415884	H22966	Hs.13471 ESTs	2.82
	427668	AA298760	Hs.180191 hypothetical protein FLJ14904	2.82
	437162	AW005505	Hs.5464 thyroid hormone receptor coactivating pr	2.81
	401091		decay accelerating factor for complement	2.81
35	425601	AW629485	Hs.140720 GSK-3 binding protein FRAT2	2.79
	428597	AK000147	Hs.295909 hypothetical protein FLJ10700	2.79
	417705	AW134952	Hs.175220 hypothetical protein FLJ14541	2.79
	438243	AI581311	ESTs	2.78
	418203	X54942	Hs.83758 CDC28 protein kinase 2	2.78
40	410704	BE076754	gb:CM1-BT0601-180200-121-b10 BT0601 Homo	2.77
	429063	AW363845	Hs.322903 ESTs, Weakly similar to A46010 X-linked	2.76
	427147	AA398587	Hs.97414 ESTs	2.76
	430552	AA176374	Hs.243886 nuclear autoantigenic sperm protein (his	2.76
	437660	W31708	Hs.55304 ESTs	2.74
45	425237	U07695	Hs.155227 EphB4	2.72
	419335	AW960146	Hs.284137 hypothetical protein FLJ12888	2.72
	426386	AA748850	Hs.125830 bladder cancer overexpressed protein	2.70
	423123	NM_012247	Hs.124027 SELENOPHOSPHATE SYNTHETASE ; Human selen	2.70
	430968	AW972830	gb:EST384925 MAGE resequences, MAGL Homo	2.70
50	420596	NM_002692	Hs.99185 polymerase (DNA directed), epsilon 2	2.68
	419741	NM_007019	Hs.93002 ubiquitin carrier protein E2-C	2.68
	401464		histone deacetylase 5	2.68
	411856	H67899	Hs.4190 Homo sapiens cDNA: FLJ23269 fis, clone C	2.68
	411365	M76477	Hs.289082 GM2 ganglioside activator protein	2.68
55	419029	AA233397	Hs.326290 hypothetical protein FLJ12581	2.67
	421654	AW163267	Hs.106469 suppressor of var1 (S.cerevisiae) 3-like	2.66
	421535	AB002359	Hs.105478 phosphoribosylformylglycinamide synthase	2.66
	423453	AW450737	Hs.128791 CGI-09 protein	2.66
	412673	AL042957	Hs.31845 ESTs	2.65
60	410006	AW732308	Hs.57783 eukaryotic translation initiation factor	2.65
	434159	AW135214	Hs.191828 ESTs	2.65
	427260	AA663848	gb:ae70b06.s1 Stratagene schizo brain S1	2.64
	439053	BE244588	Hs.6456 chaperonin containing TCP1, subunit 2 (b	2.64
	414706	AW340125	Hs.76989 KIAA0097 gene product	2.64
65	433979	AA620999	gb:ag03a08.s1 Soares_testis_NHT Homo sap	2.64
	403969		ENSP00000034663:Zinc finger protein 131	2.64
	420582	BE047878	Hs.99093 Homo sapiens chromosome 19, cosmid R2837	2.64
	418355	L42563	Hs.1165 ATPase, H ⁺ transporting, nongastric, alp	2.63
	411127	AA668995	Hs.218329 hypothetical protein	2.62
70	437205	AL110232	Hs.279243 Homo sapiens mRNA; cDNA DKFZp564D2071 (f	2.62
	412123	BE251328	Hs.73291 hypothetical protein FLJ10881	2.61
	436481	AA379597	Hs.5199 HSPC150 protein similar to ubiquitin-con	2.60
	408446	AW450669	Hs.45068 hypothetical protein DKFZp434I143	2.59
	437033	AW248364	Hs.5409 RNA polymerase I subunit	2.58
75	418592	X99226	Hs.284153 Fanconi anemia, complementation group A	2.58
	415585	R59946	Hs.184852 KIAA1553 protein	2.57
	424800	AL035588	Hs.153203 MyoD family inhibitor	2.57
	426470	AA528794	Hs.128644 ESTs	2.57
	426919	AL041228	ELAV (embryonic lethal, abnormal vision,	2.56
80	421209	AJ010230	Hs.102576 ret finger protein-like 1 antisense	2.56
	437486	AA452378	Hs.146668 Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.56
	401837		NM_025109:Homo sapiens hypothetical prot	2.56
	428743	AL080060	Hs.301549 Homo sapiens mRNA; cDNA DKFZp564H172 (fr	2.56
	422809	AK001379	Hs.121028 hypothetical protein FLJ10549	2.55

	418648	AW979223	Hs.292478	ESTs	2.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.54
	430345	AK000262	Hs.239681	hypothetical protein FLJ20275	2.54
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	2.54
5	428728	NM_016625	Hs.191381	hypothetical protein	2.53
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	2.52
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	2.52
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.52
10	422406	AF025441	Hs.116206	Opa-interacting protein 5	2.52
	433228	F28212	Hs.14953	KIAA1491 protein	2.51
	411943	BE502436	Hs.7962	ESTs, Weakly similar to S44608 C02F5.6 p	2.51
	426181	AA371422	Hs.334371	hypothetical protein MGC13096	2.50
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	2.50
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.48
15	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	2.48
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.47
	435726	BE535787	Hs.113170	ESTs	2.47
	404068			Target Exon	2.46
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	2.46
20	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.46
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.46
	429652	AA766810	Hs.259290	ESTs	2.45
	416204	AW972270	Hs.195161	ESTs	2.45
25	414713	BE465243	Hs.12664	ESTs	2.44
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.44
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.44
	435244	N77221	Hs.187624	ESTs	2.44
	402679			NM_000478:Homo sapiens alkaline phosphat	2.43
30	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	2.42
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.41
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisqu	2.41
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.41
	423232	BE244625	Hs.125742	leucine-rich neuronal protein	2.40
	427578	AI591305	Hs.169084	ESTs, Highly similar to TUL3_HUMAN TUBBY	2.40
35	409934	R91601	Hs.190466	hypothetical protein FLJ22584	2.39
	423787	AJ295745	Hs.236204	nuclear pore complex protein	2.39
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	2.39
	438869	AF075009		gb:Homo saplens full length insert cDNA	2.38
40	434981	AW182577	Hs.293077	ESTs	2.38
	417911	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (2.38
	409210	AA251812	Hs.51120	cathelicidin antimicrobial peptide	2.37
	424425	AB031480	Hs.146824	SPR1 protein	2.37
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	2.37
45	421567	AJ272137	Hs.198265	matrix metalloproteinase 25	2.37
	426159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.37
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	2.36
	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	2.36
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	2.36
50	410968	AA199907	Hs.67397	homeo box A1	2.36
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	2.36
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	2.36
	412389	AW947655		gb:RC0-MT0003-140300-031-b07 MT0003 Homo	2.35
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.35
55	403780			C4001759:gi133250[sp]P19474[RO52_HUMAN	2.34
	437681	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	2.34
	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	2.34
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	2.34
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.34
60	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	2.33
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.33
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.32
	418821	AA436002	Hs.183161	ESTs	2.32
	437437	AA226869		hypothetical protein DKFZp762L0311	2.32
65	413437	BE313164	Hs.75361	gene from NF2/meningioma region of 22q12	2.31
	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	2.30
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	2.30
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	2.30
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	2.29
70	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	2.29
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	2.29
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.28
	412721	AW183165	Hs.95600	ESTs	2.28
	404071			C12000514*:gi17302471[gb]AAF57556.1 (AE	2.27
75	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.26
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.26
	424935	AI655010	Hs.120363	hypothetical protein MGC15634	2.26
	415791	H09366	Hs.78853	uracil-DNA glycosylase	2.26
	431667	AA812573	Hs.246787	ESTs	2.26
80	424169	AA336399	Hs.153797	ESTs	2.25
	436540	BE397032	Hs.14468	hypothetical protein MGC14226	2.25
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.24
	403242			Target Exon	2.24
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.24

	421002	AF116030	Hs.100932	transcription factor 17	2.24
	438833	BE612940	Hs.88252	ESTs	2.24
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	2.23
5	433844	AA610175	Hs.179647	Homo sapiens cDNA FLJ12195 fis, clone MA	2.23
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.23
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	2.23
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.23
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.23
10	418826	AK000375	Hs.88820	HDCMC28P protein	2.23
	428612	AA770001		ESTs	2.22
	433220	AI076192	Hs.131933	ESTs	2.22
	422225	BE245652	Hs.118281	zinc finger protein 266	2.22
	437549	AA759149	Hs.126757	gb:ah70e03.s1 Soares_testis_NHT Homo sap	2.22
15	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.22
	408665	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.22
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.21
	420062	AW411096	Hs.94785	TGF(beta)-induced transcription factor 2	2.21
	432820	AI554057	Hs.152477	ESTs	2.21
20	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	2.21
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.20
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	2.20
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	2.20
	423675	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	2.20
25	433698	H24201	Hs.247423	adducin 2 (beta)	2.19
	409101	NM_004297	Hs.50612	guanine nucleotide binding protein (G pr	2.19
	435541	AA687361	Hs.221318	ESTs	2.19
	412019	AA485890	Hs.69330	Homo sapiens cDNA FLJ13835 fis, clone TH	2.19
	418753	BE217818	Hs.87016	hypothetical protein FLJ22938	2.19
30	435461	AI075846	Hs.133996	ESTs	2.19
	402260			NM_001436*:Homo sapiens fibrillarin (FBL	2.18
	421098	AI697901	Hs.192425	ESTs	2.18
	400587			C10000649*:gi 7296574 gb AAF51857.1 (AE	2.18
	407832	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.18
35	427159	U80735	Hs.173854	PAX transcription activation domain inte	2.17
	405770			NM_002362:Homo sapiens melanoma antigen,	2.17
	412722	AI343300	Hs.15091	ESTs	2.16
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	2.16
40	438192	AI859065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.16
	417420	T85150	Hs.268814	ESTs	2.16
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	2.16
	412851	AI826502	Hs.97269	ESTs	2.16
	414702	L22005	Hs.76932	cell division cycle 34	2.16
	409670	AI368109		KIAA1856 protein	2.16
45	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.15
	417863	AB000450	Hs.82771	vaccinia related kinase 2	2.15
	434750	BE019254	Hs.4112	t-complex 1	2.15
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	2.15
	418574	N28754		M-phase phosphoprotein 9	2.15
50	409019	AW385412		myosin regulatory light chain 2, smooth	2.15
	416608	R11499	Hs.189716	ESTs	2.14
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	2.14
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	2.13
	422805	AA436989	Hs.121017	H2A histone family, member A	2.13
55	410284	U50939	Hs.61828	amyloid beta precursor protein-binding p	2.13
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	2.12
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	2.12
	433252	AB040957	Hs.151343	KIAA1524 protein	2.12
	416819	U77735	Hs.80205	pim-2 oncogene	2.12
60	437218	AL117497	Hs.58185	ESTs, Weakly similar to T42727 prolifera	2.12
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	2.12
	433947	AA927996	Hs.112876	ESTs, Weakly similar to AF129535 1 F-box	2.11
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.11
	435703	AW630133	Hs.83313	GK003 protein	2.11
65	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.11
	422192	AA305159	Hs.113019	fls485	2.11
	407961	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	2.10
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.10
	414151	AW976468	Hs.257245	ESTs	2.10
70	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	2.10
	424196	AL133660	Hs.142926	Homo sapiens beta cysteine string protei	2.10
	408831	AF090114	Hs.48433	endocrine regulator	2.10
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	2.09
	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	2.09
75	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	2.09
	403532			NM_024638:Homo sapiens hypothetical prot	2.09
	432141	BE410964	Hs.272736	nuclear receptor binding protein	2.08
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.08
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	2.08
80	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	2.08
	418755	Y14443	Hs.88219	zinc finger protein 200	2.08
	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.07
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.07
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protei	2.07

5	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.07
	417230	U40998	Hs.81728	unc119 (C.elegans) homolog	2.07
	425966	NM_001761	Hs.1973	cyclin F	2.07
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	2.06
	407162	N63855	Hs.142634	zinc finger protein	2.06
	422382	D79988	Hs.115778	KIAA0166 gene product	2.06
	402677			NM_000478:Homo sapiens alkaline phosphat	2.06
	433017	Y15067	Hs.279914	zinc finger protein 232	2.05
10	424677	U09414		zinc finger protein 137 (clone pHZ-30)	2.05
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.05
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.05
	402678			Target Exon	2.05
	408146	R45621	Hs.81057	hypothetical protein MGC2718	2.05
15	420027	AF009746	Hs.94395	ATP-binding cassette, sub-family D (ALD)	2.04
	427447	T65414	Hs.6647	Homo sapiens cDNA FLJ13088 fis, clone NT	2.04
	433219	AB040916	Hs.24106	KIAA1483 protein	2.04
	431126	AF085243	Hs.283619	zinc finger protein 236	2.04
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	2.04
20	419669	AJ007041	Hs.92236	KIAA0304 gene product	2.04
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.03
	426242	AL096727	Hs.168249	Homo sapiens mRNA; cDNA DKFZp434B104 (fr	2.02
	432185	AA221032	Hs.272838	hypothetical protein FLJ10494	2.02
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	2.02
25	408636	BE294925	Hs.46680	CGI-12 protein	2.02
	420005	AW271106	Hs.133294	ESTs	2.02
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.02
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.02
	425358	AL079658	Hs.338207	FK506 binding protein 12-rapamycin assoc	2.01
30	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.01
	438450	AI050866	Hs.65853	nodal, mouse, homolog	2.00
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	2.00
	424934	U75370	Hs.153880	polymerase (RNA) mitochondrial (DNA dire	2.00
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.00
35	414251	AL042306	Hs.97689	VASA protein	2.00

TABLE 51B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
40		
45	432666 144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
	423458 30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
	418477 4172_1	BG215094 BG198867 BG196332 BG208220 BG212418
		BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092
		AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
50	436812 659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673
	436899 1000797_1	AA764852 AA736937
	437421 978554_1	AA917062 AA757369 AW592218
	430676 60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603
		AI352469 BE061601 BI062752 AW818206 BF887722
55	427521 513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165
		AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
	436909 596835_1	AW102570 AA907150 AA907120 AA737188 AI248890 AW977353
	429228 215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620
		AW969605 AI553633
60	435514 132288_1	AA683356 AW592804 AI150287
	422689 874209_1	AW954733 AA315006 AW856665
	421974 864120_1	AA301270 AA301379 AA301366
	414136 30243_1	AJ420453 AL526740 AW968449 AA459140 AA843893 AI566516 AW971760 AA430089 AI753216 AA854268 AA743075 AI864957 AA458920
		AI566634 AA211796 BG615512 BE169275 BF933253 BF969462 AA766261 AI769894 AA135833 AI831542 N63376 AA214392 AU154486
65	417886 1031334_1	AW605017 AW450072 AA446459 BE881875 AI061423 AA598549 AW439151 AA426273 Z40087 AA812434 AA135965 H04812
	418235 886897_1	AA210987 D57294 AA214584 AA207006 D56572
	414725 19377_1	BE072634 BE072653 AA830615 AA214736 AA331718
		NM_058166 AF220030 AL043894 AW974257 AA625445 AU153502 AI650537 AW612116 AI672377 AW772451 BE892241 BE501740 AA718936
		AI650276 AI654206 BE503226 AI651327 AW873562 AW271269 AW271565 AI873518 AI207150 AI338826 AI650258 AI628362 AA227117 AI207149
70		AW052076 AI470776 AA588100 AW235852 AA769791 AI701653 AK027664 AI984770 AU153469 BE222316 AA609539 BE220093 AA609112
		BI054316
	434609 14739_1	AF147390 R76593 R76594
	408065 101881_1	BI603077 AW954272 BI598724 AI003154 AA059300 AA046911 BI669907 BI600966 BI669987
	412537 14066_1	AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AI044114
75		AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364
		BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793
		AA382556 AW235763 AA927051 AI862075 BE886691 BE619282
	415684 18695_18	BF666746 D59356 BG678312 N56640 AA166861
80	433641 35983_1	AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080233 AF080233 AL535594
		AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614951
		N29986 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611
		AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833
		AA207155 BI004756 AA206262 AI365204 H77608 AW590511
	424281 892055_1	AA338252 AA338213

427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756
5	418049	AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
	12052_4	AJ314647 NM_052888 BI494693 AA835065 AI634477 AI336678 AI807696 BF477887 AI701147 Z39187 R38979 F02234 AA984711 BI222234
	3970_8	AV731417 R42406 H04996 T98498 R12489 R12577 R42405
10	433023	BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148
	245947_1	AI968683 AA846676 AA927355 H80424 AW973295 R88209 F29868 BE928871
	20459_2	T65754 AA229658 AA229857
15	437834	AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881
	2532601_1	AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478
	1054673_1	AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839
20	438243	AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420
	410704	AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260
		AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427
25	437834	BF718773 BF718645 AW074866 BE857822
	294580_1	BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296
	2532601_1	AA769294 AW749297 AW749295 AW749292 BE002573
	1054673_1	AI581311 AA781682 AA781678
30	438243	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
	410704	BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
		AW840571
35	430968	AW972830 AA489820 AA527647 AA570362
	1237115_1	AA401424 AA400100 AA663848
	11272_50	N50454 AA620999 T16375
	2076469_1	BI917595 AI203314 AL041228 AV727959 D61361 D82004 BI753157 AA961066 AI990307 BF439651 AI453076 AI376075 AI014836 AI018308
	347372_1	AW183530 AA393346 AA935601 AA628633 AI150282 AI028574 AI217182 AA431478 AW087473 AW900295 H50055 AL041229 BI917726
40	438869	AF075009 R63109 R63068
	52134_1	AW947655 AW984020
	1174403_1	NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355
	2538_1	AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205 BE090841 AW163750
45	427260	BF747730 BF898637 AI206506 AV660870 AV692110 AW386830 AV656831 N84710 AW993470 BF086802 BF758454 BG960772 BF757769
	2076469_1	BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE909924 AA708208 BG530266 BF968015 AW992930 BF888862 BG536628
	347372_1	AA143164 AW748953 BG498922 BF885190 BF889005 BF754781 BF800003 BM476529 AI627668 AW028126 AL046011 BF509668 AI017447
50	438869	AA579936 AI367597 AA699622 BE280597 AI124620 AI082548 AW274985 AA677870 AI056767 BE551689 AA287642 H94499 AI752427 AI652365
	52134_1	AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813 AI092115 BF312771 BF242859 BG533616 BG533761
	1174403_1	BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353 AU155318 BE302211 AI375022 AA085641 AU157923 H88858
	2538_1	AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296 AI184820 AI469178 AA782432 H92184 AA340562 BF195818
55	427260	AA852821 AW576342 AA827107 AA173317 AW190014 AI918514 AA729372 AA729718 AI055958 AA331424 BE328601 AA515690 BI018896
	2076469_1	AW628277 AA748368 AA626222 BG492636 AW380620 BF800058 AW370956 AA290909 R25857 BG952995 BF801437 AA172077 AU155890
	347372_1	AU149783 AI720904 AA902936 AA865727 AI470830 AV740677 AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427
60	430968	BE928472 D25910 BF758439 BF968785 BE565238 AA355981 AI905607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471
	17316_1	BG574501 AA187596 AA361196 T95557 BG531446 BG527242 BG527513 BG611106 AA085995 BF847252 BG024608 BE540261 BG531236
	5477_6	AL579993 BG108733 BG483503 BG571032 BG492505
65	425331	AA427363 AW962128 AA355353
	6087_1	BC009352 BC014630 AU131857 AL527140 AU131768 BI769362 BI753220 AU129886 AU128771 AA314135 AU126819 AI333799 AA479336
70	430968	AA258503 AL597351 AL359619 BG697218 BI254283 AI743846 AA236444 AA397533 AA247450 AI051464 AI224533 AU153442 AU151001
	17316_1	AU152621 AU151829 AU153069 AW269958 AU154195 AI862754 AI589780 AW273839 AI338155 AI126632 BE046048 AA976930 AI289304
	5477_6	AI625961 AI222288 AI280054 AA973329 AI524262 AI242371 AA296517 AI567865 AI590681 AJ346616 AW247913 AI422051 AI475352 AI689531
75	430968	AW469308 AW198034 AA936939 AU151059 AU148134 AA486419 AU151953 AI830968 BI493265 BI493264 AU149861 BE268763 AV763495
	17316_1	AW962827 BM480300 AA226869 AL529368 BM451957 AU132714 BI871319 AA380739 BI911351 BF795906 BE548853 AW579751
	5477_6	AK055746 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852
80	430968	BF173139 BE010038
	17316_1	BE219720 BF475241 AI571723 BE219848 BI789268 AI224899 AA724864 AW771467 AA480255 AW845616 AI440295 H52800 BE218790 AI681575
	5477_6	AW300064 AW262133 H21568 AI363015 AI884914 H86949
85	428612	AA770001 AA431112 AA432126
	1383189_1	AI625045 AW504152 AI469086 AA905873 AW504662 AW136114 AI927270 BE041754 AI648386 AA662655 AA400052 AI143501 AI744934
	8882_8	AI400147 AI381657 AA676551 AA974367 AW117437 AI570383 AI242456 AI274581 AA678138 R49939 AI393926 AA345854 AW605850 AI869780
90	418574	AW391171 R77044
	12009_2	AW955043 AI990326 AA776406 AI016250 AW451882 AA843678 BF916900 AW945895 AI979339 N23129 W70051 AA322672 N23137
	32320_4	BM480413 N28908 H39792 BE240826 BE882093 BE240827 AW868637 BF739795 AA700834 AA769597 AA489668 AW968806 AW085196
	15297_3	AI093280 AI218457 AA063138 AI632958 AW515005 AI570530 Z41724 AA748789 AI696584 AA062544 AA773643 AA490285
95	430935	BC017923 AA789302 AW466994 BF513878 AI819642 AI184913 AW469044 AI220572 AW072916 AI280239 AI473611 AW841126 D60937
	2518_37	AA489195 N59350 AA693435 BG531204 AA484243 AW514092
100	424677	U09414 NM_003438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW609708

TABLE 51C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406547	7711513	Minus	172780-174358
402145	8018280	Plus	113086-114800
402199	8576116	Minus	84187-84744
401435	8217934	Minus	54508-55233
402408	9796239	Minus	110326-110491
406367	9256126	Minus	58313-58489
402680	8113438	Plus	137634-137768,139702-139893,140475-14059
402299	6693370	Plus	23367-25175
401091	9958240	Plus	94760-94898

	401464	6682291	Minus	170688-170834
	403969	8569909	Plus	31237-31375,32405-32506
	401837	7630990	Minus	120993-121095,121660-121729
5	404068	3168621	Minus	18123-18766
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
	402679	8113438	Plus	132079-132216
	403780	8076989	Plus	93160-93409
	404071	7210053	Minus	167354-167859,168810-168920,169000-16910
10	403242	7637817	Minus	11297-12511
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	400587	9887626	Plus	25435-25588,25668-25747
	405770	2735037	Plus	61057-62075
	403532	8076842	Minus	81750-81901
	406137	9166422	Minus	30487-31058
15	402677	8113438	Plus	22135-22309,23063-23238
	402678	8113438	Plus	37395-37514,37866-37981

20

TABLE 52A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of testicular cancer (non-seminomatous and Seminomatous) compared to normal adult testicular tissues

25

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
30	414438	AI879277	Hs.76136	thioredoxin	51.77
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	49.93
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	49.20
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	44.46
	438091	AW373062		nuclear receptor subfamily 1, group I, m	40.70
35	406658	AI920965	Hs.77961	major histocompatibility complex, class	39.64
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	38.70
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	38.25
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	37.50
	430542	AI557486	Hs.119122	ribosomal protein L13a	37.22
40	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	35.98
	432730	AI066520	Hs.131358	ESTs	35.25
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	31.69
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	31.33
	417088	M54915	Hs.81170	pim-1 oncogene	31.20
45	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	29.93
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	29.35
	426295	AW367283		zinc finger protein 6 (CMPX1)	29.32
	406856	AW515336	Hs.29797	ribosomal protein L10	28.93
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	27.99
50	440207	AI371978	Hs.128326	ESTs	27.75
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	26.95
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.90
	420367	AA259090	Hs.257028	ESTs	26.50
	429978	AA249027		ribosomal protein S6	26.43
55	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	26.36
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	26.23
	412636	NM_004415		desmoplakin (DPI, DPLI)	26.15
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	25.25
	446899	NM_005397	Hs.16426	podocalyxin-like	25.25
60	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	25.15
	406656	M16714	Hs.89643	major histocompatibility complex, class	25.13
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	24.78
	423961	D13666	Hs.136348	periostin(OSF-2os)	24.48
	425543	R23313	Hs.334895	ribosomal protein L10a	24.38
65	420676	AI434780	Hs.4248	vav 2 oncogene	24.18
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	23.96
	440869	NM_014297	Hs.7486	protein expressed in thyroid	23.80
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	23.56
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	23.22
70	446627	AI973016	Hs.15725	hypothetical protein SBBI48	22.93
	449571	AW016812	Hs.200266	ESTs	22.83
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	22.81
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	22.68
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	22.45
75	422714	AB018335	Hs.119387	KIAA0792 gene product	22.45
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	22.30
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.69
	406648	AA563730	Hs.277477	major histocompatibility complex, class	21.58
	448588	AI970276	Hs.156905	KIAA1676	21.23
80	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	21.19
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.70
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	20.60
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	20.57

	420754	W79431	Hs.346911	ribosomal protein L22	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	20.15
	424800	AL035588	Hs.153203	MyoD family inhibitor	20.10
5	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	20.01
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	19.89
	410143	AA188169		KIAA1191 protein	19.41
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	19.08
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.03
10	425535	AB007937	Hs.158287	KIAA0468 gene product	18.78
	411573	AB029000	Hs.70823	KIAA1077 protein	18.63
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.53
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	18.52
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	18.50
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	18.50
15	429183	AB014604	Hs.197955	KIAA0704 protein	18.48
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	18.44
	450377	AB033091		KIAA1265 protein	18.40
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.15
	440528	BE313555	Hs.7252	KIAA1224 protein	18.05
20	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheri	17.98
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	17.80
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	17.75
	428782	X12830	Hs.193400	interleukin 6 receptor	17.48
25	415221	W07418	Hs.78225	annexin A1	17.47
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	17.40
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	17.30
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	17.14
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	17.13
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	17.10
30	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	17.03
	425996	W67330		hypothetical protein AL110115	16.98
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	16.98
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	16.98
35	427521	AW973352		ESTs	16.93
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.93
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	16.53
	449338	H73444	Hs.394	adrenomedullin	16.36
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	16.23
40	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	16.21
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	16.15
	427691	AW194426	Hs.20726	ESTs	16.13
	406786	AW161678	Hs.111334	ferritin, light polypeptide	16.11
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	16.10
	451106	BE382701	Hs.25960	N-MYC oncogene	16.09
45	408380	AF123050	Hs.44532	diubiquitin	16.00
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	15.93
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	15.69
50	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	15.64
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	15.55
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	15.55
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	15.53
	410185	BE294068	Hs.737	immediate early protein	15.49
55	422105	AI929700	Hs.111680	endosulfine alpha	15.23
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	15.23
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	15.05
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	15.02
	426552	BE297660	Hs.170328	moesin	14.96
60	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	14.88
	436860	H12751	Hs.5327	PRO1914 protein	14.85
	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	14.84
	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	14.78
	412623	R28898	Hs.74170	metallothionein 1E (functional)	14.70
65	408989	AW361666	Hs.49500	KIAA0746 protein	14.53
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheri	14.48
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	14.31
	410325	AB023154	Hs.62264	KIAA0937 protein	14.23
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	14.20
70	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	14.19
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	14.18
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.13
	447211	AL161961	Hs.17767	KIAA1554 protein	14.08
	417426	NM_002291	Hs.82124	laminin, beta 1	14.08
75	414420	AA043424	Hs.76095	immediate early response 3	14.04
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.02
	454413	AI653672	Hs.40092	PNAS-123	13.93
	452651	AI218918	Hs.30209	KIAA0854 protein	13.86
	450581	AF081513	Hs.25195	TGF-beta 4	13.85
80	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.78
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.63
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.59
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	13.57
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	13.53

	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	13.43
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	13.41
	447534	AW953935	Hs.288655	ESTs	13.33
5	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	13.31
	428065	AI634046	Hs.157313	ESTs	13.30
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	13.28
	436398	H87136	Hs.5174	ribosomal protein S17	13.18
	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	12.93
10	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	12.90
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	12.90
	408437	AW957744	Hs.278469	lacrimal proline rich protein	12.90
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	12.89
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.83
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	12.79
15	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	12.78
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	12.75
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	12.73
	430630	AW269920	Hs.2621	cystatin A (stefin A)	12.68
20	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	12.65
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	12.50
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	12.48
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	12.43
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.43
25	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	12.41
	412247	AF022375	Hs.73793	vascular endothelial growth factor	12.41
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	12.40
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	12.38
	432409	AA806538	Hs.130732	KIAA1575 protein	12.33
30	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.33
	419384	AA490866	Hs.39429	ESTs	12.33
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	12.32
	432805	X94630	Hs.3107	CD97 antigen	12.32
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	12.25
35	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	12.13
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	12.12
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	12.03
	402145			Target Exon	12.01
	407179	AA206465		thymosin, beta 4, X chromosome	12.00
40	433208	AW002834	Hs.24095	ESTs	11.95
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.90
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	11.83
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	11.75
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	11.75
45	427761	AA412205	Hs.140996	ESTs	11.68
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	11.58
	436075	BE090176	Hs.179902	transporter-like protein	11.50
	440774	AI420611	Hs.153934	ESTs	11.35
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	11.25
50	419223	X60111	Hs.1244	CD9 antigen (p24)	11.08
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	11.08
	444656	AI277924	Hs.145199	ESTs	10.98
	420943	AI718702	Hs.279930	major histocompatibility complex, class	10.96
	450294	H42587	Hs.238730	hypothetical protein MGC10823	10.92
55	413686	AI469213	Hs.71404	ESTs	10.83
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	10.78
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	10.75
	407252	AA659037	Hs.163780	ESTs	10.75
	445929	AI089660	Hs.323401	dpy-30-like protein	10.70
60	451864	N20370	Hs.69547	ESTs	10.69
	429307	AU076592	Hs.198951	jun B proto-oncogene	10.64
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	10.63
	447519	U46258	Hs.339665	ESTs	10.63
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	10.59
65	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	10.55
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	10.54
	437103	AW139408	Hs.152940	ESTs	10.50
	449961	AW265634	Hs.133100	ESTs	10.50
	441244	BE612935	Hs.184052	PP1201 protein	10.49
70	450139	AK001838		serum/glucocorticoid regulated kinase	10.48
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	10.48
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rholekin, clone	10.47
	446682	AW205632	Hs.211198	ESTs	10.43
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.43
75	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	10.40
	424950	AA602917	Hs.156974	ESTs	10.40
	434442	AA737415		ESTs	10.33
	438089	W05391		nuclear receptor subfamily 1, group I, m	10.33
	432559	AW452948	Hs.257631	ESTs	10.30
80	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	10.30
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	10.28
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	10.27
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	10.27
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	10.23

	445245	AB032973	Hs.12461	LCHN protein	10.18
	446488	AB037782	Hs.15119	KIAA1361 protein	10.15
	410611	AW954134	Hs.20924	KIAA1628 protein	10.15
5	425875	ALU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	10.14
	416926	H03109	Hs.263395	HT018 protein	10.07
	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	10.05
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	10.04
	411975	AI916058	Hs.144583	ESTs	10.03
10	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	10.00
	408784	AW971350	Hs.63386	ESTs	9.95
	444795	AI193356	Hs.160316	ESTs	9.93
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.90
	400440	X83957	Hs.83870	nebulin	9.90
	414829	AA321568	Hs.77436	pleckstrin	9.88
15	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.88
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	9.85
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	9.83
	446795	AI977713	Hs.156471	ESTs	9.78
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	9.67
20	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	9.65
	419904	AA974411	Hs.18672	ESTs	9.63
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	9.63
	414405	AI362533		KIAA0306 protein	9.58
25	418840	AI821614	Hs.185831	ESTs	9.53
	453716	AA037675	Hs.152675	ESTs	9.50
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	9.50
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.45
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	9.45
30	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	9.43
	434423	NM_006769	Hs.3844	LIM domain only 4	9.43
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	9.43
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	9.42
	410397	AF217517	Hs.63042	DKFZp584J157 protein	9.37
35	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	9.37
	434524	AA635931	Hs.249716	ESTs	9.36
	422960	AW890487		cadherin 13, H-cadherin (heart)	9.35
	414774	X02419	Hs.77274	plasminogen activator, urokinase	9.32
	411960	R77776	Hs.18103	ESTs	9.30
40	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	9.28
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.28
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	9.27
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	9.27
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypothe	9.25
45	427968	AI857607	Hs.181301	cathepsin S	9.23
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	9.23
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	9.23
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.18
	417315	AI080042	Hs.180450	ribosomal protein S24	9.18
50	421098	AI697901	Hs.192425	ESTs	9.18
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.18
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	9.17
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	9.17
	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.15
55	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	9.14
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.13
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	9.12
	420099	D80011	Hs.95140	KIAA0189 gene product	9.10
	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	9.08
60	441436	AW137772	Hs.185980	ESTs	9.08
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	9.08
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	9.08
	430556	AW967807	Hs.13797	ESTs	9.07
	450147	AW373713	Hs.146324	CGI-145 protein	9.06
65	442806	AW294522	Hs.149991	ESTs	9.05
	431187	AW971146	Hs.293187	ESTs	9.05
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	9.03
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	9.03
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	9.02
70	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	9.00
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.99
	432314	AA533447	Hs.312989	ESTs	8.98
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.95
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	8.94
75	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	8.93
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.90
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	8.90
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.89
	417228	AL134324	Hs.7312	ESTs	8.88
80	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	8.88
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	8.88
	438980	AW502384		gb:UL-HF-BR0p-aka-f-12-0-UL.r1 NIH_MGC_5	8.85
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	8.85
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	8.85

	430592	AJ224864	Hs.9688	leukocyte membrane antigen(IRC1)	8.83
	445612	N94126	Hs.12969	hypothetical protein	8.80
	427254	AL121523	Hs.97774	ESTs	8.80
5	428970	BE276891	Hs.194691	retinoic acid induced 3	8.80
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subunit	8.79
	430162	AW450843	Hs.346348	ESTs	8.75
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	8.73
	446659	AI335361	Hs.226376	ESTs	8.73
	447198	D61523	Hs.283435	ESTs	8.73
10	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-decay accelerating factor for complement	8.70
	401091			ESTs	8.68
	442832	AW206560	Hs.253569	ESTs	8.68
	442495	AI184717		ESTs	8.63
15	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	8.63
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	8.61
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	8.59
	425580	L11144	Hs.1907	galanin	8.55
	449656	AA002008	Hs.188633	ESTs	8.55
	412093	BE242691	Hs.14947	ESTs	8.54
20	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.54
	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.53
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	8.51
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	8.45
25	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	8.45
	425284	AF155568		NS1-associated protein 1	8.45
	441623	AA315805		desmoglein 2	8.43
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	8.42
	441021	AW578716	Hs.7644	H1 histone family, member 2	8.40
30	446630	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	8.40
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	8.35
	433655	AL036559	Hs.3463	ribosomal protein S23	8.33
	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.32
	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1-like	8.31
35	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.30
	414662	AL036058	Hs.76807	major histocompatibility complex, class	8.30
	414601	AV660804	Hs.301417	AHNAK nucleoprotein (desmoyokin)	8.29
	406699	L06505	Hs.182979	ribosomal protein L12	8.28
	443884	N20617	Hs.194397	leptin receptor	8.28
40	442821	BE391929	Hs.8752	transmembrane protein 4	8.26
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	8.24
	435968	AW161481	Hs.111577	integral membrane protein 3	8.23
	440327	R12581	Hs.191146	ESTs	8.23
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.22
45	435684	NM_001290	Hs.4980	LIM domain binding 2	8.16
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	8.15
	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	8.14
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown (H.s	8.13
	448094	H24387	Hs.32061	ESTs, Weakly similar to I38022 hypotheti	8.10
50	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	8.09
	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	8.08
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	8.07
	423523	AW299828	Hs.193580	ESTs	8.03
	426759	AI590401	Hs.21213	ESTs	8.03
55	426780	BE242284	Hs.172199	adenylate cyclase 7	8.03
	426215	AW963419	Hs.155223	stanniocalcin 2	8.03
	435748	AA699756	Hs.117335	ESTs	8.00
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	8.00
	447500	AI381900	Hs.159212	ESTs	8.00
60	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	8.00
	428728	NM_016625	Hs.191381	hypothetical protein	8.00
	434511	R28982	Hs.18106	ESTs	7.99
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	7.98
	424875	AI187945	Hs.199310	ESTs	7.95
65	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	7.95
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	7.93
	425277	NM_001241	Hs.155478	cyclin T2	7.91
	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	7.90
70	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	7.90
	429999	AI761902	Hs.99597	ESTs	7.90
	445493	AI915771		metallothionein 1E (functional)	7.89
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.88
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	7.88
75	453485	BE620712	Hs.33026	hypothetical protein PP2447	7.87
	434159	AW135214	Hs.191828	ESTs	7.85
	432666	AW204089		ESTs, Weakly similar to unnamed protein	7.83
	430915	AA488953		gb:aa55e05.r1 NCLCGAP_GCB1 Homo sapiens	7.83
	425913	AA365799		SEC22, vesicle trafficking protein (S. c	7.80
80	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	7.80
	438763	AI583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	7.79
	435905	AW997484	Hs.5003	KIAA0456 protein	7.78
	406663	U24683		immunoglobulin heavy constant mu	7.78
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.78

	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	7.75
	438962	BE046594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	7.75
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.73
5	422900	AA641201	Hs.222051	ESTs	7.73
	432598	AI341227	Hs.157106	ESTs	7.72
	449322	AI638616	Hs.196566	ESTs	7.71
	416987	D86957	Hs.80712	KIAA0202 protein	7.67
	410800	BE280421	Hs.94499	ESTs	7.67
10	416801	X98834	Hs.79971	sal (Drosophila)-like 2	7.67
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.65
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.65
	401466			vesicle-associated membrane protein 4	7.65
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	7.64
15	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.63
	457250	AA811987	Hs.125779	ESTs	7.63
	412949	AI471639	Hs.71913	ESTs	7.63
	406819	AA908472		gb:og82a10.s1 NCI_CGAP_Ov8 Homo sapiens	7.62
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.62
20	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	7.61
	435937	AA830893	Hs.119769	ESTs	7.60
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.60
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.60
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	7.56
25	418134	AA397769	Hs.86617	ESTs	7.55
	451812	X81889	Hs.152151	plakophilin 4	7.55
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.54
	429083	Y09397	Hs.227817	BCL2-related protein A1	7.54
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	7.52
30	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	7.52
	407784	AW139585	Hs.12708	ESTs	7.52
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	7.50
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	7.50
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	7.48
35	446013	AI360167	Hs.152774	ESTs	7.48
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.48
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.45
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	7.45
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	7.44
40	447082	T85314	Hs.54629	thioredoxin-like	7.43
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	7.43
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.43
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	7.43
	442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypothei	7.43
45	436394	AA531187	Hs.126705	ESTs	7.39
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	7.39
	446258	AI283476	Hs.263478	ESTs	7.38
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	7.37
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.36
50	435541	AA687361	Hs.221318	ESTs	7.35
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	7.35
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.35
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.35
	418336	BE179882		glutathione peroxidase 3 (plasma)	7.35
55	448877	AI583696	Hs.253313	ESTs	7.35
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.35
	444838	AV651680	Hs.208558	ESTs	7.33
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	7.31
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	7.30
60	441878	AI801869	Hs.127982	ESTs	7.29
	406542			C19000728*.gij12585552[sp]Q9Y2Q1J2257_HU	7.28
	408418	AW963897	Hs.44743	KIAA1435 protein	7.28
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	7.26
	442492	AA528489	Hs.234518	ribosomal protein L23	7.25
65	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	7.25
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	7.25
	426501	AW043782	Hs.293616	ESTs	7.25
	411251	R19774	Hs.22835	HHGP protein	7.25
	444670	H58373	Hs.332938	hypothetical protein MGC5370	7.25
70	418117	AI922013	Hs.83496	linker for activation of T cells	7.24
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	7.24
	434817	AA082118	Hs.102737	golliath protein	7.23
	419970	AW612022		ESTs	7.23
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	7.23
75	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	7.23
	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	7.21
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	7.21
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	7.20
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.20
80	441224	AU076964	Hs.7753	calumenin	7.18
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.18
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	7.15
	447341	AF106941	Hs.18142	arrestin, beta 2	7.15
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	7.14

	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	7.14
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.13
	421633	AF121860	Hs.106260	sorting nexin 10	7.10
5	410668	BE379794	Hs.159651	hypothetical protein	7.09
	435812	AA700439	Hs.188490	ESTs	7.08
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	7.08
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	7.08
10	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	7.06
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	7.06
	416401	N80139	Hs.268916	ESTs	7.05
	415799	AA653718	Hs.225841	DKFZP434D193 protein	7.05
	415995	NM_004573		phospholipase C, beta 2	7.05
	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.05
15	417535	AA203569	Hs.191482	ESTs	7.04
	449567	AI990790	Hs.188614	ESTs	7.03
	429355	AW973253	Hs.292689	ESTs	7.03
	442460	NM_014135	Hs.8345	PRO641 protein	7.03
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	7.03
20	430280	AA361258	Hs.237868	interleukin 7 receptor	7.03
	426124	AI268389	Hs.250697	phosphatidylinositol glycan, class F	7.02
	442685	AB033017	Hs.8594	KIAA1191 protein	7.01
	433735	AA608955	Hs.109653	ESTs	7.00
	416003	X96001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.98
25	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.96
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.95
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	6.95
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.93
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	6.93
30	451653	W18193		ESTs, Moderately similar to HERC2 [H.sap	6.93
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	6.93
	451838	AW005866	Hs.193969	ESTs	6.91
	436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-U1.s1 NCI_CGAP_Su	6.90
	443749	R38828	Hs.143463	ESTs	6.90
35	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.90
	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	6.90
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.90
	435655	AW105663	Hs.6947	HSPC069 protein	6.90
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	6.85
40	418259	AA215404		ESTs	6.85
	407244	M10014		fibrinogen, gamma polypeptide	6.85
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	6.83
	441321	H17182	Hs.7771	B-cell associated protein	6.80
	433162	AI025842		ESTs	6.80
45	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.80
	434372	AA631373		gb:np86c01.s1 NCI_CGAP_Thy1 Homo sapiens	6.80
	456629	AW891965		histone deacetylase 3	6.78
	430283	BE391688		RAB7, member RAS oncogene family	6.77
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	6.76
50	406858	AI865720	Hs.29797	ribosomal protein L10	6.75
	429582	AI569068	Hs.22247	ESTs	6.75
	401113			solute carrier family 22 (organic cation	6.75
	449576	AW014631	Hs.225068	ESTs	6.75
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	6.72
55	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.72
	430451	AA836472	Hs.297939	cathepsin B	6.72
	410503	AW975746	Hs.188662	KIAA1702 protein	6.70
	415682	AI347128	Hs.191870	ESTs	6.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Clona savignyi	6.70
60	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	6.70
	457073	AA233210	Hs.179943	ribosomal protein L11	6.69
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	6.68
	436137	AI056769	Hs.133512	ESTs	6.68
	425787	AA363867	Hs.155029	ESTs	6.67
65	437802	AI475995	Hs.122910	ESTs	6.65
	432636	AA340864	Hs.278562	claudin 7	6.65
	407340	AA810168	Hs.284289	vittiligo-associated protein VIT-1	6.65
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	6.65
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	6.63
70	441355	AI822034	Hs.137097	ESTs	6.63
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	6.63
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.63
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	6.62
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	6.60
75	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	6.60
	449057	AB037784	Hs.22941	KIAA1363 protein	6.60
	446979	AI654443	Hs.197683	ESTs	6.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	6.60
	424868	AI568170	Hs.96886	ESTs	6.59
80	409485	S80990	Hs.252136	ficolin (collagen/fibrinogen domain-cont	6.58
	451603	BE379499	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H	6.58
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.58
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	6.57
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.56

	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	6.56
	444207	AI565004		calhepsin D (lysosomal aspartyl protease	6.55
	418459	R85436	Hs.268814	ESTs	6.55
5	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.55
	406745	AW511970	Hs.279860	tumor protein, translationally-controlle	6.55
	446173	BE565849	Hs.14158	copine III	6.53
	436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	6.53
	423825	NM_004402	Hs.133089	DNA fragmentation factor, 40 kD, beta po	6.53
10	443441	AW291196	Hs.92195	ESTs	6.51
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	6.50
	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smo	6.50
	450219	AI826999	Hs.224624	ESTs	6.50
	408896	AI610447	Hs.48778	niban protein	6.50
	442618	R56222	Hs.26514	ESTs	6.49
15	422773	AB028962	Hs.301552	KIAA1039 protein	6.48
	413663	BE247585	Hs.75462	BTG family, member 2	6.48
	418905	BE539674		actinin, alpha 4	6.48
	405086			NM_006662*:Homo sapiens Snf2-related CBP	6.45
20	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	6.45
	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.45
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	6.45
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	6.43
	426496	D31765	Hs.170114	KIAA0061 protein	6.43
25	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	6.42
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [Hs	6.41
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.40
	435918	AF263538	Hs.86232	growth differentiation factor 3	6.38
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	6.38
30	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.38
	436716	AI433540		gb:ti69g05.x1 NCI_CGAP_Kid11 Homo sapien	6.38
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	6.38
	413326	H88621	Hs.19762	ESTs, Weakly similar to KIAA1140 protein	6.38
	441970	AW959918	Hs.73737	ESTs	6.38
35	430835	AI240006	Hs.192326	ESTs	6.38
	414890	BE281095	Hs.77573	uridine phosphorylase	6.37
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.37
	414768	AW376989	Hs.259855	elongation factor-2 kinase	6.36
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	6.36
40	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	6.35
	432586	AA568548		ESTs	6.35
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	6.35
	420012	AW957965	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	6.35
	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.35
45	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.35
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	6.35
	437296	AA350994	Hs.20281	KIAA1700	6.35
	427747	AW411425	Hs.180655	serine/threonine kinase 12	6.33
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	6.33
50	410387	AI277367	Hs.47094	ESTs	6.33
	413677	AW503116	Hs.301819	zinc finger protein 146	6.31
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	6.31
	443634	H73972	Hs.134460	ESTs	6.30
	409453	AI885516	Hs.95612	ESTs	6.29
55	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	6.29
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.29
	410532	T53088	Hs.155376	hemoglobin, beta	6.28
	428453	AB011110	Hs.184367	GTPase activating protein-like	6.27
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	6.26
60	458965	AA010319	Hs.60389	ESTs	6.25
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	6.25
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	6.25
	412528	AI123478	Hs.32112	ESTs	6.25
	410079	U94362	Hs.58589	glycogenin 2	6.25
65	427477	AW973119	Hs.178391	ribosomal protein L44	6.24
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.24
	435961	BE293127	Hs.283722	GTT1 protein	6.23
	424090	X99699	Hs.139262	XIAP associated factor-1	6.23
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.23
70	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	6.23
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	6.23
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	6.22
	428773	BE256238	Hs.193163	bridging integrator 1	6.20
	436372	AW972301	Hs.310286	ESTs	6.19
75	440719	AA150869	Hs.26267	ATP-dependant interferon response protei	6.18
	406685	M18728		gb:Human nonspecific crossreacting antig	6.18
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	6.17
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	6.16
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	6.15
80	406806	AW088535		ribosomal protein, large, P0	6.15
	420151	AA255931	Hs.186704	ESTs	6.14
	413441	AI929374	Hs.75367	Src-like-adaptor	6.13
	449317	AW293413	Hs.132906	19A24 protein	6.13
	421568	W85858	Hs.99804	ESTs	6.13

435919	AI052189	Hs.114104	ESTs	6.13
417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	6.13
448946	AI652855	Hs.23363	hypothetical protein FLJ10983	6.13
432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.13
406857	AA613726	Hs.29797	ribosomal protein L10	6.11
417944	AU077196	Hs.82985	collagen, type V, alpha 2	6.11
425095	AW014160	Hs.182585	KIAA1276 protein	6.10
435756	AI418466	Hs.33665	ESTs	6.10
431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	6.10
413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	6.10
451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	6.10
450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	6.08
447832	AI433357		ESTs	6.08
434421	AI915927	Hs.34771	ESTs	6.08
437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	6.08
449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	6.08
415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	6.07
433339	AF019226	Hs.8036	glioblastoma overexpressed	6.06
435511	AA683336	Hs.189046	ESTs	6.06
423458	AI204212		ESTs	6.06
442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	6.06
457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	6.06
444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathi	6.06
455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	6.05
432925	AA878324	Hs.264750	ESTs	6.05
457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	6.05
449810	AB008681	Hs.23994	acilvin A receptor, type IIB	6.04
406797	AI432224		ribosomal protein L6	6.04
450157	AW961576	Hs.60178	ESTs	6.03
422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.03
407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-link	6.03
453331	AI240665		ESTs	6.03
430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	6.02
444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isom	6.01
409945	AW015935	Hs.122642	ESTs	6.00
419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	6.00
453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	6.00
430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	6.00

TABLE 52B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW698628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581 BE880923 BG390191 AW470082 AW014585 AI423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI422030 AI348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI215830 AI283836 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085455 BE551404 AA780704 AW008596 AI796964 AA917471 AI400531 AA668626 N72207 AI306482 AW440562 AI084687 AA347280 AA063536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI916336 AI350590 BF198106 AI433377 AI300638 AI672626 AI282741 AI351487 AW105544 AA973627 AW517914 AA715424 AA508454 BF334080 AI274618 AW367201 AW572619 AW469088 AA382095 AI368364 AI146934 AI357180 AI361181 BI911347 BI871044 AA136325 BF084010 BF084007 AA335788 AI920878 AA809614 BE932941 AI678261 C75308 AI148479 BE178174 W88513 BM013627 BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI918664 AW963196 C06195 AI678018 M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BI039774 BE1713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AI0127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW955615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723

5			AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE719915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 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		BG704110 AU123329 AU122058 AU138135 BG723106 BG722291 BG831041 BG705239 BE740517 BE207133 BE252867 AU139772 BG714385
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		BM148991 BF929247 AV653435 AW250299 AW249189 BF093150 BF093173 AW205325 BF057101 BF000551 AI341108 AL162009 AK026136
		BE907957 W73238 BI711467 BG926027 AI816428 AA837518 AI754405 BG179142 AA481485 AW023435 BE855747 AI885101 N52163 AI016096
		AI090204 BE677045 AI523320 AI126855 N26501 AA043680 AA976459 AI039590 AI937917 AI361000 W94866 AI375797 AI079801 AI168236
		AA599882 AA084368 AI342635 AI190294 N26093 AI085234 AI298169 BF939715 AI223164 H98704 BE218925 N29394 AI918735 N41520 AI147784
75		AI918796 AA854317 N22193 AA199850 AI149728 AA121263 AI051074 AA565116 AI097349 N22209 AA552917 N33151 D52422 BF477483
		AA476599 AA525787 AI279198 D53353 AA738063 AA558406 BI496334 AA999948 AA425847 BI496335 AA909624 BF197591 AW023259 AI652819
		T31424 AA088213 T31115 AI206650 AA976796 AI948989 AW248762 AA449265 AA290687 AI682521 AA310227 Z38743 AA935369 AW119141
		BF941087 AI470657 AI349451 AW079338 D45665 N21640 T30071 AI446705 R60220 BE833481 R49680 R70049 R41223 R32402 R69984 R70111
80		BM476906 BE293615 BE382443 BF155692 BE720638 BE931983 BE720594 BF085890 AA336953 BF081638 AA359915 AA384116 AA360142
		BI667664 BG823235 BE315559 BE301958 BE891114 BG826267 BE253680 BG979094 AV722757 N67629 BG997927 BI915769 BG680692 R62777
		BE251116 H56358 AW369586 BG677759 BI044604 R75787 BE770960 H69529 R69983 AA259238 R97827 AA310379 W01103 AI873384
		AL554578 BF038102 H87182 H87517 H01574 T52573 N28881 AA301397 T92375 R68401 AW800466 AI268172 BE876949 D54019 AI909769
		AW798415 BI222383 AI393171 CI5260 N26959 H17129 T53095 T52494 R68602 AI364765 BF687869 AI817035 AW105354 BE293820 H14206
		BI093066 C14063 AL534349 BE255883 BE254098 AA428399 AW579360 AW579381 N53144 D60748 D54020 BG292106 H96705 D52423 T36174

			D54161 R73016 D55021 B1857200 H83444 B1016954 D54163 R15563 B1818664 BE152207 B1048502 BF885667 BE613212 BE165773 BF149332 AW607045 BE305200 AW972830 AA489820 AA527647 AA570362 BE739425 AA514221 AA865491 A1828293 AA470456 A1276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 A1432496 A1470335 A1247243 BG533994 AA513783 A1887309 AA528036 AW972006 AW873028 A1924914 A1818810 AW152378 AW084946 A1521413 A1669583 BE932521 A1581370 BE180238 AW089750 AW771461 AW089714 A1590949 A1819148 AA731056 BF815234 BF911506 AA235803 AA485373 A1735658 AW393133 AW073080 A1070637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 A1807430 A1676072 AA837010 A1452482 A1625817 AW241750 BE048616 A1290928 A1680714 AA485530 BE175687 AV648513 AW130312 A1000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 A1244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658871 BG678060 A1565004 AW819026 BE843092 AV686437 AV723049 BG616948 A1911647 A1743490 A1091096 BE857251 A1962074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE006682 BF342375 AA903144 BF338083 BF984258 AV657996 A1749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BM469076 AA533027 A1127512 A1368802 AA533141 AA700560 AW576028 A1610851 A1435361 BM129172 AW474544 BM128899 A1814292 AW502039 AA531243 BF941858 AW502037 AA702337 A1419854 AA662755 AA934364 A1300510 A1291136 AA505263 A1144527 A1076919 A1633534 A1242473 AA938561 BG055372 AA512894 A1671356 AA962403 BF808010 AA663911 AA847056 AA513301 AA369069 AA377265 BG291206 AA402298 AA885766 AW801002 AA302290 A1305842 AW800873 AA302492 AA478427 A1817291 AW801104 AW801028 AA865744 BF1155979 A1374743 AA478431 A1159846 A1369757 A1800672 BF435788 AA255451 A1937707 AW006198 A1280363 BF062434 AW801115 A1919181 F28413 W04214 AW152380 AW901567 AW901570 AA886371 AA384251 A1302846 BE701902 AA931606 H42673 R33703 AW901556 AA009816 AW901568 AW352200 AA256558 H15928 B1087170 AW800530 AA369068 N98562 H28652 N34644 H97650 H00956 W70039 A1142831 AA009817 F37136 N70289 AA531347 R72374 H27488 R66605 A1433540 AA804981 AA728984 BG015794 BE158357 BE158353 BE158358 BE158360 BE158352 BE158351 BE158355 BC022881 AU150944 BG750783 AW754175 AW857737 A1911659 A1050036 AA554053 A1826259 AA568548 A1732997 AA977633 AA865818 M18728 AW088535 A1889321 AA954221 A1337552 R42581 AW194670 AA064862 AW001147 AA864374 AA630699 AW276176 AA676615 AA857965 A1625428 AA580792 AA582038 AA581668 AA658065 AA828156 AA857160 AA936103 A1149335 AA936925 AA581684 AA954198 AW238461 A1281504 A1265812 AA583267 AW236162 AA876535 AW304286 AW474334 A1559415 A1589241 A1660952 AA641137 A1431696 A1688844 AA552513 AA564954 AW090553 A1205612 A1245753 AA954883 AA947909 A1866014 AW971213 AA493925 AA493567 AA876839 AA934462 A1628543 A1433357 AW772732 B1918168 AW779760 N48674 A1375997 AA235370 BG699146 A1913631 A1498402 A1016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 A1203107 R35004 F07491 R25094 R35360 BC018070 BG702493 A1204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539 BG215094 BG198867 BG196332 BG208220 BG212418 BG216963 BG164885 BG213710 BG204771 BG193014 BG197556 BG217481 BG198185 BG183594 B1596425 AA115605 A1589156 BF439839 BG188832 A1359615 BG190473 A1024233 BF439574 AW118065 A1672797 AA610042 BG212008 A1204382 R70913 AA033534 AA781036 A1627278 AA307285 AA034218 BG482749 AW162429 B1602460 AA721969 AA476516 AA476416 AA903019 BF110864 AA307286 AA115471 AW964555 AA423826 AA115129 A1419107 A1432224 AW276890 A1499346 AA937014 AA653573 A1318525 A1246219 AA961591 A1270640 BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 B1057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 A1161014 AA099554 BG572534 A1803329 A1809932 A1808765 AA411449 A1378760 AA976929 A1378620 AA909684 R75632 A1360919 A1350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 A1204665 BF989591 B1056086 BG001590 BF107035 BE219720 BF475241 A1571723 BE219848 B1789268 A1224899 AA724864 AW771467 AA480255 AW845616 A1440295 H52800 BE218790 A1681575 AW300064 AW262133 H21568 A1363015 A1884914 H86948		
	430968	1237115_1			
5	444207	9172_3			
10					
15	418905	517_1			
20					
25	436716	2472838_1			
	413703	376077_1			
	432586	6633_1			
	440129	2607882_1			
	406685	0_0			
	406806	0_0			
30					
	431155	1235742_1			
	447832	1036795_1			
	449625	249224_1			
35	423458	30480_1			
	455263	26143_1			
40					
	406797	0_0			
	453331	16559_1			
45					
	430504	5477_6			
50					
55	TABLE 52C				
	Pkey:	Unique number corresponding to an Eos probeset			
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.			
	Strand:	Indicates DNA strand from which exons were predicted.			
	NL_position:	Indicates nucleotide positions of predicted exons.			
60	Pkey	Ref	Strand	NL_position	
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757	
	402145	8018280	Plus	113086-114800	
	401091	9958240	Plus	94760-94898	
	401466	6682292	Plus	28748-29023	
	406542	7711499	Plus	117335-118473	
65	401113	9966541	Minus	19419-19959	
	405086	8072509	Plus	73664-73841,74081-74217,74610-74779,7492	
70	TABLE 53A:				
75	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of testicular cancer (non-seminomatous and seminomatous) compared to normal adult tissues			
	Pkey	ExAccn	UnigenelD	Unigene Title	R1
80	432666	AW204069		ESTs, Weakly similar to unnamed protein	78.20
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	75.45
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	58.80
	432730	A1066520	Hs.131358	ESTs	51.80
	450581	AF081513	Hs.25195	TGF-beta 4	48.40

	426534	U58096	Hs.2051	testis specific protein, Y-linked	44.05
	423458	AI204212		ESTs	36.60
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	34.65
5	420367	AA259090	Hs.257028	ESTs	32.60
	451106	BE382701	Hs.25960	N-MYC oncogene	30.10
	437052	AA861697	Hs.120591	ESTs	29.35
	417407	AA923278	Hs.290905	ESTs, Weakly similar to proleaze [H.sapi	29.05
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	28.45
10	420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	28.25
	407710	AW022727	Hs.23616	ESTs	26.86
	448981	AI968719	Hs.195387	ESTs	26.40
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	25.55
	420528	AF130728	Hs.98586	doublesex and mab-3 related transcriptio	25.10
15	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	23.70
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.95
	454077	AC005952	Hs.37062	insulin-like 3 (Leydig cell)	21.73
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	20.15
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	19.65
	424578	AK001973	Hs.150890	hypothetical protein	19.16
20	427335	AA448542	Hs.251677	G antigen 7B	19.05
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	18.95
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	18.86
	449322	AI638616	Hs.196566	ESTs	18.30
25	430691	C14187	Hs.157208	aristless-related homeobox protein ARX	18.00
	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (17.96
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	17.41
	418756	AA252254	Hs.226949	ESTs	17.20
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	16.20
30	447534	AW953935	Hs.288655	ESTs	16.04
	407122	H20276	Hs.31742	ESTs	15.95
	446979	AI654443	Hs.197683	ESTs	15.90
	406547			Target Exon	15.70
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.65
35	456847	AI360456	Hs.37776	ESTs	15.50
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	15.00
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	14.95
	408908	BE296227	Hs.250822	serine/threonine kinase 15	14.65
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	14.20
40	422828	AL133396		prion protein 2 (dublet)	14.08
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	14.05
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	14.05
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	13.90
	418134	AA397769	Hs.86617	ESTs	13.85
45	454438	AA224053	Hs.172405	cell division cycle 27	13.70
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	13.40
	426427	M86699	Hs.169840	TTK protein kinase	13.35
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	13.20
	419384	AA490866	Hs.39429	ESTs	13.10
50	418477	AW022983		gb:df46h12.y1 Morton Fetal Cochlea Homo	12.85
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	12.80
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.78
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	12.72
	443068	AI188710		ESTs	12.65
55	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	12.60
	420401	AK001907	Hs.97464	hypothetical protein	12.50
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	12.50
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	12.45
	406937	U14622		gb:Human transketolase-like protein gene	12.25
60	439451	AF086270	Hs.278554	heterochromatin-like protein 1	12.10
	404996			Target Exon	11.86
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	11.85
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	11.60
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	11.55
65	421241	X91817	Hs.102866	transketolase-like 1	11.50
	414972	BE263782	Hs.77695	KIAA0008 gene product	11.45
	426866	U02330	Hs.172816	neuregulin 1	11.37
	433159	AB035898	Hs.150587	kinesin-like protein 2	11.35
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	11.24
70	440207	AI371978	Hs.128326	ESTs	11.12
	407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	11.10
	450142	AW207469	Hs.24485	chondroitin sulfate proteoglycan 6 (bama	11.05
	449576	AW014631	Hs.225068	ESTs	10.95
	414251	AL042306	Hs.97689	VASA protein	10.95
75	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	10.90
	436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Su	10.85
	427521	AW973352		ESTs	10.81
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	10.80
	442832	AW206560	Hs.253569	ESTs	10.62
80	436899	AA764852		ESTs	10.60
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	10.55
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	10.45
	435206	AI432364	Hs.160594	ESTs	10.15
	433975	AA971953	Hs.122055	ESTs	10.10

	446791	AI632278	Hs.195922	ESTs	10.05
	422232	D43945	Hs.113274	transcription factor EC	10.00
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	9.71
5	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	9.50
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.44
	438188	AA779975	Hs.128859	ESTs	9.30
	418973	AA233056	Hs.191518	ESTs	9.25
	413627	BE182082	Hs.246973	intron of Bicaudal D homolog 1	9.25
10	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.15
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	9.11
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	9.08
	426518	Z43039	Hs.170198	KIAA0009 gene product	9.05
	440968	N36327		gb:yx82b06.r1 Soares melanocyte 2NbHM Ho	9.05
15	440952	AI291804	Hs.118101	ESTs	9.05
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	9.05
	442618	R56222	Hs.26514	ESTs	8.96
	419423	D26488	Hs.90315	KIAA0007 protein	8.95
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	8.80
20	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	8.76
	444971	AI651116	Hs.148659	ESTs	8.75
	436513	AJ278110	Hs.125507	DEAD-box protein	8.60
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.59
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.58
25	428847	AI954833	Hs.98881	ESTs	8.57
	408465	AW196940	Hs.253277	ESTs	8.54
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	8.53
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	8.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.50
30	450480	X82125	Hs.25040	zinc finger protein 239	8.50
	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	8.42
	413318	AJ076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	8.35
	430835	AI240006	Hs.192326	ESTs	8.33
35	416859	H43437	Hs.80305	hypothetical protein MGC14258	8.30
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	8.26
	407340	AA810168	Hs.284289	villigo-associated protein VIT-1	8.25
	449260	AA741180	Hs.29879	ESTs	8.25
40	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	8.18
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	8.17
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	8.14
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.14
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.03
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	7.98
45	410420	AA224053	Hs.172405	cell division cycle 27	7.90
	453878	AW964440	Hs.19025	DC32	7.75
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	7.66
	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	7.65
	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	7.65
50	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	7.65
	451950	AW292317	Hs.213307	ESTs	7.60
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	7.59
	435514	AW592804		ESTs	7.55
	431041	AA490967	Hs.197955	KIAA0704 protein	7.55
55	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.51
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	7.38
	409421	AA199883	Hs.67624	ESTs	7.35
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	7.35
	458570	AW971698	Hs.12627	TJ6 protein	7.30
60	441287	AW293132	Hs.131373	ESTs	7.30
	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	7.25
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.25
	441425	AA933590	Hs.28937	homeobox protein from AL590526	7.25
	446293	AI420213	Hs.149722	LIM domain transcription factor LIM-1 (h	7.21
65	414136	AA812434		SMC2 (structural maintenance of chromoso	7.20
	409089	NM_014781	Hs.50421	KIAA0203 gene product	7.19
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.18
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	7.15
	452226	AA024898	Hs.157103	ESTs	7.15
70	435918	AF263538	Hs.86232	growth differentiation factor 3	7.14
	418661	NM_001949	Hs.1189	E2F transcription factor 3	7.10
	436360	AI962796	Hs.156100	ESTs	7.10
	442950	AI500417	Hs.46764	ESTs	7.00
	415684	D59356		sorbitol dehydrogenase	7.00
75	448336	R53848	Hs.44976	ESTs	7.00
	453183	AW086185	Hs.223856	ESTs	7.00
	444434	NM_004849	Hs.11171	APG5 (autophagy 5, S. cerevisiae)-like	6.95
	422655	AJ011812	Hs.119018	transcription factor NRF	6.95
	437421	AA917062		ESTs	6.95
80	428916	AF003001	Hs.194562	telomeric repeat binding factor (NIMA-in	6.94
	408045	AW138959	Hs.245123	ESTs	6.90
	448588	AI970276	Hs.156905	KIAA1676	6.89
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	6.85
	439780	AL109688		gb:Homo sapiens mRNA full length insert	6.85

	449911	AI262106	Hs.12653	ESTs	6.85
	417791	AW965339	Hs.111471	ESTs	6.80
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
5	453160	AI263307		H2B histone family, member L	6.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.75
	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.73
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	6.70
	418379	AA218940	Hs.137516	fidgetin-like 1	6.70
10	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	6.70
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	6.69
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	6.66
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	6.65
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	6.65
15	433247	AB040948	Hs.142856	KIAA1515 protein	6.65
	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	6.65
	417886	AA214584		ESTs	6.64
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	6.62
	412537	AL031778		nuclear transcription factor Y, alpha	6.61
20	426614	AA411925	Hs.301960	ESTs	6.57
	457465	AW301344	Hs.122908	DNA replication factor	6.52
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	6.50
	440801	AA906366		ESTs	6.50
	453116	AI276680	Hs.146086	ESTs	6.50
25	436909	AA907120		ESTs	6.50
	402199			Target Exon	6.50
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	6.46
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	6.41
30	438494	AA908678	Hs.130183	ESTs	6.41
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	6.40
	408758	NM_003686	Hs.47504	exonuclease 1	6.40
	442671	AI005668	Hs.130673	EST	6.40
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.38
	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.35
35	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	6.33
	441878	AI801869	Hs.127982	ESTs	6.31
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	6.31
	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	6.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	6.30
40	421650	AA781795	Hs.122587	ESTs	6.30
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.28
	408291	AB023191	Hs.44131	KIAA0974 protein	6.26
	438180	AA808189	Hs.272151	ESTs	6.25
45	412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	6.25
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	6.20
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	6.20
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.18
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	6.12
	426223	AW977812	Hs.130391	ESTs	6.10
50	445038	AI635444	Hs.143917	dJ467N11.1 protein	6.10
	419197	N48921	Hs.27441	KIAA1615 protein	6.09
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	6.05
	436902	AW247145	Hs.192729	ESTs	6.05
	429228	AI553633		ESTs	5.99
55	457065	AI476318	Hs.192480	ESTs	5.90
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	5.90
	449132	BE045641	Hs.197573	ESTs	5.90
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.89
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	5.85
60	457289	AW573204	Hs.137078	ESTs	5.85
	433849	BE465884	Hs.280728	ESTs	5.85
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	5.85
	438450	AI050866	Hs.65853	nodal, mouse, homolog	5.81
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	5.80
65	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	5.77
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.77
	408460	AA054726	Hs.285574	ESTs	5.75
	442461	AW062564	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	5.75
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
70	428249	AA130914	Hs.183291	zinc finger protein 268	5.74
	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (5.72
	402145			Target Exon	5.71
	447178	AW594641	Hs.192417	ESTs	5.70
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	5.65
75	442980	AA857025	Hs.8878	kinesin-like 1	5.65
	419131	AA406293	Hs.109526	ESTs	5.60
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor;	5.60
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
80	440553	AA889416	Hs.344043	Homo sapiens cDNA FLJ14459 fis, clone HE	5.58
	442333	AI650877	Hs.129302	ESTs	5.58
	453941	U39817	Hs.36820	Bloom syndrome	5.57
	415799	AA653718	Hs.225841	DKFZP434D193 protein	5.57
	413623	AA825721	Hs.246973	intron of Bicaudal D homolog 1	5.55

	427147	AA398587	Hs.97414	ESTs	5.55
	451050	AW937420		ESTs	5.55
	450113	AI683098	Hs.200866	ESTs, Moderately similar to ALU7_HUMAN A	5.54
5	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	5.54
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisoqu	5.53
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransferase 3 be	5.51
	449592	AI655494	Hs.195718	ESTs	5.50
	445517	AF208855	Hs.12830	hypothetical protein	5.50
10	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ara	5.48
	430044	AA464510	Hs.152812	ESTs	5.47
	437036	AI571514	Hs.133022	ESTs	5.47
	423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	5.46
	409103	AF251237	Hs.112208	XAGE-1 protein	5.45
15	420900	AL045633	Hs.44269	ESTs	5.45
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.45
	440738	AI004650	Hs.225674	WD repeat domain 9	5.45
	412723	AA648459	Hs.335951	hypothetical protein AF301222	5.45
	441122	H56777	Hs.121084	eppin-3	5.42
20	414151	AW976468	Hs.257245	ESTs	5.40
	435663	AI023707	Hs.134273	ESTs	5.40
	448986	H42169	Hs.347310	hypothetical protein FLJ14627	5.39
	433701	AW445023	Hs.15155	ESTs	5.39
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	5.35
25	440842	AA907288	Hs.130173	ESTs	5.35
	432407	AA221036	Hs.13273	gb:zr03f12.1 Stratagene NT2 neuronal pr	5.34
	401837			NM_025109:Homo sapiens hypothetical prot	5.32
	423739	AA398155	Hs.97600	ESTs	5.31
	424315	AW614850	Hs.193384	putative 28 kDa protein	5.31
30	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.30
	415717	AA167270	Hs.130435	ESTs	5.30
	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	5.26
	427119	AW880562	Hs.272525	ESTs	5.25
	432117	AL036195	Hs.2909	protamine 1	5.24
35	446837	AW273055	Hs.156598	ESTs	5.23
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	5.21
	422797	AB033064	Hs.236463	KIAA1238 protein	5.19
	446258	AI283476	Hs.263478	ESTs	5.18
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	5.17
40	445413	AA151342	Hs.12677	CGI-147 protein	5.17
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	5.16
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.15
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	5.15
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	5.15
45	448038	AW015073	Hs.232026	ESTs, Weakly similar to RO52_HUMAN 52 KD	5.15
	430272	X04898	Hs.237658	apolipoprotein A-II	5.14
	422094	AF129535	Hs.272027	F-box only protein 5	5.13
	420424	AB033036	Hs.97594	KIAA1210 protein	5.13
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	5.10
50	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	5.10
	453448	AL036710	Hs.209527	ESTs	5.10
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	5.06
	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	5.05
55	427961	AW293165	Hs.143134	ESTs	5.05
	441553	AA281219	Hs.121296	ESTs	5.05
	429999	AI761902	Hs.99597	ESTs	5.04
	426496	D31765	Hs.170114	KIAA0061 protein	5.02
	410929	H47233	Hs.30643	ESTs	5.01
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	5.01
60	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	5.00
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.00
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	5.00
	407568	AA740964	Hs.62699	ESTs	5.00
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!!	5.00
65	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	5.00
	416350	AF188625	Hs.189507	phospholipase A2, group IID	4.99
	452197	AW023595	Hs.232048	ESTs	4.98
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.97
	403780			C4001759:gi1133250[sp]P19474[RO52_HUMAN	4.97
70	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	4.95
	418894	W73921	Hs.50743	ESTs	4.95
	426623	AA382826	Hs.132793	ESTs	4.95
	443537	D13305	Hs.203	cholecystokinin B receptor	4.94
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.94
75	453716	AA037675	Hs.152675	ESTs	4.90
	402299			Target Exon	4.90
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	4.89
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.87
	409066	AA062980	Hs.66960	ESTs	4.85
80	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.85
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
	450375	AA009647		a disintegrin and metalloproteinase doma	4.85
	416201	AA467752	Hs.195161	ESTs	4.85
	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1126 (f	4.84

5	423198	M81933	Hs.1634	cell division cycle 25A	4.82
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.81
	418971	AA360392	Hs.87113	ESTs	4.80
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.80
	409517	X90780		tropoin 1, cardiac	4.80
10	424322	AL157491	Hs.145211	Homo sapiens mRNA; cDNA DKFZp434K1111 (f	4.80
	443169	AI038687	Hs.133338	ESTs	4.80
	438624	AA889055	Hs.123468	ESTs	4.79
	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	4.76
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.76
15	443715	AI583187	Hs.9700	cyclin E1	4.76
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	4.75
	451105	AI761324		gb:w60b11.x1 NCI_CGAP_Co16 Homo sapiens	4.71
	444431	AW513324	Hs.42280	Homo sapiens, clone MGC:9010, mRNA, comp	4.71
	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	4.71
20	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	4.70
	447175	AI365208	Hs.293606	ESTs	4.70
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.69
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	4.68
	416445	AL043004	Hs.79337	KIAA0135 protein	4.66
25	429652	AA766810	Hs.259290	ESTs	4.65
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	4.65
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	4.64
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.62
	427298	AA400495		ESTs	4.62
30	412863	AA121673	Hs.59757	zinc finger protein 281	4.62
	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	4.61
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.60
	446751	AA766998	Hs.79126	Human DNA sequence from clone RP11-16L21	4.60
	432656	NM_000246	Hs.3076	MHC class II transactivator	4.60
35	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	4.60
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 leratoca	4.60
	421830	AA789269	Hs.122509	ESTs, Weakly similar to dJ1018D12.3 [H.s	4.59
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	4.58
	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	4.58
40	431721	AB032996	Hs.268044	KIAA1170 protein	4.55
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.55
	453529	AA036729	Hs.335639	ESTs	4.55
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.55
	444386	BE065183		gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.55
45	428976	AL037824	Hs.194695	ras homolog gene family, member i	4.55
	449510	AI653154	Hs.328147	ESTs	4.55
	414725	AA769791		ring finger protein 21, interferon-respo	4.54
	424153	AA451737	Hs.141496	MAGE-like 2	4.53
	414466	AA349211	Hs.76205	cytochrome P450, subfamily XIA (choleste	4.52
50	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	458443	AV647010	Hs.27	glycine dehydrogenase (decarboxylating;	4.48
	453289	AI188161	Hs.144627	ESTs	4.48
	433641	AF080229		gb:Human endogenous retrovirus K clone 1	4.45
	440196	N72847	Hs.125221	ESTs	4.45
55	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.45
	428855	AI435901	Hs.89563	nuclear cap binding protein subunit 1, 8	4.45
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	4.45
	442240	AI791883	Hs.292719	ESTs	4.45
	421917	AB028943	Hs.109445	KIAA1020 protein	4.45
60	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	4.44
	449676	AW380579	Hs.209657	ESTs	4.43
	433183	AF231338	Hs.222024	transcription factor BMAL2	4.40
	439314	AA382413	Hs.178144	ESTs	4.40
	425312	AA354940	Hs.145958	ESTs	4.39
65	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.39
	430444	AW296421	Hs.121035	ESTs	4.35
	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.35
	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.34
	418216	AA662240	Hs.283099	AF15q14 protein	4.32
70	450351	BE547267	Hs.59791	hypothetical protein MGC13183	4.32
	454073	AW206286	Hs.116727	ESTs	4.30
	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	4.30
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.30
	448877	AI583696	Hs.253313	ESTs	4.28
75	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.27
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	4.25
	430292	AK000634	Hs.238270	hypothetical protein FLJ20627	4.25
	427778	AA412323	Hs.105323	ESTs	4.25
	418768	T39310		gb:ya04a09.r2 Stratagene lung (937210) H	4.25
80	409268	AA625304		ESTs	4.25
	442010	AI032680	Hs.132213	ESTs	4.24
	452807	AA028933	Hs.162434	ESTs	4.23
	401435			C14000397*:g[i]7499898[pir]T33295 hypoth	4.23
	447519	U46258	Hs.339665	ESTs	4.21
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.21
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	4.20
	453909	AW004045	Hs.203365	ESTs	4.20

	431126	AF085243	Hs.283619	zinc finger protein 236	4.20
	429628	H09604	Hs.13268	ESTs	4.20
	415989	AI267700		ESTs	4.20
5	421373	AA808229	Hs.46677	ESTs	4.20
	433979	AA620999		gb:ag03a08.s1 Soares_testis_NHT Homo sap	4.20
	408321	AW405882	Hs.44205	cortistatin	4.19
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.17
	430335	D80007	Hs.239499	KIAA0185 protein	4.17
10	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	4.16
	438885	AI886558	Hs.184987	ESTs	4.15
	451578	NM_016323	Hs.26663	cyclin-E binding protein 1	4.15
	432446	AA542845	Hs.294088	GAJ protein	4.13
	445076	AI206888	Hs.154131	ESTs	4.11
15	420218	AW958037		ribosomal protein L4	4.10
	453628	AW243307	Hs.83937	hypothetical protein	4.10
	418459	R85436	Hs.268814	ESTs	4.10
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.08
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	4.06
20	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.06
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	4.05
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	4.05
	449687	W68520		intermediate filament protein syncoilin	4.05
	452109	AI525873	Hs.61164	hypothetical protein FLJ14909	4.05
25	401464			histone deacetylase 5	4.05
	444670	H58373	Hs.332938	hypothetical protein MGC5370	4.05
	415884	H22966	Hs.13471	ESTs	4.05
	442066	BE502147	Hs.128418	ESTs	4.04
	402098			ENSP00000217725*:Laminin alpha-1 chain p	4.02
30	404287			FGENESH predicted novel CUB-domain conta	4.01
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	4.01
	449704	AK000733	Hs.23900	GTPase activating protein	4.00
	445685	AW779829		gb:hn88a05.x1 NCI_CGAP_Kid11 Homo sapien	4.00
	444379	N99035	Hs.30352	ESTs	4.00
35	435373	AW665538	Hs.117689	ESTs	4.00
	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	4.00
	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	4.00
	418648	AW979223	Hs.292478	ESTs	4.00
	446074	AA079799	Hs.343103	hypothetical protein FLJ11896	4.00
40	447353	AI375701	Hs.25884	ESTs	4.00
	410100	AA081636	Hs.271916	ESTs, Weakly similar to S41044 chromosom	4.00
	428856	AA436735	Hs.183171	hypothetical protein FLJ22002	4.00
	445140	AI650599	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
	406367			NM_022357:Homo sapiens putative metallo	3.99
45	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	3.99
	453985	N44545	Hs.251865	ESTs	3.98
	408446	AW450669	Hs.45068	hypothetical protein DKFZp4341143	3.97
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	3.97
	414713	BE465243	Hs.12664	ESTs	3.96
50	426067	AW664691	Hs.97053	ESTs	3.96
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 utinu	3.96
	454679	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo	3.95
	451865	H43737	Hs.33186	ESTs, Weakly similar to unknown protein	3.95
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	3.95
55	445730	AI624342	Hs.179082	ESTs	3.95
	451993	AA765776	Hs.122983	ESTs	3.95
	428819	AL135623	Hs.193914	KIAA0575 gene product	3.92
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	3.91
	420812	AA715303	Hs.107369	ESTs	3.90
60	423806	AA331247	Hs.86617	ESTs	3.90
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	3.90
	449211	AI922972	Hs.196073	ESTs	3.90
	409757	NM_001898	Hs.123114	cystatin SN	3.90
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	3.89
65	432512	NM_003284	Hs.3017	transition protein 1 (during histone to	3.89
	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	3.88
	449099	AI629041	Hs.46908	ESTs	3.88
	408092	NM_007057	Hs.42650	ZW10 interactor	3.85
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	3.85
70	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.84
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.83
	433023	AW864793		thrombospondin 1	3.82
	452571	W31518	Hs.34665	ESTs	3.81
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protei	3.80
75	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.80
	420697	AA827705	Hs.26605	ESTs	3.80
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	3.80
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.80
80	411856	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	3.80
	449529	AI990559	Hs.232033	ESTs	3.80
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	3.78
	444656	AI277924	Hs.145199	ESTs	3.77
	448674	W31178	Hs.154140	ovary-specific acidic protein	3.77
	415829	AW450198	Hs.163742	ESTs	3.76

	436188	AK001049	Hs.48712	hypothetical protein FLJ20736	3.75
	402178			C19001998*:gil6453813[ref][NP_008926.2] b	3.75
	418179	X51630	Hs.1145	Wilms tumor 1	3.75
5	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.75
	429063	AW363845	Hs.322903	ESTs, Weakly similar to A46010 X-linked	3.75
	437440	AA846804		ESTs	3.75
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associate	3.74
	438456	AA913381	Hs.20594	ESTs	3.73
10	418821	AA436002	Hs.183161	ESTs	3.73
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.73
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.71
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	3.70
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	3.70
15	414206	AW276887	Hs.46609	ESTs	3.70
	427761	AA412205	Hs.140996	ESTs	3.69
	428728	NM_016625	Hs.191381	hypothetical protein	3.68
	452631	AI188658	Hs.87496	ESTs	3.68
	427719	AI393122	Hs.134726	ESTs	3.68
20	431869	AA521136	Hs.190176	ESTs	3.67
	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.67
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.66
	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.66
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.65
25	456030	AA136106	Hs.184852	KIAA1553 protein	3.65
	402408			NM_030920*:Homo sapiens hypothetical pro	3.65
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	3.65
	416608	R11499	Hs.189716	ESTs	3.65
	417553	L09190		trichohyalin	3.65
30	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.65
	431077	AI689133	Hs.115660	hypothetical protein FLJ12810	3.64
	452461	N78223	Hs.108106	transcription factor	3.60
	437660	W31708	Hs.55304	ESTs	3.60
	420552	AK000492	Hs.98806	hypothetical protein	3.60
35	419926	AW900892	Hs.93796	DKFZP586D2223 protein	3.59
	420161	AI683069	Hs.120817	ESTs	3.59
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.59
	449571	AW016812	Hs.200266	ESTs	3.56
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	3.55
40	441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein	3.55
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	3.55
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.55
	437700	AA766060	Hs.301209	myeloid/lymphoid or mixed-lineage leukem	3.55
	438176	AW138970	Hs.122113	ESTs	3.55
45	453062	AW207538	Hs.61603	KIAA1677	3.55
	447064	AB002350	Hs.17262	KIAA0352 gene product	3.55
	430056	X97548	Hs.228059	KRAB-associated protein 1	3.54
	418049	AA211467		Homo sapiens, Similar to nuclear localiz	3.54
	434288	AW189075	Hs.116265	fibrillin3	3.54
50	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	3.52
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.52
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	3.52
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	3.51
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.50
55	449467	AW205006	Hs.197042	ESTs	3.50
	405935			Target Exon	3.50
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	3.50
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.50
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.49
60	429183	AB014604	Hs.197955	KIAA0704 protein	3.49
	428878	AA436884	Hs.48926	ESTs	3.49
	418203	X64942	Hs.83758	CDC28 protein kinase 2	3.49
	435068	H16262	Hs.31415	ESTs	3.48
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.48
65	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.48
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.48
	406542			C19000728*:gil12585552[sp]Q9Y2Q1[Z257_HU	3.47
	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.46
	402099			ENSP00000217725*:Laminin alpha-1 chain p	3.45
70	418826	AK000375	Hs.88820	HDCMC28P protein	3.45
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	3.45
	427617	D42063	Hs.199179	RAN binding protein 2	3.45
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.45
	400268			NM_003292:Homo sapiens translocated prom	3.45
75	443596	AW026048	Hs.134124	ESTs	3.45
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	3.45
	416031	T30290	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	3.45
	435244	N77221	Hs.187824	ESTs	3.45
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.45
80	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.45
	420686	AI950339	Hs.40782	ESTs	3.44
	429467	NM_004477	Hs.203772	FSHD region gene 1	3.43
	448769	N66037	Hs.38173	ESTs	3.43
	423453	AW450737	Hs.128791	CGI-09 protein	3.41

	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.41
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.41
	404068			Target Exon	3.40
	401644			Target Exon	3.40
5	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	3.40
	452907	BE256966	Hs.31652	ESTs, Moderately similar to I54374 gene	3.40
	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.39
	452404	AW450675	Hs.212709	ESTs	3.39
10	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	3.39
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	3.39
	440606	AI828751		ESTs, Weakly similar to I38022 hypotheti	3.38
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.37
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.37
15	446214	AK001322	Hs.14347	hypothetical protein FLJ10460	3.36
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.36
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.36
	421633	AF121860	Hs.106260	sorting nexin 10	3.36
	438192	AI859065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	3.36
20	436511	AA721252	Hs.291502	ESTs	3.35
	402680			Target Exon	3.35
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.35
	449477	AI652602	Hs.197043	ESTs	3.35
	413686	AI469213	Hs.71404	ESTs	3.35
25	401091			decay accelerating factor for complement	3.35
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.35
	433220	AI076192	Hs.131933	ESTs	3.34
	453200	AA033832	Hs.212433	ESTs	3.33
	427239	BE270447		ubiquitin carrier protein	3.33
30	418355	L42563	Hs.1165	ATPase, H7 transporting, nongastric, alp	3.33
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide syntha	3.31
	441243	AI767056	Hs.193002	ESTs	3.30
	440716	AW105245	Hs.146509	ESTs	3.30
	400587			C10000649*.gil7296574[gb]AAF51857.1[(AE	3.30
35	401148			Target Exon	3.30
	411752	AW236047	Hs.126497	ESTs	3.30
	433252	AB040957	Hs.151343	KIAA1524 protein	3.30
	434008	AA740878	Hs.112982	ESTs	3.30
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.30
40	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.30
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.29
	452761	BE244742	Hs.30532	CGI-77 protein	3.29
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	3.29
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.28
45	432809	AA565509	Hs.131703	ESTs	3.27
	449426	T92251	Hs.198882	ESTs	3.27
	425174	D87450	Hs.154978	KIAA0261 protein	3.25
	435159	AA668879	Hs.116649	ESTs	3.25
	446597	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	3.25
50	411554	W22895	Hs.112360	prominin (mouse)-like 1	3.25
	447555	AI391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	3.25
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.25
	445093	AI207197		ESTs	3.25
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.24
55	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.24
	453293	AA382267	Hs.10653	ESTs	3.24
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.23
	430552	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	3.22
	411975	AI916058	Hs.144583	ESTs	3.22
60	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.22
	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.21
	436515	AJ278111	Hs.195292	putative tumor antigen	3.21
	456505	AA504595		ESTs	3.21
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	3.21
65	452794	AI192444	Hs.25892	ESTs, Weakly similar to I37356 epithelia	3.20
	427314	AB033024	Hs.175475	KIAA1198 protein	3.20
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.20
	452028	AK001859	Hs.27595	hypothetical protein FLJ21142	3.20
	421002	AF116030	Hs.100932	transcription factor 17	3.20
70	422225	BE245652	Hs.118281	zinc finger protein 266	3.20
	437549	AA759149	Hs.128757	gb:ah70e03.s1 Soares_testis_NHT Homo sap	3.20
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	3.20
	427642	R40761	Hs.9834	ESTs	3.20
	442765	BE567353	Hs.99480	ESTs	3.20
75	410048	W76467	Hs.343874	proline oxidase homolog	3.20
	412008	NM_001841	Hs.73037	cannabinoid receptor 2 (macrophage)	3.20
	423675	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	3.20
	453895	AA039843	Hs.61948	Homo sapiens, clone MGC:16466, mRNA, com	3.20
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.19
80	428612	AA770001		ESTs	3.19
	422805	AA436989	Hs.121017	H2A histone family, member A	3.19
	444371	BE540274	Hs.239	forkhead box M1	3.18
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.17
	451684	AF216751	Hs.26813	CDA14	3.17

5	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	3.17
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.16
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.16
	444823	BE262989	Hs.12045	putative protein	3.15
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.15
10	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.15
	447801	H88923	Hs.270247	Homo sapiens cDNA FLJ11977 fis, clone HE	3.15
	424188	AW954552	Hs.142634	zinc finger protein	3.15
	436941	AA860383	Hs.292791	ESTs	3.15
	400592			Target Exon	3.15
15	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.15
	450405	AI694913	Hs.279637	ESTs	3.15
	414161	AA136106	Hs.184852	KIAA1553 protein	3.15
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	3.14
	438538	AA832203	Hs.291955	ESTs	3.14
20	441013	AI125252	Hs.126419	ESTs	3.14
	450431	AW136797	Hs.266041	ESTs	3.14
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	3.13
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.13
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.12
25	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	3.12
	412673	AL042957	Hs.31845	ESTs	3.11
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.11
	423419	R55336	Hs.23539	ESTs	3.11
	428925	AW242474	Hs.98960	ESTs	3.11
30	426108	AA622037	Hs.166468	programmed cell death 5	3.10
	439398	AA284267	Hs.221504	ESTs	3.10
	449138	AW294215	Hs.195631	ESTs	3.10
	441795	N58115	Hs.21137	AD024 protein	3.10
	456053	S57498	Hs.76252	endothelin receptor type A	3.10
35	403610			C3001199:gil7494834 pir T15308 hypothet	3.10
	421281	AI299139	Hs.17517	ESTs	3.10
	429274	AI379772	Hs.99206	ESTs	3.10
	438243	AI581311		ESTs	3.10
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.09
40	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.08
	416443	N69469	Hs.194225	ESTs	3.08
	421230	AW958439	Hs.105633	ESTs	3.07
	427906	AA864330	Hs.166520	ESTs	3.07
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.06
45	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.06
	445679	AI343868	Hs.301059	hypothetical protein FLJ12488	3.06
	434456	AW452621	Hs.116832	ESTs	3.05
	433228	F28212	Hs.14953	KIAA1491 protein	3.05
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	3.05
50	415227	AW821113	Hs.72402	ESTs	3.05
	421184	NM_003616	Hs.102456	survival of motor neuron protein interac	3.05
	438869	AF075009		gb:Homo sapiens full length insert cDNA	3.05
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	3.04
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.04
55	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.04
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	3.04
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	3.04
	435726	BE535787	Hs.113170	ESTs	3.03
	426386	AA748850	Hs.125830	bladder cancer overexpressed protein	3.03
60	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.02
	427953	AA417944	Hs.44331	ESTs	3.01
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.01
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	3.00
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	3.00
65	434776	AA648988		gb:ns41f11.s1 NCI_CGAP_GCB1 Homo sapiens	3.00
	414132	AI801235	Hs.48480	ESTs	3.00
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
	433493	AA594915	Hs.155087	ESTs	3.00
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	3.00
70	453416	NM_003037	Hs.32970	signaling lymphocytic activation molecu	3.00

TABLE 53B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

75	Pkey	CAT Number	Accession
	432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
80	423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
	430676	60836_2	BG215094 BG198867 BG196332 BG208220 BG212418
85	422828	227063_1	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603
	418477	4172_1	AI352469 BE061601 BI052752 AW818206 BF887722
90	443068	18695_17	BE671981 BE503379 AI655440 AI337054 AI288920 AI242370 AI825182 AA758081 BF855141 BF091068
	436812	659779_1	BC022538 AI990847 BF478249 BG217896 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092
95			AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
			AV752763 AI032142 N30308 N22181 H95390 AW675632
100			AW978773 AW298067 AA810101 AW194180 AA731645 AI690673

5	427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892 AA764852 AA736937 AW954733 AA315006 AW856665 AI964001 AI634418 AW236545 AI824860 BF223710 AW139686 AI672051 AI655566 AW025712 N36327 BF222876 N34083 AA911045 N40303 AW835451
	436899	1000797_1	BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433
	422689	874209_1	AA301270 AA301379 AA301366
	440968	518029_1	AA683356 AW592804 AI150287 AF147390 R76593 R76594 AJ420453 AL526740 AW968449 AA459140 AA843893 AI566516 AW971760 AA430089 AI753216 AA854268 AA743075 AI864957 AA458920 AI566634 AA211796 BG615512 BE169275 BF983253 BF969462 AA766261 AI769894 AA135833 AI831542 N63376 AA214392 AU154486 AW605017 AW450072 AA446459 BE881875 AI061423 AA598549 AW439151 AA426273 Z40087 AA812434 AA135965 H04812 BF666746 D59356 BG678312 N56640 AA166861 AA917062 AA757369 AW592218 AL109688 R23665 R26578 BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336 AA210987 D57294 AA214584 AA207006 D56572 AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114 AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364 BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793 AA382556 AW235763 AA927051 AI862075 BE886691 BE619282 AA906366 AA938956 AI910938 AW102570 AA907150 AA907120 AA737188 AI248890 AW977353 BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633 BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 BE072634 BE072653 AA830615 AA214736 AA331718 AA218925 AW962081 AA354237 BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758
10	427486	684159_1	NM_000363 X54163 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI657074 C03333 AI193911 C05024 C03193 AI950215 C05070 C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255 T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339 AK056685 BG399272 AA187835 BF821903 AV660550 AV660556 AV660502 BG564397 BE379584 BF446961 AI653056 AW973709 AI653173 BG054997 AI266043 BI054879 AI656750 AI492830 AW021142 AI472184 AW170056 AI082443 AI167921 D59940 BI492088 H74180 AW130886 AI348677 AI278577 AA761517 AI698203 AA115535 AI264790 AW205074 AA860452 AA554902 AI000715 D62102 BE544768 AI376090 D59939 AW224249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832 BI015205 AI761324 AW880937 AW880941 AA338252 AA338213 AK055746 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852 BF173139 BE010038 AA933717 BF061897 AW628327 AA641788 AA400495 BE065183 AI144398 BE065367 BF377924
	421974	864120_1	NM_058166 AF220030 AL043894 AW974257 AA625445 AU153502 AI650537 AW612116 AI672377 AW772451 BE892241 BE501740 AA718936 AI650276 AI654206 BE503226 AI651327 AW873562 AW271269 AW271565 AI873518 AI207150 AI338826 AI650258 AI628362 AA227117 AI207149 AW052076 AI470776 AA588100 AW235852 AA769791 AI701653 AK027664 AI984770 AU153469 BE222316 AA609539 BE220093 AA609112 BI054316 AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594 AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614951 N29986 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611 AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833 AA207155 BI004756 AA206262 AI365204 H77608 AW590511 T39328 T39310 T39303 T39284 BE893356 AA625304 AI765607 AI624898 R76060 AA069651 BG998885 R35783 BF086499 AA428755 AI245055 BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236 N50454 AA620999 T16375 AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727 T65754 AA229658 AA229857 AK056550 AK056356 AI928212 AI742073 AW300558 BG058755 AA058343 AI554842 AW207438 BF059981 BF444954 AW026234 AI620104 AA973460 AI370934 N63066 AA493129 AW590888 AI682952 AI167202 AA631394 AI421915 AI222883 BF477519 AI208777 AA765849 AI675076 AI370922 AI339579 AA486224 AA453524 AW771805 AI492842 H54679 AA961022 AW023555 H06192 AA910222 AI660021 AI032525 AI375480 AI361860 AI032919 AA833599 BG057928 AA553913 AW235737 AA002124 AA913636 F04607 AI867699 AA648100 BE091446 AA486378 BE002022 H84627 BI059837 BF917659 BF917100 BF917043 BF917104 BF916878 BG290981 AW954251 AA757126 H11545 AA353384 N48448 AA379845 AA004943 AA379928 AA002123 BM470118 AL598847 AL598830 BG899239 R57470 BF939179 AI650642 AI758851 BF352505 W68422 W35297 H11435 AA937499 AI783996 R12500 AI619557 N39093 Z41619 H22849 AA004942 R09436 R02403 T90942 T85823 BG029683 AI248120 BI850480 AW779829 N22494 BE155042 BE155040 BE154987 BE155012 BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573 AW813110 BF771370 BF771371 AW813113 AW003381 BI862319 AA204955 BF240507 BG212143 AW205739 BI760647 BM129481 BI760482 AW300025 AI288591 AW236114 AI302852 AI038548 AI797207 AA534496 BG188194 AA921877 BG191846 BG182959 BE620243 BF217428 BC009514 BM463015 AL529077 BM051874 BG773269 BM314351 BM314660 AW629666 AA316207 AI623431 AA504153 AA314700 BG195449 BG614101 BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148 AI968683 AA846676 AA927355 H80424 AW973295 R88209 F29868 BE928871 AA846804 AA757581 AI050950 AI092024 AA838807
	437421	978554_1	
	439780	49082_1	
15	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
20	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
25	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
30	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
35	453160	6028_5	
	415684	18695_18	
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	415684	18695_18	
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45	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
50	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
55	453160	6028_5	
	415684	18695_18	
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	439780	49082_1	
60	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
65	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
70	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
75	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
80	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
85	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
90	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
95	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
100	453160	6028_5	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	

417553	258857_1	AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204699 W60115 N56751 N30878 AI769345 R71250 AI363766 R22777 R17009 R27985 R28243
408065	101881_1	BI603077 AW954272 BI598724 AI003154 AA0593C0 AA046911 BI669907 BI600966 BI669987
418049	12052_4	AJ314647 NM_052888 BI494693 AA835065 AI634477 AI336678 AI807696 BF477887 AI701147 Z39187 R38979 F02234 AA984711 BI222234
430968	1237115_1	AV731417 R42406 H04996 T98498 R12489 R12577 R42405
400268	840_4	AW972830 AA489820 AA527647 AA570362
		U69668 AA448366 X63105 BC016514 BE694436 AI655840 AW235355 BG427984 AA612862 AA448223 BM145813 BM194565 AI870824 BE973573
		BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687
		BF908518 BF907890 R11490 AL536642 BF109180 AA953881 AI783716 BE622908 AI621005 AW148784 AI690114 AW275000 AI765790 BF222859
		AW167268 AI990460 AW300443 AA779660 AI620568 BF115024 BE504703 AW628332 AI922851 BE006636 AU158376 AI168279 AA809916
		AI69757 AA830828 AA830388 N64324 AI049683 AA970275 BF477364 BG261301 AA326388 AU150565 AU158374 AA687967 N58510 AI650450
		AL549572 BF349280 BF349269 BM463016 AW836798 AL120958 AW836891 AW385525 BE175733 BE175727 BE175723 BF092430 BI061782
		AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW847833 AL536643 AW366516 AW391532
		BE934857 BF925057 AW438446 R86246 AW179270 BE087782 BI832144
		BC017350 BC021031 AI220219 AI828751 AW134498 BE139642 AA894554 AI278594 AV747315 BE561749 BI085890 T80117 H69682 N70904
		AV741999 H70098
		AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE139953 BE049086 AI334881
		AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478
		AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839
		AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420
		AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260
		AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427
		BF718773 BF718645 AW074866 BE857822
		AI207197 BF773544 AW196462
		BC017965 AW969075 AA279982 AA504511 AI219979 AA504595 AI245579 AA278181 BG485019 BI049312
		AA770001 AA431112 AA432126
		AL079309 AA281819
		AI732997 AA977633 AA865818
		AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
		BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
		AW840571
		AI581311 AA781682 AA781678
		AF075009 R63109 R63068
		AW974599 AA648988 R98760

TABLE 53C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406547	7711513	Minus	172780-174358
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
402199	8576116	Minus	84187-84744
402145	8018280	Plus	113086-114800
401837	7630990	Minus	120993-121095,121660-121729
403780	8076989	Plus	93160-93409
402299	6693370	Plus	23367-25175
401435	8217934	Minus	54508-55233
401464	6682291	Minus	170688-170834
402098	8117697	Minus	44186-44330
404287	2326514	Plus	53134-53281
406367	9256126	Minus	58313-58489
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
402178	8575912	Plus	391138-391711
403433	9719611	Minus	72225-72437
402408	9796239	Minus	110326-110491
405935	6758795	Minus	163112-163652
406542	7711499	Plus	117335-118473
402099	8117697	Plus	121553-121742,123265-123423
404068	3168621	Minus	18123-18766
401644	8576138	Plus	82655-83959
402680	8113438	Plus	137634-137768,139702-139893,140475-14059
401091	9958240	Plus	94760-94898
400587	9887626	Plus	25435-25588,25668-25747
401148	2547238	Minus	22521-23053
403432	9719611	Minus	68204-68392
400592	9887642	Minus	24642-24815
403610	8308266	Plus	157705-157860

TABLE 54A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of normal testis to normal adult tissues
 R2: Ratio of "average" normal testis to "average" testicular cancer

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
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	401979		C17000767:gil11990770[emb]CAC19651.1 (A	10.08	43.3
	421825	AA298758	Hs.183747	ESTs, Moderately similar to CALB_HUMAN C	10.35
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.74
5	441728	AI797395	Hs.169797	Homo sapiens BOULE (BOULE) mRNA, complet	10.54
	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	4.86
	415211	R64730.	Hs.155986	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	6.93
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	4.94
	449108	AI140683	Hs.98328	hypothetical protein MGC13040	7.94
10	420437	AA992768	Hs.97633	A kinase (PRKA) anchor protein 4	16.75
	436632	AA724299	Hs.304020	ESTs, Weakly similar to CRTC_HUMAN CALRE	6.51
	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	4.96
	406409			Target Exon	3.98
	427060	AW378993	Hs.90286	ESTs	3.56
15	427310	AI613480	Hs.47152	teklin 3	4.50
	427166	AA431576	Hs.99154	ESTs	4.28
	427178	AA398866	Hs.97542	Homo sapiens testis-development related	10.19
	410694	AL137538	Hs.65500	Homo sapiens mRNA; cDNA DKFZp434N2019 (f	5.76
	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.24
20	427441	AA412605	Hs.343879	SPANX family, member C	10.45
	438057	AW294544	Hs.125785	ESTs, Weakly similar to CORB MOUSE CORNI	18.57
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	5.18
	427293	AA705799	Hs.183714	ESTs	10.79
	444963	AI916973	Hs.213603	ESTs	3.18
25	428608	AI699329	Hs.99168	ESTs, Weakly similar to AF132972 1 CGI-3	15.40
	453178	AA496086	Hs.61648	ESTs	4.13
	428618	AA885360		Target CAT	7.53
	401741			Target Exon	10.41
	422086	AW182930	Hs.250182	ESTs	4.39
30	426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	7.04
	442373	AI377758	Hs.164799	testes development-related NYD-SP17	8.23
	427455	AF173081	Hs.178215	Vertebrate LIN7 homolog 1, Tax interacti	3.03
	437248	AW449340	Hs.93090	ESTs	9.06
	426608	AA444162	Hs.99344	hypothetical protein PRTD-NY3	3.68
35	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	9.70
	422358	AL133030	Hs.115429	Homo sapiens mRNA for KIAA1666 protein,	11.85
	451610	AW118604	Hs.207126	ESTs	5.63
	410630	BE044562	Hs.266847	ESTs, Weakly similar to KIAA1214 protein	4.38
	426677	AW949856	Hs.97165	ESTs	6.58
40	437558	AI126471	Hs.124112	ESTs, Moderately similar to H5J2_HUMAN D	4.47
	423088	NM_006687	Hs.123530	actin-like 7A	15.07
	426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	18.55
	421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	13.93
	429877	W37337	Hs.103014	ESTs	6.97
45	413114	AI825838	Hs.75206	protein phosphatase 3 (formerly 2B), cat	3.78
	412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	22.03
	411844	AI807681	Hs.144658	ESTs, Weakly similar to T17257 hypotheti	7.34
	436868	AA974253	Hs.120319	Homo sapiens autoimmune infertility-rela	4.16
	426599	AW183574		ESTs	6.29
50	426683	AI073430	Hs.146775	ESTs, Weakly similar to T30993 hypotheti	10.89
	426930	AA393442		ESTs	5.06
	427836	AA416642	Hs.116176	ESTs	4.79
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	5.11
55	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	21.26
	434150	BE047007	Hs.116116	testis specific, 10	4.85
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	10.29
	422116	H64205	Hs.111850	mitochondrial capsule selenoprotein	9.12
	433724	AI827749	Hs.144924	serine/threonine protein kinase SSTK	22.24
60	410187	AA860341	Hs.104680	ESTs	3.03
	419584	AF053356	Hs.283764	F-box only protein 24	6.43
	458182	AI147996	Hs.155833	ESTs, Weakly similar to spliceosomal pro	9.90
	418665	T19204	Hs.195685	ESTs	7.14
	426646	AA382787	Hs.122713	ESTs	7.03
	420349	NM_016611	Hs.97174	potassium inwardly-rectifying channel, s	14.90
65	428624	AI125222	Hs.98712	hypothetical protein DKFZp434H0311	3.71
	420710	NM_007009	Hs.99875	zona pellucida binding protein	20.78
	434317	AI674095		ESTs	3.98
	443432	AI056863	Hs.339871	ESTs	3.46
	425709	AA383076	Hs.159274	outer dense fibre of sperm tails 1	23.21
70	426670	AA383047	Hs.310210	ESTs	6.92
	408613	AW242086	Hs.253967	ESTs	5.77
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	9.23
	434133	AI655275	Hs.236635	ESTs, Weakly similar to ATHUB actin beta	7.46
	427294	AA412594	Hs.125902	ESTs	3.44
75	427262	AA448509	Hs.128652	ESTs	5.66
	429851	AA459835	Hs.120573	hypothetical protein DKFZp434K1172	9.01
	406378			NM_021247*:Homo sapiens protamine 3 (PRM	3.96
	425865	AA393491	Hs.183740	ESTs	9.15
	428665	NM_017481	Hs.189184	ubiquitin 3	11.07
80	439379	AA835002	Hs.125611	ESTs	5.06
	427520	BE467881	Hs.97489	ESTs, Weakly similar to B28096 line-1 pr	9.29
	458940	BE149824	Hs.132888	KIAA1674	3.11
	426620	AW450252		ESTs	12.27
	429516	AI653299	Hs.99354	ESTs, Weakly similar to hyperpolarizatio	9.15

	426736	AA431615	Hs.130722	ESTs	3.58	6.1
	427843	AC005622	Hs.180943	hypothetical protein R30953_1	6.34	6.1
	426639	AI799059	Hs.112807	ESTs	6.93	6.0
5	438637	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein	3.04	6.0
	433795	AI216683	Hs.122599	ESTs, Weakly similar to ALU7_HUMAN ALU S	10.45	5.9
	441232	AI656050	Hs.7086	hypothetical protein MGC12435	4.27	5.9
	433943	AA992805	Hs.44865	lymphoid enhancer-binding factor 1	6.87	5.8
	426955	AA393669	Hs.238094	ESTs	4.75	5.8
10	428918	AL036967	Hs.2324	protamine 2	38.40	5.8
	427851	AA846543	Hs.98257	ESTs	15.87	5.8
	428208	AA442327	Hs.104854	ESTs	6.34	5.7
	422207	AI828862	Hs.10964	ESTs	6.43	5.7
	431153	AW972342	Hs.77823	hypothetical protein FLJ21343	9.24	5.7
	419350	AC005328		Homo sapiens chromosome 19, cosmid R2666	14.94	5.6
15	427107	AA889586	Hs.180346	ESTs	6.25	5.6
	429461	AI188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	3.92	5.6
	432512	NM_003284	Hs.3017	transition protein 1 (during histone to	22.03	5.6
	434451	AW445179	Hs.121438	ESTs	7.89	5.5
20	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1126 (f	11.26	5.5
	427214	AA442240	Hs.178213	ESTs	8.41	5.5
	458658	AI301117	Hs.122055	ESTs	4.35	5.5
	457034	AA398061	Hs.296587	Homo sapiens chromosome 21 segment HS21C	11.29	5.4
	423120	AW160551	Hs.124021	soggy-1 gene	8.88	5.4
25	438983	AF085884	Hs.20029	proacrosin binding protein sp32 precursor	22.69	5.4
	426619	AI357194	Hs.119284	ESTs	7.07	5.4
	440822	AI554897		Homo sapiens clone 191B7 placenta expres	3.60	5.4
	416205	AA176396	Hs.169624	ESTs	10.26	5.4
	426712	AW173177	Hs.197755	hypothetical protein MGC5356	8.17	5.3
30	427840	AI216654	Hs.98251	ESTs	6.44	5.3
	439314	AA382413	Hs.178144	ESTs	8.35	5.3
	426943	BE551631	Hs.20969	ESTs	6.31	5.2
	409209	AA460160	Hs.73217	ESTs	7.85	5.2
	441710	AI187883	Hs.127510	ESTs, Weakly similar to ENC1_HUMAN ECTOD	7.73	5.1
35	420571	AA442366	Hs.98952	Human DNA sequence from clone RP1-39G22	9.39	5.1
	428563	AA431616	Hs.98660	ESTs	14.94	5.1
	433994	AL042483	Hs.335499	ESTs	6.84	5.0
	441856	AI674774	Hs.128014	ESTs	3.74	5.0
	427789	AA412428	Hs.48642	hypothetical protein FLJ23093	4.29	5.0
40	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	4.14	4.9
	430232	AA469940	Hs.105324	ESTs, Moderately similar to FRHUH ferrit	10.66	4.9
	421850	AW274576	Hs.121021	ESTs	12.27	4.9
	449436	AA860329	Hs.279307	hypothetical protein DKFZp434I2117	4.50	4.9
	426699	AA383337	Hs.121269	ESTs	5.67	4.9
45	426627	AF012359	Hs.195685	ESTs	20.66	4.9
	427285	AA401664	Hs.97784	ESTs	4.72	4.8
	423693	AL133633	Hs.131779	Homo sapiens mRNA; cDNA DKFZp434E2118 (f	6.03	4.8
	457019	AA421844	Hs.12830	hypothetical protein	3.87	4.8
	405264			NM_030813*:Homo sapiens suppressor of po	4.48	4.8
50	450606	AI668605	Hs.60380	ESTs, Moderately similar to ALU6_HUMAN A	3.76	4.8
	421378	L77564	Hs.103978	serine/threonine kinase 22B (spermiogene	7.35	4.8
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	8.66	4.7
	427423	BE267041	Hs.177926	exonuclease NEF-sp	19.27	4.7
	438756	AW081754	Hs.303923	hypothetical protein DKFZp434L1717	12.05	4.7
55	424197	AF096834	Hs.142989	germ cell specific Y-box binding protein	17.70	4.7
	423284	AC005764	Hs.126496	Homo sapiens chromosome 19, cosmid R3134	7.50	4.7
	432117	AL036195	Hs.2909	protamine 1	55.33	4.7
	424426	AI476416	Hs.132888	KIAA1674	5.41	4.6
	437387	AI198874	Hs.28847	AD026 protein	5.04	4.6
60	420718	NM_002301	Hs.99881	lactate dehydrogenase C	9.18	4.6
	420768	AI468780	Hs.292503	ESTs, Weakly similar to T47142 hypotheti	5.70	4.6
	423677	M86808	Hs.131361	pyruvate dehydrogenase (lipoamide) alpha	10.93	4.5
	436661	AI125270	Hs.128069	ESTs, Weakly similar to T19142 hypotheti	3.82	4.5
	427749	BE045979	Hs.98095	Homo sapiens cDNA: FLJ23052 fis, clone L	6.45	4.5
65	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	11.29	4.5
	427877	AW138725	Hs.178067	ESTs	4.09	4.5
	426623	AA382826	Hs.132793	ESTs	26.62	4.5
	429965	AL040379	Hs.99551	Homo sapiens cDNA FLJ11789 fis, clone HE	13.25	4.5
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.88	4.4
70	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosom	3.46	4.4
	421938	AA405951		gb:zu66c01.r1 Soares_testis_NHT Homo sap	4.69	4.4
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	19.15	4.4
	426710	BE041517	Hs.143893	ESTs	5.57	4.4
	428710	AI890919	Hs.126780	ESTs, Weakly similar to T12519 hypotheti	11.86	4.4
75	438641	AW138484	Hs.190653	ESTs	6.19	4.4
	420614	AL110291	Hs.99364	putative transmembrane protein	6.86	4.4
	422705	NM_006686	Hs.119287	actin-like 7B	9.73	4.4
	421805	AL042716	Hs.130947	hypothetical protein DKFZp434N1415	5.89	4.4
	448963	AA459796	Hs.331247	Homo sapiens, clone IMAGE:3610712, mRNA,	6.77	4.3
80	426738	AA421097	Hs.291902	ESTs	3.49	4.3
	440403	AW665135	Hs.130531	ESTs	6.97	4.3
	456085	AI184560	Hs.130352	ESTs, Weakly similar to A47582 B-cell gr	6.30	4.3
	439594	AI245026	Hs.111099	hypothetical protein MGC10974	7.85	4.3
	428909	AI190714	Hs.98945	ESTs	7.79	4.3

	426735	T78716	Hs.120446	ESTs	5.10	4.3
	438653	AW188099	Hs.131813	ESTs	5.29	4.3
	443038	AI968058	Hs.209206	ESTs, Weakly similar to S38782 actin bet	7.29	4.2
5	428677	AI657119	Hs.120036	tropoin I, cardiac	10.73	4.2
	424220	AK000869	Hs.143251	hypothetical protein	9.13	4.2
	426299	H93373	Hs.169222	acrosomal vesicle protein 1	4.87	4.2
	428871	AA913840	Hs.98903	ESTs	3.76	4.2
	410163	AF151977	Hs.59260	NTT5 protein	7.29	4.2
10	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.29	4.2
	427757	AI142295	Hs.129794	ESTs	3.57	4.1
	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	11.13	4.1
	401692			C16000122:gij5689527[dbj]BAA83047.1} (A	6.37	4.1
	403783			NM_031956:Homo sapiens NYD-SP14 protein	3.74	4.0
15	421611	AA459841	Hs.97309	ESTs	11.51	4.0
	404271			ENSP00000244792*:Phosphoglycerate kinase	4.02	4.0
	441800	AW027571	Hs.7973	hypothetical protein DKFZp434G156; KIAA1	8.86	4.0
	423000	AF049615	Hs.122959	Huntingtin interacting protein M	3.60	4.0
	423118	AL035460	Hs.124009	Human DNA sequence from clone RP5-860F19	4.84	4.0
20	420419	AA397796	Hs.11614	HSPC065 protein	4.07	3.9
	435897	AF269223	Hs.128322	I-complex 11 (a murine tcp homolog)	23.29	3.9
	428516	R38137	Hs.156469	ESTs, Moderately similar to KIAA0940 pro	5.28	3.9
	427179	AA400590	Hs.97543	ESTs	6.18	3.9
	426609	AL040604	Hs.99344	hypothetical protein PRTD-NY3	10.07	3.9
25	452579	AA131657	Hs.23830	ESTs	5.24	3.9
	441443	BE465999	Hs.129293	ESTs	4.60	3.9
	427709	AI631811	Hs.180403	STRIN protein	3.82	3.9
	435484	AA682756	Hs.88051	ESTs	5.10	3.9
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	4.61	3.8
30	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	7.14	3.8
	421620	AA446183	Hs.91885	ESTs, Weakly similar to I55214 salivary	5.20	3.8
	427086	AA436131	Hs.188781	ESTs	5.76	3.8
	420475	AW408407	Hs.187018	ESTs	3.99	3.8
	441357	AI240184	Hs.343487	ESTs	4.63	3.8
35	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	8.04	3.8
	441806	AI024442	Hs.346385	ESTs	5.48	3.8
	413209	AW083791	Hs.21263	suppressor of potassium transport defect	9.02	3.8
	414544	AA149285	Hs.115659	hypothetical protein MGC5521	10.15	3.8
	427251	AI026844	Hs.98843	ESTs, Highly similar to GRA2_HUMAN GLYCI	7.69	3.8
40	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	3.46	3.7
	442589	BE409869		protein kinase, cAMP-dependent, regulato	4.50	3.7
	425841	BE262951	Hs.99052	ESTs	8.26	3.7
	410350	AA446395	Hs.62595	chromosome 9 open reading frame 9	7.64	3.7
	440487	AI203685	Hs.135763	ESTs	5.90	3.7
45	419455	AW172570	Hs.14600	ESTs	4.23	3.7
	436588	AA759233		ESTs	5.04	3.7
	421610	AA393168	Hs.90034	hypothetical protein FLJ21916	5.53	3.7
	441982	AI216902	Hs.48802	ESTs	4.79	3.6
	427288	AI139000	Hs.97792	hypothetical protein DKFZp434I099	5.17	3.6
50	414439	W45387	Hs.100007	regulatory factor X, 2 (influences HLA c	4.43	3.6
	401798			Target Exon	4.83	3.6
	433395	AF039442	Hs.160881	Homo sapiens colon cancer antigen NY-CO-	3.17	3.6
	438064	AI476330	Hs.234934	ESTs	3.56	3.6
	426658	AA397912	Hs.115366	Human DNA sequence from clone RP4-803K15	7.26	3.6
55	431986	AA536130		Novel human gene mapping to chomosome 20	6.13	3.6
	427872	AA835058	Hs.9622	Human DNA sequence from clone RP1-261G23	4.04	3.6
	437896	AA813689	Hs.123436	ESTs, Weakly similar to KIAA1205 protein	4.69	3.6
	420431	AB007131		Homo sapiens cDNA FLJ12825 fis, clone NT	4.24	3.5
	409467	Z22780	Hs.307358	cylicin, basic protein of sperm head cyl	5.13	3.5
60	422770	AL117544	Hs.120021	DKFZP434I092 protein	8.02	3.5
	437399	AI808626	Hs.121188	ESTs, Weakly similar to T29922 hypotheti	5.03	3.5
	428448	AA625766	Hs.98609	ESTs, Weakly similar to A Chain A, Coagu	4.30	3.5
	426705	AL042749	Hs.97714	ESTs	10.45	3.5
	427312	AA400657	Hs.135283	ESTs	4.47	3.5
65	423329	AF054910	Hs.127111	teklin 2 (testicular)	4.40	3.5
	439290	AI638094	Hs.236896	ESTs	3.29	3.4
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	6.18	3.4
	420500	AC005261	Hs.98338	serine/threonine kinase 13 (aurora/PL1-	6.24	3.4
	441168	AI198850	Hs.131654	DMRT-like family B with proline-rich C-t	10.39	3.4
70	420482	X57655	Hs.98243	serine protease inhibitor, Kazal type, 2	20.38	3.4
	426988	AI208684	Hs.163960	Homo sapiens heat shock transcription fa	5.02	3.4
	444968	AW628609	Hs.148653	ESTs	5.10	3.4
	429210	AA448011	Hs.131918	ESTs	4.22	3.4
	442970	R28215	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	4.20	3.4
75	422782	AL133054	Hs.120369	hypothetical protein DKFZp434H2215	4.72	3.4
	436601	AA969884		ESTs	4.84	3.4
	421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	7.83	3.4
	415705	U06632	Hs.966	collin	6.30	3.4
	435587	AF215924	Hs.97899	putative allantoicase	3.48	3.3
80	427572	AA417291	Hs.97978	hypothetical protein MGC4766 similar to	3.54	3.3
	427541	AI798983	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.33	3.3
	429404	NM_005738	Hs.201672	ADP-ribosylation factor-like 4	3.57	3.3
	415014	AW954064	Hs.24951	ESTs	4.03	3.3
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	10.76	3.3

	412092	H43229	Hs.125201	ESTs, Weakly similar to I38022 hypotheti	5.27	3.3
	441579	AW468847	Hs.127194	ESTs	7.13	3.3
	420619	AF130255	Hs.99430	testis zinc finger protein	5.19	3.3
5	425368	AB014595	Hs.155976	cullin 4B	3.07	3.3
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.52	3.3
	429938	BE296804	Hs.226377	phosphate cytidyltransferase 2, ethano	3.03	3.3
	453017	R84301	Hs.31387	DKFZP564J0123 protein	3.30	3.3
	424466	AL040420	Hs.148250	Homo sapiens mRNA; cDNA DKFZp434N1535 (f	4.81	3.3
10	442084	H81173	Hs.34596	ESTs	4.78	3.3
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	4.63	3.3
	434183	AW104257	Hs.123426	ESTs, Weakly similar to SN1L_HUMAN PROBA	5.73	3.3
	428093	AW594506	Hs.104830	ESTs	6.95	3.3
	433982	AA724720	Hs.112941	ESTs	5.11	3.2
15	429821	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (fr	4.04	3.2
	408415	AW418788		ESTs, Weakly similar to S43569 R01H10.5	3.49	3.2
	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.77	3.2
	402857			Target Exon	3.19	3.2
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	3.69	3.2
20	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	14.29	3.2
	427748	AA421041		ESTs	4.57	3.2
	422794	AJ011733	Hs.120857	synaptogyrin 4	4.23	3.2
	417488	AL046052	Hs.321046	hypothetical protein FLJ11743	3.57	3.2
	440115	R41808		ESTs, Weakly similar to B Chain B, Solut	4.67	3.2
25	437143	AW204056	Hs.8917	ESTs	4.16	3.2
	417473	M55268	Hs.82201	casein kinase 2, alpha prime polypeptide	4.02	3.2
	426594	AA884317	Hs.97130	ESTs	3.45	3.2
	428733	AA346824	Hs.191996	Homo sapiens organic cation transporter	6.29	3.2
	440864	AI382142	Hs.132104	ESTs	8.48	3.2
30	427141	AW628007	Hs.97643	testis-specific protein TSP-NY	5.60	3.2
	431534	AL137531	Hs.258990	Homo sapiens mRNA; cDNA DKFZp434F0919 (f	5.10	3.2
	438670	AI275803	Hs.123428	ESTs	4.08	3.2
	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	4.26	3.2
	452251	R37132	Hs.65009	ESTs	4.01	3.1
35	444141	AW629475	Hs.8977	ESTs, Weakly similar to RED1_HUMAN DOUBL	4.89	3.1
	428254	AK000542	Hs.183362	hypothetical protein FLJ20535	5.23	3.1
	421621	AL045589	Hs.180197	ESTs	7.09	3.1
	451017	BE391847	Hs.181173	hypothetical protein MGC10771	3.57	3.1
	457138	AW140059	Hs.98579	ESTs	13.17	3.1
40	428524	AA429772		ESTs	4.40	3.1
	428726	AA432195	Hs.98694	ESTs	6.47	3.1
	431310	AW327889	Hs.252433	Homo sapiens cDNA FLJ13794 fis, clone TH	4.07	3.1
	428076	AA420979	Hs.234895	ESTs, Weakly similar to Lysozyme [H.sapi	5.97	3.1
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.45	3.1
45	424450	AL137526	Hs.147472	dynein intermediate chain 2	6.01	3.1
	433963	AI218808	Hs.187778	ESTs	5.68	3.1
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.20	3.1
	440933	AI208217		ESTs	3.44	3.1
	441854	AA215990	Hs.99841	ESTs, Weakly similar to dJ1108D11.1 [H.s	4.03	3.1
50	423313	NM_014269	Hs.126838	a disintegrin and metalloproteinase doma	6.36	3.1
	428630	AA431270	Hs.140646	ESTs	3.59	3.1
	448813	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	5.63	3.0
	434720	AI208541	Hs.189160	ESTs, Weakly similar to cytochrome c-lik	6.04	3.0
	436328	AI201145	Hs.122042	Human DNA sequence from clone RP4-576H24	7.10	3.0
55	429293	AI767879	Hs.99214	ESTs	5.69	3.0
	427255	AA400082	Hs.343593	ESTs, Weakly similar to TD54_HUMAN TUMOR	5.37	3.0
	440713	AA904448	Hs.126368	ESTs	6.28	3.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	7.88	3.0
	423218	NM_015896	Hs.167380	BLu protein	6.68	3.0
60	444644	AW070634	Hs.144794	ESTs	5.00	3.0
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.75	3.0
	427829	AI188225		ESTs	7.36	3.0
	426879	AI969340	Hs.115437	hypothetical protein MGC3048	7.24	3.0
	427362	AA625582	Hs.97752	EST	4.38	3.0
65	441973	T60072	Hs.10688	ESTs, Weakly similar to HRIHFB2157 [H.sa	4.06	2.9
	428989	AF104260	Hs.194712	piwi (Drosophila)-like 1	4.45	2.9
	438735	M76676		ESTs	3.81	2.9
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	11.37	2.9
	427586	AA609661	Hs.190592	ESTs, Moderately similar to WASP-family	6.26	2.9
70	427306	AI476743	Hs.229275	ESTs	3.00	2.9
	418725	AL117637	Hs.306094	DKFZP434I225 protein	7.13	2.9
	456748	AW137749	Hs.125902	ubiquitin specific protease 2	3.48	2.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.60	2.9
	433836	AA610065	Hs.179646	ESTs	3.33	2.9
75	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.22	2.9
	437426	AW136558	Hs.125246	ESTs	4.49	2.9
	405528			C2002647:gi 4507721 ref NP_003310.1 tit	6.03	2.9
	442977	AW291731	Hs.144090	ESTs	4.23	2.9
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	13.24	2.8
80	424275	AW673173	Hs.144505	DKFZP566F0546 protein	5.60	2.8
	426667	AA770016	Hs.121192	ESTs	3.64	2.8
	410202	AB023213	Hs.60177	KIAA0996 protein	3.00	2.8
	428080	AI198656	Hs.98330	ESTs	4.09	2.8
	427252	AA400069	Hs.97757	hypothetical protein FLJ13031	4.34	2.8

	458255	AW140126	Hs.132357	ESTs	3.23	2.8
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.95	2.8
	440582	AA993337	Hs.129082	ESTs	5.29	2.8
	435566	AI457958	Hs.80464	hepatitis B virus x-interacting protein	3.28	2.8
5	433771	AI028794	Hs.112684	ESTs	3.36	2.8
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypothe	5.30	2.8
	426703	AI221893	Hs.121549	ESTs	3.93	2.8
	430251	AA609246	Hs.181451	ESTs	4.04	2.8
	427184	AI969361	Hs.180471	ESTs	6.78	2.8
10	439909	AW450062	Hs.187134	ESTs, Moderately similar to AF263742 1 g	3.65	2.8
	448885	AW003686	Hs.30325	ESTs, Highly similar to AF200923 1 tesli	3.34	2.7
	450340	AA442322	Hs.60288	ESTs	5.39	2.7
	428100	AW665592	Hs.190413	ESTs	5.32	2.7
	449333	AI203021		ESTs	4.35	2.7
15	429861	AI989571	Hs.99510	ESTs	3.28	2.7
	426622	AL044400	Hs.25371	ESTs, Weakly similar to A37232 mucin, tr	5.38	2.7
	427256	AL042436	Hs.97723	ESTs	4.08	2.7
	408407	AF214680	Hs.44685	C3HC4-like zinc finger protein	3.27	2.7
	403328			Target Exon	4.26	2.7
20	436264	AA707457	Hs.120014	ESTs	3.58	2.7
	427104	AA398187	Hs.104682	ESTs, Weakly similar to mitochondrial ci	3.68	2.7
	426640	AI200961	Hs.98104	ESTs	4.60	2.7
	428789	AW296167	Hs.91930	ESTs	4.23	2.7
25	435274	AA887547	Hs.150905	ESTs	4.25	2.7
	426612	AA922067	Hs.184185	ESTs	7.17	2.7
	435110	N42688	Hs.81001	F-box only protein 25	4.85	2.7
	433792	AA778661		ESTs	4.06	2.7
	423278	AL117627	Hs.126289	Homo sapiens mRNA; cDNA DKFZp434B115 (fr	3.04	2.7
30	427284	AA400298	Hs.144696	ESTs	5.81	2.6
	423375	Z94277	Hs.127689	type 1 protein phosphatase inhibitor	3.36	2.6
	422362	Z46967	Hs.115460	calicin	4.72	2.6
	439993	T18864	Hs.144924	serine/threonine protein kinase SSTK	5.03	2.6
	409364	AI480252	Hs.137368	ESTs	7.22	2.6
35	419224	NM_012189	Hs.314452	fibrousheathin II	13.86	2.6
	428915	AI041278	Hs.87908	Snf2-related CBP activator protein	4.73	2.6
	427181	AI183653	Hs.27888	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.21	2.6
	442122	AI932330		ESTs	3.07	2.6
	424812	AF059252	Hs.153299	DOM-3 (C. elegans) homolog Z	3.80	2.6
40	430956	AI183529	Hs.2706	glutathione peroxidase 4 (phospholipid h	3.19	2.6
	427234	AA399667	Hs.104675	ESTs	3.43	2.6
	423005	AL080148	Hs.123004	DKFZP434B204 protein	3.53	2.6
	428214	AA936282	Hs.120397	ESTs	4.14	2.6
	452613	AA461599	Hs.23459	ESTs	7.78	2.6
45	410380	AL133068	Hs.62880	novel protein similar to mouse MOV10	3.45	2.6
	452537	AW247390	Hs.77735	hypothetical protein FLJ11618	3.43	2.6
	401712			Target Exon	4.51	2.6
	429186	BE503443	Hs.112095	hypothetical protein DKFZp434F1819	5.90	2.6
	438124	AA778610	Hs.122045	ESTs	3.43	2.6
50	422937	U03270	Hs.122511	centrin, EF-hand protein, 1	3.60	2.6
	410279	BE271977	Hs.61809	hypothetical protein FLJ14117	4.36	2.6
	428625	W87565	Hs.18566	ESTs	5.29	2.6
	433439	AA431176	Hs.133230	ribosomal protein S15	3.50	2.5
	433760	AW592321		ESTs	3.26	2.5
55	431219	AI190773	Hs.127204	ESTs, Weakly similar to similar to CR16,	5.10	2.5
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	8.07	2.5
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.56	2.5
	445158	AI992108	Hs.127206	ESTs	3.60	2.5
	440860	R10482	Hs.132876	ESTs	4.26	2.5
60	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.95	2.5
	433281	N48673	Hs.146037	hypothetical protein DKFZp434C135	5.68	2.5
	429369	AI269514	Hs.129802	ESTs	3.49	2.5
	433949	AI674766	Hs.112877	ESTs	5.15	2.5
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	10.46	2.5
65	414708	AA393379	Hs.97415	ESTs, Weakly similar to T33068 hypothe	3.87	2.5
	408485	AW274294	Hs.144092	ESTs, Weakly similar to A Chain A, Sacch	6.10	2.4
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	5.64	2.4
	426956	AA393673		ESTs, Weakly similar to ALU5_HUMAN ALU S	4.68	2.4
	429152	AA447209	Hs.99099	Homo sapiens NYD-SP28 mRNA, complete cds	4.34	2.4
70	426247	U92992	Hs.98834	ESTs	5.40	2.4
	427589	T19219	Hs.97978	hypothetical protein MGC4766 similar to	3.40	2.4
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2 (testis)	5.85	2.4
	453353	U33055	Hs.32959	G protein-coupled receptor kinase 2 (Dro	4.82	2.4
	413372	H55532		tubulin, alpha 2	9.32	2.4
75	411737	AW160339	Hs.71791	hypothetical protein	5.26	2.4
	453868	NM_014433	Hs.35984	rhabdoid tumor deletion region protein 1	3.05	2.4
	427098	AA398161	Hs.97602	ESTs	3.21	2.4
	427165	AA429709	Hs.99336	ESTs, Weakly similar to T15446 hypothe	4.27	2.4
	425808	AA364109	Hs.177990	ESTs	7.80	2.4
80	444790	AB030506	Hs.11955	B9 protein	3.32	2.4
	426718	AA383555	Hs.126413	ESTs	4.20	2.4
	411441	AL042355	Hs.70202	WD repeat domain 10	6.14	2.4
	450852	AI983354	Hs.7740	oxysterol binding protein-like 1	4.97	2.3
	427054	AA421240	Hs.97570	ESTs	3.10	2.3

5	438633	AI653327	Hs.123501	ESTs	3.46	2.3
	427199	AW015836	Hs.292919	ESTs	4.31	2.3
	440182	AA868919	Hs.250110	ESTs	3.03	2.3
	435517	AA926626	Hs.130177	ESTs	3.64	2.3
	446309	BE044261	Hs.149774	ESTs	3.52	2.3
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	4.23	2.3
	433829	AI190715	Hs.102021	ESTs	6.08	2.3
	429485	AW197086	Hs.99338	ESTs	3.14	2.3
10	423058	AW964568	Hs.111591	ESTs	3.36	2.3
	433822	AI218609	Hs.112772	ESTs	3.83	2.3
	442268	BE278064	Hs.8179	hypothetical protein, clone 2746033	3.00	2.3
	434298	AA860090	Hs.116290	ESTs	3.71	2.3
	440720	AW662776	Hs.336943	Human DNA sequence from clone RP11-60H7	3.08	2.3
15	427554	AW246578	Hs.179615	hypothetical protein FLJ10058	3.39	2.3
	414251	AL042306	Hs.97689	VASA protein	11.25	2.3
	430254	AI809520		ESTs	3.27	2.3
	437418	AI478954	Hs.59459	ESTs	3.43	2.2
	437522	AA983844	Hs.121383	ESTs	4.15	2.2
20	422808	AA449014	Hs.121025	chromosome 11 open reading frame 5	3.09	2.2
	436695	AA725655	Hs.120480	ESTs	5.26	2.2
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	6.78	2.2
	421625	AA405386	Hs.178004	ESTs	3.22	2.2
	434807	AA364183	Hs.323443	hypothetical protein FLJ11806	5.51	2.2
25	428174	AA913321	Hs.126778	ESTs	3.09	2.2
	409735	AL035295	Hs.56175	H.sapiens gene from PAC 106H8, similar t	3.11	2.2
	444467	AI150368		ESTs	3.81	2.2
	433832	AA918018	Hs.172516	ESTs	6.94	2.2
	440036	AW593295	Hs.210956	ESTs	5.87	2.2
30	415240	AA161411	Hs.58668	chromosome 21 open reading frame 57	3.66	2.2
	432538	BE258332	Hs.278362	male-enhanced antigen	3.58	2.1
	440882	AI205777	Hs.129538	ESTs	3.83	2.1
	436605	AI187742		ESTs	3.41	2.1
	422990	AF035620	Hs.122764	BRCA1 associated protein	5.66	2.1
35	432174	AW590264	Hs.132806	ESTs	3.05	2.1
	409267	NM_012453	Hs.52515	transducin (beta)-like 2	5.46	2.1
	423021	AL036111	Hs.292767	ESTs	3.87	2.1
	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	5.25	2.1
	433812	AA725026	Hs.97165	ESTs, Weakly similar to T31611 hypotheti	3.62	2.1
40	456924	AI631510	Hs.196956	ESTs, Highly similar to match to EST AA3	4.38	2.1
	437249	AA432202	Hs.103147	hypothetical protein FLJ21347	3.38	2.1
	426038	AA368101	Hs.99052	ESTs	3.03	2.1
	427065	AA397903	Hs.236635	gb:z189f12.r1 Soares_testis_NHT Homo sap	3.23	2.1
	428824	W23624	Hs.173059	ESTs	3.07	2.1
45	428224	X54017	Hs.183088	acrosin	3.18	2.1
	436954	AA740151	Hs.130425	ESTs	3.20	2.1
	444470	AA412195	Hs.13740	ESTs	4.27	2.1
	457579	AB030816	Hs.36761	HRAS-like suppressor	5.30	2.1
	427886	AA417083	Hs.104789	ESTs	3.49	2.1
50	439273	AW139099	Hs.269701	ESTs	3.83	2.1
	434318	AW207552	Hs.116328	ESTs, Weakly similar to A39564 transcrip	4.01	2.1
	427015	AA397520		ESTs	4.28	2.1
	421598	AW630942	Hs.106061	RD RNA-binding protein	3.30	2.1
	427236	AA399859	Hs.148271	ESTs	3.07	2.1
55	434520	AA205273	Hs.177011	hypothetical protein	3.19	2.0
	456051	T85626	Hs.76239	hypothetical protein FLJ20608	3.11	2.0
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	8.41	2.0
	451807	W52854		hypothetical protein FLJ23293 similar to	3.52	2.0
	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	4.73	2.0
60	420484	W32963	Hs.98289	VRK3 for vaccinia related kinase 3	3.86	2.0
	414181	AK000476	Hs.75798	hypothetical protein	3.33	2.0
	424558	AF038847	Hs.150490	FK506-binding protein 6 (36kD)	7.70	2.0

TABLE 54B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

70	Pkey	CAT Number	Accession
	428618	2668_1	BC017998 BI826643 BG715794 BG722697 BI460787 BG773459 H52859 AI652853 AI990773 AW665193 AW340601 AA913806 AI337099 BE045942 AW572790 AW515652 H15004 AA909115 BI465310 BI462024 BI561578 BI463075 BG722527 R86003 BG623286 H15003 BI562131 BG435272
	426599	10110_1	BE736800 BM471423 AL557221 BG763302 BF742196 BF991016 BG200112 BF920027 BG576409 BG332214 BI830957 AI827504 AW183574 AI805171 AI126491 AA448257 AI090641 AW183329 AA994873 AI203663 BE041513 AA382260 AA382261 AL554887 BE273483
75	426930	1310779_1	AI809889 AA393442 AI150574 AI200886 AI221692 AA608977 AA813213
	434317	599587_1	AI209094 AI377740 AW117382 AW182289 AI674095 AW188019 AA897352 AA931314 AA923336 AW665317 AA629314 AA776691 AA906846 AA974625 AA884357 AI808590
	426620	142987_1	AL042392 AI147451 AA758821 AW450252 AA399310 AI656343 AI636668 AW515660 AI190733 AI025812 AA723645 AA709253 AA725709 AA398244 AA382463 AI139837
80	419350	13086_1	AI218809 BC014609 BG724383 AI024359 AA904573 AI138595 AA868685 AI768931 BI828436 BG717350 BG719800 AW182303 AA448181 BI826670 BI827131 BI830254 BI824155 BI831745 T19190 BI830415
	440822	532606_1	BG207562 BG192113 AA977616 AW274024 AI554897 AI221379 AA969158 AA906867 AI873494 AI015039
	421938	863689_1	AA412383 AA300675 BG773248 AA412243 AA405951

442589	33097_2	NM_004157 X14968 BG480488 BE409869 BG723898 BG476313 AU121626 BE386516 AI969297 AW172340 AA889668 R23436 AI015037 BE250558 BF590945 AW385993 BF983000 AA070235 AL556082 M78388 AW504473 AW370139 BG913697 BE899096 BG827945 BE741233 AI015465 AW370169 BE297350 AA093249 AI122828 AA909991 AA759233 AI591713 BF197609 AI985094 AW448916 AI243277 AL449630 AL449629 AW241405 AW205071 AI671586 AI652354 AI638465 AW590359 AW662771 AW594067 BE502532 AI218894 BE466416 BF056295 AI247366 AI990484 AI917746 AW665925 AI216456 AW182169 AA969884 AA723888 AI018419 BI602176 BI603138 BI459895 BI755030 AW418788 AA883999 AA724858 AI480311 AW196355 AI004813 AI651117 BE814363 AW589856 AA448124 AA447982 BI461166 AA405629 AI208966 AA421041 AA815377 AA411954 BF980396 R51074 BF979883 AI539370 BM128735 AA993397 AI611039 AW593985 R41808 AI208080 AA442862 AA429772 AI125404 AW593312 AI247364 AI208217 AA910021 AI915307 AI190292 AI188225 AA416673 AA416596 AA952898 AA972172 AA906874 MF6676 NM_022571 BG772522 BF516449 AI537485 AW517245 BF762536 AA634446 AW196331 AI203035 BG722281 AK056320 AL522040 BI793043 AW071691 AI433682 AA865414 AA702684 BI792794 H96879 R52351 AA211126 AA442875 N25725 AA482563 N33446 N25222 Z41110 N26507 N73447 N24077 N20492 AW275550 H99619 AL518306 AL522041 AW959849 AL518307 AA725907 AI655113 AI309906 F10184 BM451081 BE257595 BG721625 BI828509 BG700470 F12568 Z45396 BI829288 AA364618 AA364851 AA421448 T74231 R52350 AA482415 AI203021 T88948 AI565842 AI024286 AA769898 AA778661 AA868972 AA609524 AI932330 AI190707 AI376782 AA976847 AA609179 AW592321 AA758282 AI214437 AW072537 AA781937 BI831486 AW190479 AI472793 AA460217 AA459937 BF082576 AA393673 AA398702 NM_006001 L11645 AI205604 AI207994 AI187362 AA709190 BI462421 BG772170 BG771655 BI553260 BF126025 BF125857 BI462670 BG724164 BI562424 BG721652 BI559662 BG722455 BI596415 BG717561 BG722138 BG773507 BG720572 C03867 AI016802 AL042663 AA770436 AA435720 T19365 AA626698 AA759057 AI208021 BF507844 AI208058 AA412719 AA426374 AI208775 AA977217 AA758055 F34585 AA180062 BG700885 AA868017 AW341719 AA971332 AI688794 Z20462 AI808145 AW665263 AA884952 AA906136 AW663704 AI150368 AI216464 AI125340 AI125684 AI377949 AI126470 AI218351 AW665355 AI243952 AW663454 AI240603 AI187742 AA884214 AA723933 AA857437 AI968733 AI968938 AA992784 AA397520 AW235244 BM479185 AL552795 AL577722 BF038888 BM127617 BF510346 AW450652 AA865478 AW449519 BM127314 AI806539 AW449522 AA993634 AI827626 AA904788
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TABLE 54C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401979	2828778	Minus	75693-75851,76977-77112
406409	9256364	Minus	141101-141256
401741	2982169	Plus	196686-196823,200241-200381
406378	9256142	Minus	126408-126800
405264	7329374	Plus	28556-28684
401692	3540172	Plus	26365-26510
403783	8081824	Plus	128412-128635
404271	9828129	Minus	56392-57645
401798	6730720	Plus	22831-23448
402857	9801539	Plus	13402-14133
405528	9581957	Minus	22418-22687
403328	8469086	Minus	120428-120703
401712	6682593	Minus	76410-76527,76692-76829,78737-78866,8024

TABLE 55A:

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigenelD:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues

Pkey	ExAccn	UnigenelD	Unigene Title	R1
416680	AW245540	Hs.79516	brain abundant, membrane attached signal	48.80
423961	D13666	Hs.136348	periostin(OSF-2os)	43.30
412948	BE243313	Hs.334851	LIM and SH3 protein 1	42.50
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	36.80
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	29.80
414438	AI879277	Hs.76136	thioredoxin	29.40
406658	AI920965	Hs.77961	major histocompatibility complex, class	29.25
446899	NM_005397	Hs.16426	podocalyxin-like	28.70
411573	AB029000	Hs.70823	KIAA1077 protein	28.40
432730	AI066520	Hs.131358	ESTs	28.00
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	28.00
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	27.90
446619	AJ076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	26.80
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	25.00
418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	24.15

	406856	AW515336	Hs.29797	ribosomal protein L10	23.66
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	23.60
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (ig),	23.60
5	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	22.35
	417426	NM_002291	Hs.82124	laminin, beta 1	21.60
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	21.55
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	21.50
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	21.50
10	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	20.90
	412636	NM_004415		desmoplakin (DPI, DP11)	20.90
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	20.30
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	19.45
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	19.30
15	406648	AA563730	Hs.277477	major histocompatibility complex, class	19.10
	412247	AF022375	Hs.73793	vascular endothelial growth factor	17.45
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	17.40
	424800	AL035588	Hs.153203	MyoD family inhibitor	17.20
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	16.90
20	415314	N88802	Hs.5422	glycoprotein M6B	16.80
	406656	M16714	Hs.89643	major histocompatibility complex, class	16.75
	426295	AW367283		zinc finger protein 6 (CMPX1)	16.25
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	16.00
25	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	15.85
	417088	M54915	Hs.81170	p1m-1 oncogene	15.60
	449338	H73444	Hs.394	adrenomedullin	15.51
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	15.33
	414420	AA043424	Hs.76095	immediate early response 3	15.30
	425543	R23313	Hs.334895	ribosomal protein L10a	15.10
30	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	15.00
	420754	W79431	Hs.346911	ribosomal protein L22	14.92
	410397	AF217517	Hs.63042	DKFZp564J157 protein	14.86
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	14.70
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	14.60
35	406786	AW161678	Hs.111334	ferritin, light polypeptide	14.57
	422105	AI929700	Hs.111680	endosulfine alpha	14.57
	422714	AB018335	Hs.119387	KIAA0792 gene product	14.25
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.05
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.00
40	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	14.00
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	13.95
	410185	BE294068	Hs.737	immediate early protein	13.85
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	13.60
	410611	AW954134	Hs.20924	KIAA1628 protein	13.60
45	448588	AI970276	Hs.156905	KIAA1676	13.40
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	13.10
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.00
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	13.00
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	13.00
50	454413	AI653672	Hs.40092	PNAS-123	12.90
	415221	W07418	Hs.78225	annexin A1	12.89
	425535	AB007937	Hs.158287	KIAA0468 gene product	12.48
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	12.45
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.40
55	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	12.19
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	12.12
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	12.07
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	11.90
	408437	AW957744	Hs.278469	lacrimal proline rich protein	11.80
60	430542	AI557486	Hs.119122	ribosomal protein L13a	11.51
	424670	W61215	Hs.116651	epithelial V-like antigen 1	11.50
	432409	AA806538	Hs.130732	KIAA1575 protein	11.50
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	11.44
	425996	W67330		hypothetical protein AL110115	11.40
65	449961	AW265634	Hs.133100	ESTs	11.40
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	11.25
	407179	AA206465		thymosin, beta 4, X chromosome	11.21
	412623	R28898	Hs.74170	metallothionein 1E (functional)	11.10
	429978	AA249027		ribosomal protein S6	11.10
70	450377	AB033091		KIAA1265 protein	11.10
	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	11.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	11.00
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	11.00
	451106	BE382701	Hs.25960	N-MYC oncogene	10.93
75	426552	BE297660	Hs.170328	moesin	10.91
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	10.90
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	10.80
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	10.80
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rhotekin, clone	10.75
80	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.70
	435056	AW023337	Hs.5422	glycoprotein M6B	10.70
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	10.70
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	10.65
	420676	AI434780	Hs.4248	vav 2 oncogene	10.60

	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	10.60
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	10.50
	436075	BE090176	Hs.179902	transporter-like protein	10.30
5	450139	AK001838		serum/glucocorticoid regulated kinase	10.30
	427691	AW194426	Hs.20726	ESTs	10.26
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	10.15
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	10.10
	440528	BE313555	Hs.7252	KIAA1224 protein	10.06
10	423184	NM_004428	Hs.1624	ephrin-A1	10.05
	450847	NM_003155	Hs.25590	stanniocalcin 1	9.90
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.90
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), miloc	9.90
	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	9.89
15	435918	AF263538	Hs.86232	growth differentiation factor 3	9.89
	411251	R19774	Hs.22835	HHGP protein	9.80
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	9.75
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	9.75
	425580	L11144	Hs.1907	galanin	9.60
20	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	9.60
	413813	M96956	Hs.75561	lateral carcinoma-derived growth factor 1	9.60
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.60
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	9.53
	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	9.51
25	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	9.42
	416926	H03109	Hs.263395	HT018 protein	9.41
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	9.40
	428065	AI634046	Hs.157313	ESTs	9.40
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	9.39
30	410325	AB023154	Hs.62264	KIAA0937 protein	9.30
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.30
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	9.29
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	9.24
	447211	AL161961	Hs.17767	KIAA1554 protein	9.22
35	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	9.20
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	8.93
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	8.90
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.90
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	8.90
40	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.84
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	8.80
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	8.70
	426215	AW963419	Hs.155223	stanniocalcin 2	8.70
	446627	AI973016	Hs.15725	hypothetical protein SBB148	8.60
45	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	8.60
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	8.50
	445245	AB032973	Hs.12461	LCHN protein	8.50
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.40
50	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	8.35
	410143	AA188169		KIAA1191 protein	8.35
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.30
	433208	AW002834	Hs.24095	ESTs	8.30
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.25
55	432559	AW452948	Hs.257631	ESTs	8.20
	450581	AF081513	Hs.25195	TGF-beta 4	8.10
	450157	AW961576	Hs.60178	ESTs	8.10
	444795	AI193356	Hs.160316	ESTs	8.10
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	8.05
60	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	8.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	8.00
	419970	AW612022		ESTs	8.00
	411975	AI916058	Hs.144583	ESTs	7.95
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	7.90
65	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	437103	AW139408	Hs.152940	ESTs	7.90
	432636	AA340864	Hs.278562	claudin 7	7.87
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	7.84
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	7.80
70	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.80
	450147	AW373713	Hs.146324	CGI-145 protein	7.75
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.70
	449571	AW016812	Hs.200266	ESTs	7.70
	429355	AW973253	Hs.292689	ESTs	7.70
75	446488	AB037782	Hs.15119	KIAA1361 protein	7.70
	414774	X02419	Hs.77274	plasminogen activator, urokinase	7.69
	422424	AI186431	Hs.296638	prostate differentiation factor	7.67
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	7.65
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	7.65
	451812	X81889	Hs.152151	plekophilin 4	7.65
80	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	7.60
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	7.60
	422746	NM_004484	Hs.119651	glypican 3	7.60
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	7.57

5	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.57
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	7.55
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	7.53
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	7.50
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	7.50
10	419223	X60111	Hs.1244	CD9 antigen (p24)	7.47
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.44
	401466			vesicle-associated membrane protein 4	7.43
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	7.40
	413686	AI469213	Hs.71404	ESTs	7.40
15	408605	AF025374	Hs.46465	T-cell, immune regulator 1	7.40
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.30
	444838	AV651680	Hs.208558	ESTs	7.30
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	7.28
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	7.20
20	452924	AW580939	Hs.97199	complement component C1q receptor	7.15
	436398	H87136	Hs.5174	ribosomal protein S17	7.15
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.10
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.10
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	7.10
25	401192			Target Exon	7.08
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	7.08
	402474			NM_004079: Homo sapiens cathepsin S (CTSS	7.00
	449567	AI990790	Hs.188614	ESTs	7.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to t38022 hypot	7.00
30	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	7.00
	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor Nb:HOT H	7.00
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	6.90
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	6.87
	442492	AA528489	Hs.234518	ribosomal protein L23	6.84
35	417365	D50683	Hs.82028	transforming growth factor, beta recepto	6.80
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-in	6.80
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	6.80
	435684	NM_001290	Hs.4980	LIM domain binding 2	6.80
	442685	AB033017	Hs.8594	KIAA1191 protein	6.79
40	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	6.77
	411789	AF245505	Hs.72157	Adiccan	6.76
	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	6.75
	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	6.74
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.72
45	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	6.70
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytolaclin)	6.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.70
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	6.70
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	6.70
50	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	6.70
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	6.66
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	6.65
	406858	AI865720	Hs.29797	ribosomal protein L10	6.65
	435748	AA699756	Hs.117335	ESTs	6.63
55	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	6.62
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	6.62
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.61
	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.60
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	6.55
60	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	6.50
	450294	H42587	Hs.238730	hypothetical protein MGC10823	6.45
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	6.45
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	6.43
	402145			Target Exon	6.43
65	414662	AL036058	Hs.76807	major histocompatibility complex, class	6.42
	436860	H12751	Hs.5327	PRO1914 protein	6.40
	438962	BE046594		gb:hn41c11.x1 NCL_CGAP_RDF2 Homo sapiens	6.40
	435937	AA830893	Hs.119769	ESTs	6.40
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	6.40
70	446173	BE565849	Hs.14158	copine III	6.39
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	6.36
	412093	BE242691	Hs.14947	ESTs	6.34
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.30
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.30
75	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.30
	447519	U46258	Hs.339665	ESTs	6.30
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	6.30
	434423	NM_006769	Hs.3844	LIM domain only 4	6.30
	434524	AA635931	Hs.249716	ESTs	6.30
80	441970	AW959918	Hs.73737	ESTs	6.30
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	6.30
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	6.25
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	6.23
	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.20
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.20
	447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f	6.20
	417315	AI080042	Hs.180450	ribosomal protein S24	6.20

	418840	AI821614	Hs.185831	ESTs	6.20
	410668	BE379794	Hs.159651	hypothetical protein	6.16
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.13
5	413840	AI301558		RNA binding motif protein, X chromosome	6.13
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	6.12
	450944	AA554989		sudD (suppressor of bimD6, Aspergillus n	6.10
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	6.10
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.10
10	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	6.10
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.10
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	6.10
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.09
	435812	AA700439	Hs.188490	ESTs	6.06
	432805	X94630	Hs.3107	CD97 antigen	6.06
15	441283	AA927670	Hs.131704	ESTs	6.06
	417632	R20855	Hs.5422	glycoprotein M6B	6.00
	435905	AW997484	Hs.5003	KIAA0456 protein	6.00
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	5.99
20	429083	Y09397	Hs.227817	BCL2-related protein A1	5.95
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	5.95
	425291	AA354572		gb:EST62857 Jurkat T-cells V Homo sapien	5.95
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	5.93
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	5.90
25	447217	BE465754	Hs.17778	neuropilin 2	5.90
	417228	AL134324	Hs.7312	ESTs	5.86
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.86
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.84
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.84
30	414483	R25513	Hs.10683	ESTs	5.82
	428570	AA430321	Hs.293945	ESTs	5.81
	443194	AI954968		matrix Gla protein	5.80
	429582	AI569068	Hs.22247	ESTs	5.80
	414405	AI362533		KIAA0306 protein	5.80
35	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	5.80
	437739	AW579216	Hs.264610	ESTs, Moderately similar to lbd1 [H.sapi	5.80
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	5.80
	442821	BE391929	Hs.8752	transmembrane protein 4	5.77
	434511	R28982	Hs.18106	ESTs	5.76
40	406745	AW511970	Hs.279860	tumor protein, translationally-controlle	5.70
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	5.70
	453115	AW772041	Hs.18439	ESTs, Moderately similar to JC5238 galac	5.70
	406857	AA613726	Hs.29797	ribosomal protein L10	5.69
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	5.68
45	444273	AI903474	Hs.230	fibromodulin	5.65
	441623	AA315805		desmoglein 2	5.63
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	5.63
	440099	AL080058	Hs.6909	DKFZP564G202 protein	5.60
50	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	5.60
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associated	5.60
	422610	AF153820	Hs.1547	potassium inwardly-rectifying channel, s	5.60
	438278	BE409248	Hs.57988	hypothetical protein FLJ22357 similar to	5.58
	430451	AA836472	Hs.297939	cathepsin B	5.57
	406699	L06505	Hs.182979	ribosomal protein L12	5.53
55	458965	AA010319	Hs.60389	ESTs	5.50
	430592	AJ224864	Hs.9688	leukocyte membrane antigen(IRC1)	5.50
	433655	AL036559	Hs.3463	ribosomal protein S23	5.50
	428471	X57348	Hs.184510	stratifin	5.42
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	5.40
60	417849	AW291587	Hs.82733	nidogen 2	5.40
	408989	AW361666	Hs.49500	KIAA0746 protein	5.40
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	5.40
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	5.40
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	5.40
65	406819	AA908472		gb:og82a10.s1 NCL_CGAP_Ov8 Homo sapiens	5.39
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.36
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.34
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.34
	427968	AI857607	Hs.181301	cathepsin S	5.32
70	429307	AU076592	Hs.198951	jun B proto-oncogene	5.30
	424950	AA602917	Hs.156974	ESTs	5.30
	410619	BE512730	Hs.65114	keratin 18	5.30
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.27
	425430	BE185921	Hs.98073	ESTs, Moderately similar to Z195_HUMAN Z	5.27
75	411165	NM_000169	Hs.69089	galactosidase, alpha	5.26
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	5.26
	435631	BE254086	Hs.29647	uncharacterized hematopoietic stem/proge	5.24
	418905	BE539674		actinin, alpha 4	5.23
	449303	AK001495	Hs.23467	hypothetical protein FLJ10633	5.22
80	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	5.20
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	5.20
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	5.20
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	5.20

	409604	AW444448	Hs.49124	ESTs	5.20
	432581	AU076465	Hs.278441	KIAA0015 gene product	5.16
	430556	AW967807	Hs.13797	ESTs	5.16
5	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5.16
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subunit	5.15
	454227	AW963897	Hs.44743	KIAA1435 protein	5.15
	429367	AB007867	Hs.278311	plexin B1	5.12
	452191	AU076408	Hs.28309	UDP-glucose dehydrogenase	5.11
10	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis, clone NT	5.11
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	5.10
	443030	R68048	Hs.9238	hypothetical protein FLJ23516	5.10
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	5.10
	424875	AI187945	Hs.199310	ESTs	5.10
15	427641	AI270591	Hs.146116	ESTs	5.10
	442806	AW294522	Hs.149991	ESTs	5.10
	442495	AI184717		ESTs	5.10
	439941	AI392640	Hs.18272	amino acid transporter system A1	5.10
	444981	AW855398	Hs.12210	hypothetical protein FLJ13732 similar to	5.09
20	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.07
	418117	AI922013	Hs.83496	linker for activation of T cells	5.06
	431824	AW972842		gb:EST384937 MAGE resequences, MAGL Homo	5.06
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	5.06
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	5.03
25	431805	NM_014053	Hs.270594	FLVCR protein	5.00
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	5.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	5.00
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	5.00
	443634	H73972	Hs.134460	ESTs	5.00
30	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	5.00
	444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathi	4.97
	422200	AA080895	Hs.347969	cytochrome c oxidase subunit IV	4.95
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	4.94
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	4.94
35	452063	R53185	Hs.32366	ESTs, Weakly similar to TWST_HUMAN TWIST	4.93
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.93
	429558	AI391454	Hs.207251	nucleolar autoantigen (55kD) similar to	4.92
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	4.92
	433162	AI025842		ESTs	4.92
40	406797	AI432224		ribosomal protein L6	4.91
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	4.90
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	4.90
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	4.90
	447832	AI433357		ESTs	4.90
45	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697 hypotheti	4.90
	413593	AA205248		gb:zq78c12.r1 Stratagene hNT neuron (937	4.90
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	4.90
	441224	AU076964	Hs.7753	calumenin	4.90
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	4.90
50	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.90
	417308	H60720	Hs.81892	KIAA0101 gene product	4.90
	438763	AI583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	4.89
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.89
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	4.88
55	421748	NM_014718	Hs.107809	KIAA0726 gene product	4.87
	427486	AA974433		fibroblast growth factor 4 (heparin secr	4.86
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	4.82
	406867	AA157857	Hs.182265	keratin 19	4.81
	449378	AW664026	Hs.59892	ESTs	4.81
60	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	4.80
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	4.80
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.80
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	4.79
65	441321	H17182	Hs.7771	B-cell associated protein	4.75
	448896	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr	4.75
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	4.73
	449317	AW293413	Hs.132906	19A24 protein	4.73
	436372	AW972301	Hs.310286	ESTs	4.71
70	422082	AA016188	Hs.111244	hypothetical protein	4.70
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	4.70
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	4.70
	446659	AI335361	Hs.226376	ESTs	4.70
	414829	AA321568	Hs.77436	pleckstrin	4.70
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	4.70
75	417677	NM_016055	Hs.82389	CGI-118 protein	4.70
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.70
	423766	AA303799	Hs.300141	ribosomal protein L39	4.70
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	4.69
80	453485	BE620712	Hs.33026	hypothetical protein PP2447	4.67
	452973	H88409	Hs.40527	ESTs	4.67
	427816	AA159248	Hs.180909	peroxiredoxin 1	4.67
	406794	AI890243		ribosomal protein L6	4.66
	449475	AI348027	Hs.108557	hypothetical protein PP1057	4.65

	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.64
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	4.62
	407874	AI766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	4.61
	417535	AA203569	Hs.191482	ESTs	4.61
5	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	4.61
	408491	AI088063	Hs.7882	ESTs	4.60
	428398	AI249368	Hs.98558	ESTs	4.60
	410295	AA741357		nidogen (enactin)	4.60
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	4.60
10	440327	R12581	Hs.191146	ESTs	4.60
	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.60
	426141	C05886	Hs.293972	ESTs	4.60
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	4.59
15	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.58
	416987	D86957	Hs.80712	KIAA0202 protein	4.57
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.57
	416581	H66276	Hs.108288	ESTs	4.56
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	4.56
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	4.56
20	413663	BE247585	Hs.75462	BTG family, member 2	4.55
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, rec	4.54
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	4.53
	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	4.52
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	4.51
25	440774	AI420611	Hs.153934	ESTs	4.51
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	4.51
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	4.51
	449267	AI638640	Hs.220624	ESTs	4.51
30	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.50
	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	4.50
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypothe	4.50
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	4.50
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	4.50
35	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	406623	X69392	Hs.91379	ribosomal protein L26	4.49
	456642	AW451623	Hs.109752	putative c-Myc-responsive	4.47
	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.47
	408307	AI761786	Hs.204674	ESTs	4.46
	428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito	4.46
40	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.45
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	4.45
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	4.45
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.44
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	4.44
45	428773	BE256238	Hs.193163	bridging integrator 1	4.43
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	4.43
	437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	4.43
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	4.43
50	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	4.42
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	4.41
	424868	AI568170	Hs.96886	ESTs	4.41
	408380	AF123050	Hs.44532	diubiquitin	4.40
	411960	R77776	Hs.18103	ESTs	4.40
55	428782	X12830	Hs.193400	interleukin 6 receptor	4.40
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	4.40
	456629	AW891965		histone deacetylase 3	4.40
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	4.40
	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypothe	4.39
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	4.39
60	427779	AA906997	Hs.180780	TERA protein	4.38
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.37
	413276	Z24725	Hs.75260	mitogen inducible 2	4.36
	452651	AI218918	Hs.30209	KIAA0854 protein	4.35
65	453467	AI535997	Hs.30089	ESTs	4.35
	435961	BE293127	Hs.283722	GTT1 protein	4.35
	415691	AW963979	Hs.24723	ESTs	4.34
	435968	AW161481	Hs.111577	integral membrane protein 3	4.34
	420099	D80011	Hs.95140	KIAA0189 gene product	4.33
70	421522	R48881	Hs.102991	hypothetical protein FLJ13956	4.33
	457073	AA233210	Hs.179943	ribosomal protein L11	4.31
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.31
	420732	AA789133	Hs.63525	ESTs	4.30
	432731	R31178	Hs.287820	fibronectin 1	4.30
75	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.30
	408784	AW971350	Hs.63386	ESTs	4.30
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	4.30
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.30
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	4.30
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.30
80	413677	AW503116	Hs.301819	zinc finger protein 146	4.29
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.28
	408896	AI610447	Hs.48778	niban protein	4.26
	433550	AA989061	Hs.177376	ESTs	4.26

	406230		Target Exon	4.25
	435655	AW105663	Hs.6947 HSPC069 protein	4.25
	448717	R67419	Hs.21851 Homo sapiens cDNA FLJ12900 fis, clone NT	4.24
5	437386	W52452	ribosomal protein L10	4.24
	416759	AK000978	Hs.79741 hypothetical protein FLJ10116	4.23
	447341	AF106941	Hs.18142 arrestin, beta 2	4.22
	410423	AW402432	Hs.63489 protein tyrosine phosphatase, non-recept	4.22
	409453	AI885516	Hs.95612 ESTs	4.22
10	428453	AB011110	Hs.184367 GTPase activating protein-like	4.22
	444681	AJ243937	Hs.288316 chromosome 6 open reading frame 9	4.21
	416072	AL110370	Hs.79000 growth associated protein 43	4.20
	450937	R49131	Hs.26267 ATP-dependant interferon response protei	4.20
	447595	AW379130	Hs.18953 phosphodiesterase 9A	4.20
15	418452	BE379749	Hs.85201 C-type (calcium dependent, carbohydrate-	4.20
	430594	AK000790	Hs.246885 hypothetical protein FLJ20783	4.20
	425259	AL049280	Hs.155397 Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.20
	431560	BE244135	Hs.260238 hypothetical protein FLJ10842	4.20
20	439403	BE265745	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.20
	409245	AA361037	IRNA isopentenylpyrophosphate transferas	4.18
	437296	AA350994	Hs.20281 KIAA1700	4.17
	406877	AA226392	Hs.179943 ribosomal protein L11	4.17
	419652	AL157485	Hs.91973 hypothetical protein	4.15
	406661	X66975	Hs.172550 polypyrimidine tract binding protein (ha	4.15
25	452432	AW206008	Hs.283378 Homo sapiens cDNA: FLJ21778 fis, clone H	4.14
	448782	AL050295	KIAA0758 protein	4.14
	407110	AA018042	Hs.252085 Prader-Willi/Angelman syndrome-5	4.14
	422960	AW890487	cadherin 13, H-cadherin (heart)	4.13
30	432841	M93425	Hs.62 protein tyrosine phosphatase, non-recept	4.12
	415857	AA866115	Hs.127797 Homo sapiens cDNA FLJ11381 fis, clone HE	4.11
	420298	AI199510	Hs.267912 ESTs, Weakly similar to ALU7_HUMAN ALU S	4.11
	419726	U50330	Hs.1274 bone morphogenetic protein 1	4.11
	426075	AW513691	Hs.270149 ESTs, Weakly similar to 2109260A B cell	4.10
	430255	AK000703	Hs.323822 Homo sapiens mRNA for KIAA1551 protein,	4.10
35	418699	BE539639	Hs.173030 ESTs, Weakly similar to ALU8_HUMAN ALU S	4.10
	443035	Z45822	Hs.8906 Homo sapiens clone 24889 mRNA sequence	4.10
	457415	AK000010	Hs.258798 hypothetical protein FLJ20003	4.10
	412220	BE350058	Hs.36787 chromodomain helicase DNA binding protei	4.10
	427509	M62505	Hs.2161 complement component 5 receptor 1 (C5a l	4.10
40	444633	AF111713	Hs.286218 junctional adhesion molecule 1	4.10
	441384	AA447849	Hs.288660 Homo sapiens cDNA: FLJ22182 fis, clone H	4.09
	431958	X63629	Hs.2877 cadherin 3, type 1, P-cadherin (placenta	4.09
	422310	AA316622	Hs.98370 cytochrome P450, subfamily IIS, polypept	4.08
	439815	AA206079	Hs.6693 hypothetical protein FLJ20420	4.07
45	417930	H81136	Hs.334604 Homo sapiens mRNA for KIAA1870 protein,	4.06
	418458	AA332941	Hs.85226 lipase A, lysosomal acid, cholesterol es	4.06
	424464	R68537	Hs.17962 ESTs	4.06
	417035	AA192455	Hs.22968 Homo sapiens clone IMAGE:451939, mRNA se	4.06
	412627	BE391959	Hs.74276 chloride intracellular channel 1	4.06
50	414890	BE281095	Hs.77573 uridine phosphorylase	4.05
	452248	AA093668	Hs.28578 muscleblind (Drosophila)-like	4.05
	450887	AA011518	Hs.271778 ESTs, Weakly similar to I38022 hypotheti	4.05
	444224	AV648599	Hs.199438 ESTs	4.05
	451351	AW058261	Hs.321435 ESTs, Weakly similar to ALU1_HUMAN ALU S	4.04
55	407792	AI077715	Hs.39384 putative secreted ligand homologous to f	4.04
	439864	AI720078	Hs.291997 ESTs, Weakly similar to A47582 B-cell gr	4.04
	408745	AW936356	Hs.300925 ESTs, Weakly similar to A46010 X-linked	4.03
	409132	AJ224538	Hs.50732 protein kinase, AMP-activated, beta 2 no	4.01
	410597	W16518	Hs.279518 amyloid beta (A4) precursor-like protein	4.01
60	409485	S80990	Hs.252136 ficolin (collagen/fibrinogen domain-cont	4.01
	426398	BE256390	Hs.169718 calponin 2	4.01
	417777	AI823763	Hs.7055 ESTs, Weakly similar to I78885 serine/th	4.01
	446979	AI654443	Hs.197683 ESTs	4.00
	416000	R82342	Hs.79856 ESTs, Weakly similar to S65657 alpha-1C-	4.00
65	426647	AA243464	Hs.294101 pre-B-cell leukemia transcription factor	4.00
	436394	AA531187	Hs.126705 ESTs	4.00
	409956	AW103364	Hs.727 inhibin, beta A (activin A, activin AB a	4.00
	414602	AW630088	Hs.76550 Homo sapiens mRNA; cDNA DKFZp564B1264 (f	4.00
	446013	AI360167	Hs.152774 ESTs	4.00
70	452404	AW450675	Hs.212709 ESTs	4.00
	444736	AA533491	Hs.23317 hypothetical protein FLJ14681	4.00
	438590	AA811465	Hs.123375 ESTs	4.00
	451838	AW005866	Hs.193969 ESTs	4.00
	449832	AA694264	Hs.60049 ESTs	4.00

TABLE 55B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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413787	7612_1	BC003047 S80794 NM_003405 X78138 AY007132 L08439 AW340648 AW131665 AI082748 AI470204 BI711078 BF350700 BI496963 AI087141 AA720684 AA862331 AA605146 BM313650 AI089749 AI359738 N69107 AW995424 AI086917 AI083995 AW340217 N99662 AI829449 AI089839 AI608761 AI342365 AI199076 AA908944 AI248943 AU160053 AI191245 AI218477 AI077943 AA864930 AI310394 AA872478 AI279782 W61343 AA565955 W46596 AA126874 AA223241 AA491574 R84813 AA491520 BG055114 AI469689 BE464590 AW664539 H67097 AL534332 C21397 AI085941 AW028427 BG939820 AI697089 AI039008 AI125315 AI655561 AW150042 L20422 X57345 BI458375 AU142852 BI666601 BE888276 AU119302 BI603754 BG705953 BI598754 BE296713 BG002538 BF951911 N29226 BE909424 AV698274 AV683116 AV708195 AA127798 AI124697 D54224 F08031 AA340253 BF923383 BM467808 BI546644 BG777200 BG705941 BG468577 AU127209 AW403970 BI597630 BI458091 AV689560 BI669267 BG506219 BI837163 BI667275 AA343750 BE783112 BF671405 BF954720 H67636 H69456 AA484894 BI869271 BF998207 N31547 BF945817 BF947918 N90630 BG980194 AA156681 BI493502 AW273118 AI473820 AA608688 AI359337 AV712091 AA084101 BF592036 H13301 AI864305 AA505883 AI423963 AW084401 AI917740 R69858 AA033631 N79982 BE885276 AI635674 AA096126 AA700018 AV707753 AI082545 AU145681 AA629032 AI421367 AA740589 AA150830 AI248541 AA988608 AA150478 W65437 BM310234 AA262704 T28031 AI811116 BM272753 H21979 T15405 AA938406 F04963 AI188296 AW152629 AA905196 BG223058 AI831016 AI766457 AI811102 AA776573 AI922133 AI775958 AI261476 AA219489 AI688035 AI872093 BE537084 AW189078 D82630 AI123121 AL583492 BE350791 R69901 W65436 BE155392 BI089081 BE155394 AL120538 AW166100 AI359620 AI174338 N20527 W47413 AA155615 AI272249 H25293 BE614558 H69864 AW383484 H78021 H11617 R56892 H23204 N21530 R82499 AW383522 AA774536 AL534331 W94127 W46459 AI866231 AA513281 AA192465 H69844 W85827 AW383642 AW383529 AA171496 AI537424 BE814866 BF823254 R25553 AI080917 AI559406 M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW3730827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI647252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AU149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 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W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365155 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 BE880923 BG390191 AW470082 AW014585 AI423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI422030 AI348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI215830 AI283836 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085545 BE551404 AA4780704 AW008596 AI796964 AA917471 AI400531 AA668626 N72207 AI306482 AW440562 AI084687 AA347280 AA063536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI916336 AI350590 BF198106 AI433377 AI300638 AI672626 AI282741 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	430068	1177709_2	AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843
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			BF668788 BE083134 AW631281 BG193052 BG183095 BE440088 BG185728 AI499579 AA188162 AA864282 BI493352 AA155854 AA836749
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			AI088473 AA916151 AW473324 BG901177 BE439998 AW023269 BE813871 AW999947 BE839108 AV707983 AA369722 AW796627 AW890608
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	418905	517_1	AA908472
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	431824	1237125_1	AW972842 AA516061 AA630205
	433162	2167905_1	AI742311 AI025842 AA578843
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	447197	2176805_1	R36075 R36167 AI366546
	447832	1036795_1	AI628543 AI433357 AW772732
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	406794	0_0	AI890243
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413703 376077_1
406870 0_0
456629 207_22

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437386 5541_2

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439403 4937_10
409245 3199_2

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448782 34980_1

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422960 11862_2

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TABLE 55C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

65

Pkey	Ref	Strand	Nt_position
401466	6682292	Plus	28748-29023
401192	9719502	Minus	69559-70101
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402145	8018280	Plus	113086-114800
406230	4760409	Plus	71716-72515

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TABLE 56A:

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of seminomatous testicular cancer compared to normal adult testicular tissues

80

Pkey	ExAccn	UnigenelD	Unigene Title	R1
414438	AI879277	Hs.76136	thioredoxin	47.30

AI336371 AI989381 AI131425 AI147483 AI311537 AW338638 AI141649 AA709414 AI187177 AA780884 AI333805 AA045312 AI623918 AI349421
W63753 W70299 AA557276 AA299007 N98212 W74064 N24823 T54892 AA054724 W73059 AI869152 N93462 N71889 AI573432 R71628
AA303089 AI498550 T60941 AV706417 AW067848 AI150677 AW338118 AI336313 AA826256 AI139518 AA662948 AA902723 AI970175 W68682
AI089380 AI148372 H99951 AW183001 AI270317 AA532767 AA044727 AA931652 R82469 AA150261 W67788 H67495 R80715 AW149812 N78914
AI862034 W61122 AW023118 W69375 T88917 T47984 N21531 R35646 AA055544 H15534 AA688295 AA090586 AA044764 BF994641 R79547
N21313 BF674610 H02874 AW975323 R16904 AA328030 AA054671 R79546 BF832310 AI249109
BG015794 BE158357 BE158353 BE158358 BE158362 BE158351 BE158355
AA075144
AW891965 AW604749 BE080872 R15559 BE177623 AW883520 AW945343 AI246167 T07082 AW805679 W96278 AA135796 W32615 AW995418
AW801688 BE003837 AW801621 AW385721 AW385742 AW385714 AW604757 W87409 AW604738 AW385757 AW580796 AW801247 BE003239
BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW362791 AW604759 AW866589 AW604758 N44337 AI378548
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AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE067470 AW894935 BE082529 AI248811 BE179917 BE002200
AW607506 AW392889 AW894560 AW381360 AI904206 AW863533 C00609 AW381372 BE082530 AW898120 BE075323 AW392799 AW601420
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AW610318 AW996909 AW610296 AW901923 AW880003 AI762171 AW062582 AW368713 AW062593 AW176663 AW842064 AW842089
AW842095 AI243049 AW902074 AW062592 AW176664 AW751692 BE087703 AI907439 BE009686 BE172115 BE077030 AW608556 AW835577
AI909628 BE077029 AW176241 BE077552 BE160370 BE160288 AW835656 AW606765 AW606770 AW835678 AW606758 AW606778 AI907484
BE172821 AW606768 AW999517 AW844165 BE171738 AW751683 AW610493 BE177484 BE177487 AA090510 AW841117 BE173367 AW999878
AI124870 BE163472 AW841823 AW379762 AW893297 AI290296 BE089132 AA610287 AW176676 AW607622 BE172639 AW893232 AA329629
BE089008 BE178350 BE178214 BE063291 AW820236 AW999653 BE089486 BE173126 BE171775 BE185787 AA558280 AI174840 AW999912
BE218391 BE172734 BE178021 BE172738 BE173324 AW603494 AL036722 R38192 R60905 H53721 H41052 AL037917 R37795 AW998972
AA767189 AW044272 H50689 AA768399 AA767764 AI087888 H44202 BE222792 N90597 W81396 N90615 AI935353 BE501168 F10945
AW118215 AI970480 AI627641 AW236081 AA574090 AI627652 AI681913 AI759983 N69591 N69276 BE467722 AW392780 BE172467 H92861
AI524921 F02989 Z39328 F02705 F01414 T88678 AI215165 H87220 AW374781
BM476605 BI545004 BI834636 BG112453 BI199049 BG112759 AA149846 H97925 AA306121 AA313204 W52451 AI734997 AA931168 AA429766
N47913 AA584321 BF940241 AI083648 AI089410 AI347705 AI343661 AI186232 AI889031 N98464 AI820039 AI459034 AV652512 AA622990
BE857200 AA932998 AA740573 AI826264 AA865683 AI344550 AI027349 AI056087 AA442777 AA603724 AA873347 AI056717 AI092185 AI032895
AA535689 BF806025 BF806061 BF805985 BF746099 BF746097 AI309259 AI597603 BF806066 AI090653 AI129205 AI248410 H72993 AW615341
BF805990 BF805982 AA993819 T34373 T35604 H56242 AA648145 T35907 BF808691 N94015 AV703438 BG774276 H82341 R76371
AK056692 AF086220 AI375066 AA284293 W32566 AW797961 AA960897 AA504145
AF030234 BC017465 BG008526 AW505550 BM450141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857
AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R66856 H01374 BI257369 BI259830
AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024
BF093291 AW021929 H22650 AA459715 BG496341 BE697763 BI254209 BG499543 H42946 BI059780 BI086741 H87896 H87599 BF691752
BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF909744 AW966003 AV714014 BI492868 BI495144 AA921845
AI693426 AI652147 AI435449 N47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897
AW665247 AW340077 N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AI080245
AA884954 AI125702 AI382934 AA931835 AI358631 AW439905 AI027833 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI768667
AA948472 AI819214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AI492769 D56771 AA095911 BE222062
D56772 AW372265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI492848
H16217 H21980 H22651 H88179 H87354 H44052 H25165 H44128
AB018301 AL050295 BF513128 AW385080 AL551708 AI352542 AI829703 AI819388 AW629019 AW073189 AW273857 AW118768 AI453845
AI452494 AA886341 AI057144 AA904647 AI423547 AW263913 AI094774 AI434419 AI039546 AI002491 AI240412 Z25099 AA995178 AW050649
AW026140 AI796309 AI584012 BE166666 AI767591 AI309041 AA724059 AI695284 AI245095 T63971 Z40627 BE166681 BG570071 BF921915
BI562702 BG506502 AV658066 R48378 AA121543 AI096938 AA618131 H40993 R48277 AI352281 BG540263 BG538901 N95226 AI356752
AI221152 Z28777 R16574 AW966449 AA044116 AW797518 BI010405 AA044288 AI093508 BE140169 T64039 BG433106 AW130367 AW130361
N73937 AA127680 AW044037 AI096437 AA384077 BF941499 T93764 BG003285
BF090249 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119
AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260

	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	44.80
	438091	AW373062		nuclear receptor subfamily 1, group I, m	40.10
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	34.90
5	417088	M54915	Hs.81170	p1m-1 oncogene	31.10
	430542	AI557486	Hs.119122	ribosomal protein L13a	29.60
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	29.10
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	28.15
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	28.13
10	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	28.10
	406658	AI920965	Hs.77961	major histocompatibility complex, class	27.85
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	27.70
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	27.20
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.30
15	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	25.80
	429978	AA249027		ribosomal protein S6	25.40
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	24.60
	440207	AI371978	Hs.128326	ESTs	24.50
	425543	R23313	Hs.334895	ribosomal protein L10a	24.30
20	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	24.10
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	24.05
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	24.00
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	22.90
	420367	AA259090	Hs.257028	ESTs	22.90
25	406856	AW515336	Hs.29797	ribosomal protein L10	22.77
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	22.75
	412636	NM_004415		desmoplakin (DPI, DPII)	22.40
	420676	AI434780	Hs.4248	vav 2 oncogene	22.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	21.40
30	446627	AI973016	Hs.15725	hypothetical protein SBBI48	21.20
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	21.10
	420754	W79431	Hs.346911	ribosomal protein L22	20.98
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	20.90
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	20.80
35	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	19.50
	422714	AB018335	Hs.119387	KIAA0792 gene product	19.15
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.00
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	18.50
40	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.50
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.00
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	17.90
	448588	AI970276	Hs.156905	KIAA1676	17.70
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	17.50
45	428782	X12830	Hs.193400	interleukin 6 receptor	17.40
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIb	17.20
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	17.15
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	17.10
	440528	BE313555	Hs.7252	KIAA1224 protein	17.06
50	410143	AA188169		KIAA1191 protein	17.05
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.90
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	16.70
	429183	AB014604	Hs.197955	KIAA0704 protein	16.70
	450937	R49131	Hs.25267	ATP-dependant interferon response protei	16.60
55	449571	AW016812	Hs.200266	ESTs	16.50
	432730	AI066520	Hs.131358	ESTs	16.20
	426295	AW367283		zinc finger protein 6 (CMPX1)	16.15
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	15.90
60	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	15.80
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	15.80
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	15.50
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	14.90
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	14.90
65	406656	M16714	Hs.89643	major histocompatibility complex, class	14.85
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	14.71
	450377	AB033091		KIAA1265 protein	14.70
	425996	W67330		hypothetical protein AL110115	14.60
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	14.60
70	427691	AW194426	Hs.20726	ESTs	14.42
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	14.35
	451106	BE382701	Hs.25960	N-MYC oncogene	14.21
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	14.13
	436860	H12751	Hs.5327	PRO1914 protein	13.90
75	446899	NM_005397	Hs.16426	podocalyxin-like	13.90
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	13.75
	408380	AF123050	Hs.44532	diubiquitin	13.70
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	13.40
80	427521	AW973352		ESTs	13.30
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.25
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	13.23
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	13.23
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	12.70
	426552	BE297660	Hs.170328	moesin	12.69

5	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.55
	436398	H87136	Hs.5174	ribosomal protein S17	12.50
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.30
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.30
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	12.28
10	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	12.25
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	12.25
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	12.20
	419384	AA490866	Hs.39429	ESTs	12.20
	410185	BE294068	Hs.737	immediate early protein	12.15
15	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	12.05
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.00
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	11.90
	408989	AW361666	Hs.49500	KIAA0746 protein	11.80
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	11.80
20	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.80
	410325	AB023154	Hs.62264	KIAA0937 protein	11.70
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	11.70
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	11.61
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	11.60
25	454413	AI653672	Hs.40092	PNAS-123	11.60
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	11.40
	428065	AI634046	Hs.157313	ESTs	11.40
	432805	X94630	Hs.3107	CD97 antigen	11.36
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.35
30	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	11.30
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	11.30
	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	11.11
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	11.00
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.00
35	406786	AW161678	Hs.111334	ferritin, light polypeptide	10.95
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	10.90
	444656	AI277924	Hs.145199	ESTs	10.90
	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	10.85
	440774	AI420611	Hs.153934	ESTs	10.82
40	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	10.80
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	10.80
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.80
	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	10.70
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	10.65
45	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	10.60
	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	10.43
	424800	AL035588	Hs.153203	MyoD family inhibitor	10.40
	446682	AW205632	Hs.211198	ESTs	10.40
	447211	AL161961	Hs.17767	KIAA1554 protein	10.31
50	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	10.30
	422105	AI929700	Hs.111680	endosulfine alpha	10.21
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	10.20
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	10.20
	452651	AI218918	Hs.30209	KIAA0854 protein	10.15
55	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	10.11
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	10.10
	427761	AA412205	Hs.140996	ESTs	10.10
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	9.90
	402145			Target Exon	9.82
60	413686	AI469213	Hs.71404	ESTs	9.80
	446488	AB037782	Hs.15119	KIAA1361 protein	9.80
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	9.80
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	9.80
	407179	AA206465		thymosin, beta 4, X chromosome	9.72
65	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	9.70
	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	9.70
	446795	AI797713	Hs.156471	ESTs	9.70
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	9.65
	451864	N20370	Hs.69547	ESTs	9.65
70	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	9.60
	419904	AA974411	Hs.18672	ESTs	9.60
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.60
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	9.52
	424950	AA602917	Hs.156974	ESTs	9.50
75	447534	AW953935	Hs.288655	ESTs	9.50
	419223	X60111	Hs.1244	CD9 antigen (p24)	9.41
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.40
	422960	AW890487		cadherin 13, H-cadherin (heart)	9.33
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	9.32
80	408784	AW971350	Hs.63386	ESTs	9.30
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.30
	432409	AA806538	Hs.130732	KIAA1575 protein	9.30
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	9.30
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.22
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.20
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.20
	434524	AA635931	Hs.249716	ESTs	9.20

	450294	H42587	Hs.238730	hypothetical protein MGC10823	9.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.10
	434442	AA737415		ESTs	9.10
5	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.03
	447519	U46258	Hs.339665	ESTs	9.00
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	8.98
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	8.90
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypothe	8.90
10	442806	AW294522	Hs.149991	ESTs	8.90
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	8.89
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	8.81
	408437	AW957744	Hs.278469	lacrimal proline rich protein	8.80
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	8.80
15	431187	AW971146	Hs.293187	ESTs	8.80
	421098	AI697901	Hs.192425	ESTs	8.70
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	8.70
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	8.70
	401091			decay accelerating factor for complement	8.62
20	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	438089	W05391		nuclear receptor subfamily 1, group I, m	8.60
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	8.60
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	8.59
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	8.56
	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.50
25	414829	AA321568	Hs.77436	pleckstrin	8.50
	430162	AW450843	Hs.346348	ESTs	8.50
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	8.50
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.45
	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.43
30	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	8.40
	433208	AW002834	Hs.24095	ESTs	8.40
	428970	BE276891	Hs.194691	retinoic acid induced 3	8.38
	425284	AF155568		NS1-associated protein 1	8.33
35	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.33
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	8.30
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	8.30
	453716	AA037675	Hs.152675	ESTs	8.30
	418840	AI821614	Hs.185831	ESTs	8.20
40	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	8.20
	449656	AA002008	Hs.188633	ESTs	8.20
	425535	AB007937	Hs.158287	KIAA0468 gene product	8.17
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.13
	432559	AW452948	Hs.257631	ESTs	8.10
45	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.10
	420099	D80011	Hs.95140	KIAA0189 gene product	8.01
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	8.00
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.00
	434423	NM_006769	Hs.3844	LIM domain only 4	8.00
50	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	8.00
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	7.92
	433655	AL036559	Hs.3463	ribosomal protein S23	7.89
	435968	AW161481	Hs.111577	integral membrane protein 3	7.89
	434511	R28982	Hs.18106	ESTs	7.88
55	423523	AW299828	Hs.193580	ESTs	7.86
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	7.84
	411960	R77776	Hs.18103	ESTs	7.80
	434159	AW135214	Hs.191828	ESTs	7.80
	447500	AI381900	Hs.159212	ESTs	7.80
60	406699	L06505	Hs.182979	ribosomal protein L12	7.75
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	7.68
	426759	AI590401	Hs.21213	ESTs	7.66
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.62
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	7.60
65	444795	AI193356	Hs.160316	ESTs	7.60
	406663	U24683		immunoglobulin heavy constant mu	7.59
	442821	BE391929	Hs.8752	transmembrane protein 4	7.56
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.52
	407252	AA659037	Hs.163780	ESTs	7.50
70	414405	AI362533		KIAA0306 protein	7.50
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.50
	429999	AI761902	Hs.99597	ESTs	7.50
	441436	AW137772	Hs.185980	ESTs	7.50
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	7.50
75	420943	AI718702	Hs.279930	major histocompatibility complex, class	7.46
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.43
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.42
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	7.41
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	7.40
80	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	7.40
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	7.40
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	7.40
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	7.40
	432598	AI341227	Hs.157106	ESTs	7.38

	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.34
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.30
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.30
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.30
5	437103	AW139408	Hs.152940	ESTs	7.30
	442495	AI184717		ESTs	7.30
	445929	AI089660	Hs.323401	dpy-30-like protein	7.30
	446013	AI360167	Hs.152774	ESTs	7.30
10	436075	BE090176	Hs.179902	transporter-like protein	7.20
	450139	AK001838		serum/glucocorticoid regulated kinase	7.20
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	7.17
	406819	AA908472		gb:og82a10.s1 NCI_CGAP_Ov8 Homo sapiens	7.16
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.12
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	7.10
15	413886	AW958264	Hs.103832	similar to yeast Upt3, variant B	7.10
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	7.10
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	7.10
	427254	AL121523	Hs.97774	ESTs	7.10
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.10
20	438980	AW502384		gb:U1-HF-BR0p-aka-f-12-0-U1.r1 NIH_MGC_5	7.10
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	7.10
	441878	AI801869	Hs.127982	ESTs	7.09
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.04
25	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	7.00
	417315	AI080042	Hs.180450	ribosomal protein S24	7.00
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.00
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.00
	445245	AB032973	Hs.12461	LCHN protein	7.00
30	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.00
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	6.97
	410397	AF217517	Hs.63042	DKFZp564J157 protein	6.96
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	6.96
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	6.95
	418134	AA397769	Hs.86617	ESTs	6.90
35	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	6.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	6.90
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	6.89
	451838	AW005866	Hs.193969	ESTs	6.88
40	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	6.87
	453485	BE620712	Hs.33026	hypothetical protein PP2447	6.85
	401466			vesicle-associated membrane protein 4	6.84
	457073	AA233210	Hs.179943	ribosomal protein L11	6.83
	412093	BE242691	Hs.14947	ESTs	6.83
45	442492	AA528489	Hs.234518	ribosomal protein L23	6.83
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	6.83
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	6.82
	416401	N80139	Hs.268916	ESTs	6.80
	426501	AW043782	Hs.293616	ESTs	6.80
50	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	6.80
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	6.80
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.80
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.79
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	6.77
55	425277	NM_001241	Hs.155478	cyclin T2	6.72
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	6.70
	428728	NM_016625	Hs.191381	hypothetical protein	6.70
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	6.70
	433735	AA608955	Hs.109653	ESTs	6.70
60	430556	AW967807	Hs.13797	ESTs	6.69
	417535	AA203569	Hs.191482	ESTs	6.69
	418117	AI922013	Hs.83496	linker for activation of T cells	6.67
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.65
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	6.62
65	447341	AF106941	Hs.18142	arrestin, beta 2	6.61
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	6.60
	442460	NM_014135	Hs.8345	PRO0641 protein	6.60
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	6.59
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.57
70	415221	W07418	Hs.78225	annexin A1	6.56
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.54
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	6.51
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	6.50
	441224	AU076964	Hs.7753	calumenin	6.50
75	443749	R38828	Hs.143463	ESTs	6.50
	448094	H24387	Hs.32061	ESTs, Weakly similar to I38022 hypotheti	6.50
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	6.40
	418259	AA215404		ESTs	6.40
	421633	AF121860	Hs.106260	sorting nexin 10	6.40
80	435937	AA830893	Hs.119769	ESTs	6.40
	445612	N94126	Hs.12969	hypothetical protein	6.40
	451653	W18193		ESTs, Moderately similar to HERC2 [H.sap	6.40
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.40
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	6.39

5	434817	AA082118	Hs.102737	goliath protein	6.38
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	6.35
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.34
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.33
	435812	AA700439	Hs.188490	ESTs	6.31
	401113			solute carrier family 22 (organic cation	6.30
	408418	AW963897	Hs.44743	KIAA1435 protein	6.30
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.30
10	426780	BE242284	Hs.172199	adenylate cyclase 7	6.30
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	6.30
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	6.30
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	6.30
	449576	AW014631	Hs.225068	ESTs	6.30
15	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	6.30
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.27
	411975	AI916058	Hs.144583	ESTs	6.26
	452852	AK001972	Hs.30822	hypothetical protein FLJ111110	6.25
	433162	AI025842		ESTs	6.23
20	449322	AI638616	Hs.196566	ESTs	6.22
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	6.20
	440327	R12581	Hs.191146	ESTs	6.20
	442832	AW206560	Hs.253569	ESTs	6.20
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	6.20
25	427968	AI857607	Hs.181301	calthepsin S	6.18
	414662	AI036058	Hs.76807	major histocompatibility complex, class	6.16
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.16
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	6.15
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.15
30	445493	AI915771		metallothionein 1E (functional)	6.15
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.14
	427477	AW973119	Hs.178391	ribosomal protein L44	6.14
	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypothi	6.13
	443441	AW291196	Hs.92195	ESTs	6.12
35	413677	AW503116	Hs.301819	zinc finger protein 146	6.11
	406797	AI432224		ribosomal protein L6	6.10
	406857	AA613726	Hs.29797	ribosomal protein L10	6.10
	410387	AI277367	Hs.47094	ESTs	6.10
	410503	AW975746	Hs.188662	KIAA1702 protein	6.10
40	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	6.10
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.08
	406877	AA226392	Hs.179943	ribosomal protein L11	6.07
	407784	AW139585	Hs.12708	ESTs	6.05
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.05
45	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	6.01
	412949	AI471639	Hs.71913	ESTs	6.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	6.00
	435756	AI418466	Hs.33665	ESTs	6.00
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.00
50	441623	AA315805		desmoglein 2	5.98
	416926	H03109	Hs.263395	HT018 protein	5.96
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subuni	5.95
	441244	BE612935	Hs.184052	PP1201 protein	5.95
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.95
55	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	5.94
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	5.92
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	5.91
	433891	AA613792		gb:nc097h03.s1 NCI_CGAP_Pr2 Homo sapiens	5.90
	406542			C19000728*:gij12585552 sp Q9Y2Q1 Z257_HU	5.90
60	406858	AI865720	Hs.29797	ribosomal protein L10	5.90
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.90
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	5.90
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	5.90
	455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	5.90
65	441321	H17182	Hs.7771	B-cell associated protein	5.88
	429083	Y09397	Hs.227817	BCL2-related protein A1	5.87
	406806	AW088535		ribosomal protein, large, P0	5.87
	416987	D86957	Hs.80712	KIAA0202 protein	5.86
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	5.83
70	428773	BE256238	Hs.193163	bridging integrator 1	5.83
	406794	AI890243		ribosomal protein L6	5.82
	457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	5.82
	435511	AA683336	Hs.189046	ESTs	5.81
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.80
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	5.80
75	412528	AI123478	Hs.32112	ESTs	5.80
	424875	AI187945	Hs.199310	ESTs	5.80
	426981	AL044675	Hs.173081	KIAA0530 protein	5.80
	447711	AI459554	Hs.161286	ESTs	5.80
80	449961	AW265634	Hs.133100	ESTs	5.80
	416759	AK000978	Hs.79741	hypothetical protein FLJ10116	5.80
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	5.79
	422773	AB028962	Hs.301552	KIAA1039 protein	5.78
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	5.78

	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.77
	449317	AW293413	Hs.132906	19A24 protein	5.75
	425787	AA363867	Hs.155029	ESTs	5.73
5	414890	BE281095	Hs.77573	uridine phosphorylase	5.72
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	5.71
	435961	BE293127	Hs.283722	GTT1 protein	5.71
	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	5.70
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	5.70
10	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	5.70
	446659	AI335361	Hs.226376	ESTs	5.70
	457250	AA811987	Hs.125779	ESTs	5.70
	414150	AA136026		gb:zn88d07.r1 Stratagene lung carcinoma	5.68
	439924	AI985897	Hs.125293	ESTs	5.67
15	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.66
	451812	X81889	Hs.152151	plakophilin 4	5.65
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	5.63
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	5.63
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	5.60
20	431770	BE221880	Hs.268555	5'-3' exonuclease 2	5.60
	436511	AA721252	Hs.291502	ESTs	5.60
	446630	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	5.60
	406623	X69392	Hs.91379	ribosomal protein L26	5.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.57
25	416047	BE439894	Hs.78991	DNA segment, numerous copies, expressed	5.56
	437296	AA350994	Hs.20281	KIAA1700	5.56
	453985	N44545	Hs.251865	ESTs	5.56
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	5.55
	448877	AI583696	Hs.253313	ESTs	5.53
30	435748	AA699756	Hs.117335	ESTs	5.52
	420732	AA789133	Hs.63525	ESTs	5.51
	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	5.50
	430915	AA488953		gb:aa55e05.r1 NCI_CGAP_GCB1 Homo sapiens	5.50
	436716	AI433540		gb:tl69g05.x1 NCI_CGAP_Kid11 Homo sapien	5.50
35	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	5.50
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	5.50
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	5.50
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associa	5.50
	433701	AW445023	Hs.15155	ESTs	5.49
40	427640	AF058293	Hs.180015	D-dopachrome tautomerase	5.47
	420552	AK000492	Hs.98806	hypothetical protein	5.45
	449338	H73444	Hs.394	adrenomedullin	5.42
	427176	AW381569	Hs.40334	ESTs	5.42
	409945	AW015935	Hs.122642	ESTs	5.40
45	421568	W85858	Hs.99804	ESTs	5.40
	423961	D13666	Hs.136348	periostin(OSF-2os)	5.40
	440719	AA150869	Hs.26267	ATP-dependant interferon response protei	5.40
	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	5.40
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	5.40
50	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	5.40
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	5.39
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	5.38
	439815	AA206079	Hs.6693	hypothetical protein FLJ20420	5.37
	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	5.37
55	457465	AW301344	Hs.122908	DNA replication factor	5.37
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.36
	409485	S80990	Hs.252136	ficollin (collagen/fibrinogen domain-cont	5.35
	430283	BE391688		RAB7, member RAS oncogene family	5.33
	406814	AA642947	Hs.119122	ribosomal protein L13a	5.33
60	409019	AW385412		myosin regulatory light chain 2, smooth	5.30
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	5.30
	412623	R28898	Hs.74170	metallothionein 1E (functional)	5.30
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	5.30
	418702	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	5.30
65	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.30
	422900	AA641201	Hs.222051	ESTs	5.30
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	5.30
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.30
	427774	AA278583	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA	5.30
70	430177	AW969233	Hs.302746	MSTP028 protein	5.30
	430835	AI240006	Hs.192326	ESTs	5.30
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	5.30
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	5.30
	447082	T85314	Hs.54629	thioredoxin-like	5.30
75	415995	NM_004573		phospholipase C, beta 2	5.29
	424578	AK001973	Hs.150890	hypothetical protein	5.27
	441303	AW293081	Hs.241801	ESTs	5.27
	427816	AA159248	Hs.180909	peroxiredoxin 1	5.27
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.26
80	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	5.24
	444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isome	5.23
	415121	D60971	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	5.21
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.21
	405086			NM_006662*:Homo sapiens Snf2-related CBP	5.20

	413401	AI361861	Hs.118659	ESTs	5.20
	418459	R85436	Hs.268814	ESTs	5.20
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.20
	426496	D31765	Hs.170114	KIAA0061 protein	5.20
5	431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp564F133 (fr	5.20
	434372	AA631373		gb:np86c01.s1 NCI_CGAP_Thy1 Homo sapiens	5.20
	436812	AW298067		gb:Ul-H-BW0-ajp-g-09-0-Ul.s1 NCI_CGAP_Su	5.20
	441390	AI692560	Hs.131175	ESTs	5.20
	449419	R34910	Hs.119172	ESTs	5.20
10	453127	AI696671	Hs.294110	ESTs	5.20
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	5.20
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	5.19
	451814	AA847992	Hs.137003	ESTs	5.18
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	5.18
15	406799	AA908548		gb:og83g12.s1 NCI_CGAP_Ov8 Homo sapiens	5.16
	413963	R84282	Hs.75643	nuclear factor (erythroid-derived 2), 45	5.15
	422293	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	5.14
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	5.12
	414768	AW376989	Hs.259855	elongation factor-2 kinase	5.12
20	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	5.12
	430478	NM_014349	Hs.241535	apolipoprotein L, 3	5.11
	420151	AA255931	Hs.186704	ESTs	5.11
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	5.10
	419317	AA236282	Hs.172318	ESTs	5.10
25	424699	AW206227	Hs.287727	hypothetical protein FLJ23132	5.10
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	5.10
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	5.10
	431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	5.10
	436137	AI056769	Hs.133512	ESTs	5.10
30	440948	AW188311	Hs.128619	ESTs	5.10
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	5.09
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.09
	417228	AL134324	Hs.7312	ESTs	5.09
	424868	AI568170	Hs.96886	ESTs	5.08
35	418905	BE539674		actinin, alpha 4	5.08
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.07
	442618	R56222	Hs.26514	ESTs	5.06
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.06
40	406813	AW276131		ribosomal protein L13a	5.06
	454128	AL031259	Hs.41639	programmed cell death 2	5.05
	440709	AW797724	Hs.130350	ESTs	5.05
	436372	AW972301	Hs.310286	ESTs	5.05
	446173	BE565849	Hs.14158	copine III	5.05
45	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	5.04
	418876	AA740616		gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens	5.03
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	5.00
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	5.00
	410800	BE280421	Hs.94499	ESTs	5.00
	431451	AA761378	Hs.192013	ESTs	5.00
50	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.00
	435655	AW105663	Hs.6947	HSPC069 protein	5.00
	435919	AI052189	Hs.114104	ESTs	5.00
	436394	AA531187	Hs.126705	ESTs	5.00
55	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	5.00
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	5.00
	442685	AB033017	Hs.8594	KIAA1191 protein	5.00
	444454	BE018316	Hs.11183	sorting nexin 2	5.00
	444670	H58373	Hs.332938	hypothetical protein MGC5370	5.00
60	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.00
	450113	AI683098	Hs.200866	ESTs, Moderately similar to ALU7_HUMAN A	5.00
	450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	5.00
	450887	AA011518	Hs.271778	ESTs, Weakly similar to I38022 hypothei	5.00
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	5.00
65	457068	X69391		ribosomal protein L6	5.00
	406793	AW264291	Hs.5662	guanine nucleotide binding protein (G pr	4.97
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	4.95
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.94
	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	4.92
70	400281			Eos Control	4.91
	414420	AA043424	Hs.76095	immediate early response 3	4.90
	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.90
	434666	AF151103	Hs.112259	T cell receptor gamma locus	4.90
	449057	AB037784	Hs.22941	KIAA1363 protein	4.90
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.90
75	451598	N29102	Hs.118078	ESTs	4.90
	409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	4.88
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	4.88
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.86
80	447150	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r	4.86
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.85
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	4.85
	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	4.84
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	4.84

	406781	AA639388		gb:nq88b06.s1 NCI_CGAP_Co9 Homo sapiens	4.83
	449810	AB008681	Hs.23994	activin A receptor, type IIB	4.82
	410323	AI241708	Hs.296322	Homo sapiens cDNA: FLJ22844 fis, clone K	4.81
5	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	4.81
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.81
	400424	AJ276316	Hs.287374	zinc finger protein 304	4.80
	411573	AB029000	Hs.70823	KIAA1077 protein	4.80
	421045	BE144608	Hs.55533	ESTs	4.80
10	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.80
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.80
	438590	AA811465	Hs.123375	ESTs	4.80
	442071	BE048433	Hs.276043	ESTs	4.80
	449567	AI990790	Hs.188614	ESTs	4.80
	453213	AA082650	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	4.80
15	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	4.78
	437802	AI475995	Hs.122910	ESTs	4.77
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.77
	421932	W51778	Hs.323949	kangai 1 (suppression of tumorigenicity	4.74
20	428453	AB011110	Hs.184367	GTPase activating protein-like	4.74
	413441	AI929374	Hs.75367	Src-like-adapter	4.74
	446560	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	4.73
	435541	AA687361	Hs.221318	ESTs	4.71
	410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	4.70
25	412766	BE544475	Hs.54347	ESTs	4.70
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.70
	418973	AA233056	Hs.191518	ESTs	4.70
	421433	AI829192	Hs.22380	ESTs	4.70
	432925	AA878324	Hs.264750	ESTs	4.70
30	438869	AF075009		gb:Homo sapiens full length insert cDNA	4.70
	442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypotheti	4.70
	447198	D61523	Hs.283435	ESTs	4.70
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	4.70
	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	4.66
35	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	4.66
	447817	BE620775	Hs.4866	Homo sapiens cDNA FLJ14387 fis, clone HE	4.65
	416062	AA724811	Hs.334791	Homo sapiens cDNA FLJ14609 fis, clone NT	4.65
	406661	X66975	Hs.172550	polypyrimidine tract binding protein (he	4.64
	424582	AF026849	Hs.150922	BCS1 (yeast homolog)-like	4.64
40	411165	NM_000169	Hs.69089	galactosidase, alpha	4.63
	435905	AW997484	Hs.5003	KIAA0456 protein	4.63
	445776	NM_001310	Hs.13313	cAMP responsive element binding protein-	4.62
	424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	4.62
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	4.62
45	410668	BE379794	Hs.159651	hypothetical protein	4.61
	406774	AW518383	Hs.177592	ribosomal protein, large, P1	4.60
	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.60
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	4.60
	415682	AI347128	Hs.191870	ESTs	4.60
50	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	4.60
	419970	AW612022		ESTs	4.60
	420012	AW957965	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	4.60
	431574	AW572659	Hs.261373	hypothetical protein dJ434014.3	4.60
	432586	AA568548		ESTs	4.60
55	437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	4.60
	441355	AI822034	Hs.137097	ESTs	4.60
	444539	AI955765	Hs.146907	ESTs, Weakly similar to 2004399A chromos	4.60
	458965	AA010319	Hs.60389	ESTs	4.60
	406655	M21533	Hs.277477	major histocompatibility complex, class	4.60
60	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	4.60
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.59
	423766	AA303799	Hs.300141	ribosomal protein L39	4.59
	451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
	450043	AA885699	Hs.24332	CGI-26 protein	4.56
65	447742	AF113925	Hs.19405	caspase recruitment domain 4	4.54
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.54
	426395	BE151985		hypothetical protein FLJ23316	4.53
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	4.53
	423799	AW026300	Hs.132906	19A24 protein	4.53
70	445093	AI207197		ESTs	4.52
	428044	AA093322	Hs.301404	RNA binding motif protein 3	4.52
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	4.51
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	4.50
	427747	AW411425	Hs.180655	serine/threonine kinase 12	4.50
75	406745	AW511970	Hs.279860	tumor protein, translationally-controlle	4.50
	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	4.50
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	4.50
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	4.50
	429687	AI675749	Hs.211608	nucleoporin 153kD	4.50
80	436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	4.50
	437634	AW293046	Hs.255158	ESTs	4.50
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	4.50
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	4.50
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	4.50

	450497	H64159	Hs.15328	ESTs	4.50
	417497	AW402482	Hs.82212	CD53 antigen	4.50
	447667	AL117611	Hs.19150	Homo sapiens mRNA; cDNA DKFZp564A2164 (f	4.49
5	413856	D13639	Hs.75586	cyclin D2	4.49
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	4.49
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.48
	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.48
	446021	BE389213	Hs.286	ribosomal protein L4	4.47
10	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.46
	412819	T25829	Hs.24048	FK506 binding protein precursor	4.46
	448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.45
	401846			NM_000988*:Homo sapiens ribosomal protei	4.44
	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	4.43
15	442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	4.43
	436623	AI417073	Hs.107265	ESTs	4.42
	412146	M92444	Hs.73722	APEX nuclease (multifunctional DNA repai	4.42
	437042	AK000702	Hs.5420	hypothetical protein FLJ20695	4.42
	416754	H07145	Hs.6799	ESTs, Weakly similar to T12483 hypotheti	4.41
20	436671	AW137159	Hs.183291	ESTs	4.40
	410079	U94362	Hs.58589	glycogenin 2	4.40
	420150	AA648712	Hs.29798	KIAA1712 protein	4.40
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	4.40
	428931	AA994979	Hs.98967	ATPase, H(-)-transporting, lysosomal, non	4.40
25	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	4.40
	430280	AA361258	Hs.237868	interleukin 7 receptor	4.40
	438330	AW450572	Hs.257316	ESTs	4.40
	438962	BE046594		gb:hn41c11.x1 NCL_CGAP_RDF2 Homo sapiens	4.40
	444794	AI419991	Hs.145225	ESTs	4.40
30	445100	AW188205	Hs.12311	Homo sapiens clone 23570 mRNA sequence	4.40
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	4.40
	449832	AA694264	Hs.60049	ESTs	4.40
	452404	AW450675	Hs.212709	ESTs	4.40
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.39
35	425097	NM_014247		PDZ domain containing guanine nucleotide	4.37
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.37
	406742	AI468091	Hs.279860	tumor protein, translationally-controlle	4.35
	425095	AW014160	Hs.182585	KIAA1276 protein	4.34
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, rec	4.34
40	442333	AI650877	Hs.129302	ESTs	4.33
	424971	AA479005	Hs.154036	tumor suppressing subtransferable cand'id	4.32
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.32
	437386	W52452		ribosomal protein L10	4.31
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	4.30
45	408875	NM_015434	Hs.48604	DKFZP434B168 protein	4.30
	409604	AW444448	Hs.49124	ESTs	4.30
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.30
	419423	D26488	Hs.90315	KIAA0007 protein	4.30
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	4.30
50	422797	AB033064	Hs.236463	KIAA1238 protein	4.30
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.30
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	4.30
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	4.30
	436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	4.30
55	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	4.30
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	4.30
	452994	AW962597	Hs.31305	KIAA1547 protein	4.30
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.30
	437250	BE257342	Hs.94576	hypothetical protein MGC3062	4.29
60	440910	H97875	Hs.117974	ESTs	4.29
	406853	AA614553	Hs.252259	hypothetical protein FLJ23059	4.28
	432295	BE091049	Hs.343665	ribosomal protein S15a	4.28
	400244			Eos Control	4.28
	413518	BE149455	Hs.75415	beta-2-microglobulin	4.28
65	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.27
	406746	AA580395	Hs.279860	tumor protein, translationally-controlle	4.26
	400395	AF111167		v-fos FBJ murine osteosarcoma viral onco	4.26
	443229	AI057129	Hs.133396	ESTs	4.26
	450201	T97838	Hs.25722	ESTs	4.25
70	409636	AA305729	Hs.18272	amino acid transporter system A1	4.25
	422082	AA016188	Hs.111244	hypothetical protein	4.24
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	4.24
	453902	BE502341	Hs.3402	ESTs	4.24
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	4.22
75	404854			Target Exon	4.21
	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.20
	400440	X83957	Hs.83870	nebulin	4.20
	415049	N67334	Hs.50158	ESTs	4.20
	418304	AA215702		gb:zr97g10.r1 NCL_CGAP_GCB1 Homo sapiens	4.20
80	423180	AF068302	Hs.125031	choline/ethanolaminephosphotransferase	4.20
	424684	AW752714	Hs.5174	ribosomal protein S17	4.20
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	4.20
	438141	AW946871		gb:RC2-ET0022-080500-012-d02 ET0022 Homo	4.20
	438607	AW080237	Hs.252884	ESTs	4.20

451952	AL120173	Hs.301663	ESTs	4.20
455397	AW936332		gb:QV4-DT0021-281299-070-g01 DT0021 Homo	4.20
417116	Z43916	Hs.7634	hypothetical protein FLJ12287 similar to	4.19
453247	T80198	Hs.111806	ESTs	4.19
430451	AA836472	Hs.297939	cathepsin B	4.19
414283	AW960011	Hs.154993	ESTs	4.18
452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.18
450746	D82673	Hs.278589	general transcription factor II, i	4.16
444797	AB018333	Hs.12002	KIAA0790 protein	4.16
445718	H79791	Hs.15227	ESTs	4.15
425783	AI026740	Hs.1948	ribosomal protein S21	4.15
414837	U24266	Hs.77448	aldehyde dehydrogenase 4 family, member	4.15
406710	AI708347	Hs.184014	ribosomal protein L31	4.15
424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	4.14
422343	AI628633	Hs.346823	gb:ty77d05.x1 NCL_CGAP_Kid11 Homo sapien	4.13
416207	NM_014745	Hs.79077	Homo sapiens, clone MGC:2908, mRNA, comp	4.13
406724	C14071	Hs.234518	ribosomal protein L23	4.12
449475	AI348027	Hs.108557	hypothetical protein PP1057	4.12
413828	L19067		v-rel avian reticuloendotheliosis viral	4.11
416819	U77735	Hs.80205	pim-2 oncogene	4.11
436674	AA725002	Hs.272018	low molecular mass ubiquinone-binding pr	4.11
405266			Target Exon	4.10
408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	4.10
410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	4.10
420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.10
423096	AA732684	Hs.278428	progesterone induced protein	4.10
428328	AA426080	Hs.292812	ESTs, Weakly similar to I38022 hypothi	4.10
429355	AW973253	Hs.292689	ESTs	4.10
433308	AA582718	Hs.291650	ESTs	4.10
443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.10
450850	AA648886	Hs.151999	ESTs	4.10
453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	4.10
406854	AA613705	Hs.252259	ribosomal protein S3	4.10
410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	4.09
419612	AI498267	Hs.110613	KIAA0421 protein	4.09
434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.08
439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	4.08
441374	AA043696	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564C1216 (f	4.08
443415	AI056523	Hs.133472	ESTs	4.08
424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	4.07
422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.07
400233			Eos Control	4.06
421959	AW751497	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.06
442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	4.06
424795	AW102850	Hs.153177	ribosomal protein S28	4.05
446231	NM_002163	Hs.14453	interferon consensus sequence binding pr	4.05
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	4.05
427681	AB018263	Hs.180338	tumor necrosis factor receptor superfam	4.05
409061	AI204994	Hs.7874	Homo sapiens cDNA: FLJ21435 fis, clone C	4.03
413891	BE271020		tumor suppressor deleted in oral cancer-	4.03
414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	4.02
417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.02
410584	AB011112		KIAA0540 protein	4.01
417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.00
423645	AI215632	Hs.147487	ESTs	4.00
430048	T65054	Hs.73605	ESTs	4.00
431113	AK000673	Hs.274337	hypothetical protein FLJ20666	4.00
434170	AA626509	Hs.122329	ESTs	4.00
434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	4.00
435391	AA704588	Hs.58934	ESTs	4.00
446768	AV660305	Hs.110286	ESTs	4.00
448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	4.00
451831	NM_001674	Hs.460	activating transcription factor 3	4.00

TABLE 56B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552

			BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
429978	35194_2		BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260821 AI767525 R31663 BI918664 AW963196 C06195 AI678018
442562	39593_1		AK056685 BG399272 AA187835 BF821903 AV660550 AV660556 AV660502 BG564397 BE379584 BF446961 AI653056 AW973709 AI653173 BG054997 AI266043 BI054879 AI656750 AI492830 AW021142 AI472184 AW170056 AI082443 AI167921 D59940 BI492088 H74180 AW130886 AI348677 AI278577 AA761517 AI698203 AA115535 AI264790 AW205074 AA860452 AA554902 AI000715 D62102 BE544768 AI376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832
412636	1438_1		M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361143 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494059 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 BC003047 S80794 NM_003405 X78138 AY007132 L08439 AW340648 AW131665 AI082748 AI470204 BI711078 BF350700 BI496963 AI087141 AA720684 AA862331 AA605146 BM313650 AI089749 AI359738 N69107 AW995424 AI086917 AI083995 AW340321 N99662 AI829449 AI089839 AI608761 AI342365 AI199076 AA908944 AI248943 AU160053 AI191245 AI218477 AI077943 AA864930 AI310394 AA872478 AI279782 W61343 AA565955 W46596 AA126874 AA223241 AA491574 R84813 AA491520 BG055114 AI469689 BE464590 AW664539 H67097 AI534332 C21397 AI085941 AW028427 BG939820 AI697089 AI039008 AI125315 AI655561 AW150042 L20422 X57345 AI458375 AU142852 BI666601 BE888276 AU119302 BI603754 BG705953 BI598754 BE296713 BG002538 BF951911 N29226 BE909424 AV688274 AV683116 AV708195 AA127798 AI124697 D54224 F08031 AA340253 BF923383 BM467808 BI546644 BG777200 BG705941 BG468577 AU127209 AW403970 BI697630 BI458091 AV689560 BI689267 BG506219 BI837163 BI667275 AA343750 BE783112 BF671405 BF954720 H67636 H69456 AA448494 BI869271 BF998207 N31547 BF945817 BF947918 N90630 BG980194 AA156681 BI493502 AW273118 AI473820 AA608688 AI359337 AV712091 AA084101 BF592036 H13301 AI864305 AA505883 AI423963 AW084401 AI917740 R69858 AA033631 N79982 BE885276 AI635674 AA096126 AA700018 AV707753 AI082545 AU145681 AA629032 AI421367 AA740589 AA150830 AI248541 AA988608 AA150478 W65437 BM310234 AA262704 T28031 AI811116 BM272753 H21979 T15405 AA938406 F04963 AI88296 AW152629 AA905196 BG223058 AI831016 AI766457 AI811102 AA776573 AI922133 AA775958 AI261476 AA219489 AI688035 AI872093 BE537084 AW189078 D82630 AI123121 AI583492 BE350791 R69901 W65436 BE155392 BI089081 BE155394 AL120538 AW166100 AI359620 AI174338 N20527 W47413 AA155615 AI272249 H25293 BE145558 H69864 AW383484 H78021 H11617 R56892 H23204 N21530 R82499 AW383522 AA774536 AL534331 W94127 W46459 AI866231 AA513281 AA192465 H69844 W85827 AW383642 AW383529 AA171496 AL537424 BE814866 BF823254 R82553 AI089817 AI559406 AK000357 AI571830 AA579613 AG68790 BF939495 BF196886 AI990982 BF591561 AI809189 AW410232 BF739769 AI144392 BF438721 AI707495 AI423359 N52503 BE855784 N94367 AI023931 AA563662 AI744624 AI221298 AI299523 AI299520 BI491312 AI452711 AI360730 AA622643 AW195955 AA470473 AW392767 AI218127 AA873430 AA906005 AA748160 H89523 AW020252 AW664988 AA970424 AW869079 AI581622 AI361357 AA468498 AW008694 AA903275 AI187724 AI187718 AA890505 BF092771 AI066655 BE714172 BG289028 AW080390 BE001197 BF132049
413787	7612_1		BE880923 BG390191 AW470082 AW014585 AI423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI422030 AI348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI215830 AI283836 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085455 BE551404 AA780704 AW008596 AI796964 AA917471 AI400531 AA668626 N72207 AI306482 AW440562 AI084687 AA347280 AA063536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI916336 AI350590 BF198106 AI433377 AI300638 AI672626 AI282741 AI351487 AW105544 AA973627 AW517914 AA715424 AA508454 BF334080 AI274618 AW367201 AW572619 AW469088 AA382095 AI368364 AI146934 AI357180 AI361181 BI911347 BI871044 AA136325 BF084010 BF084007 AA335788 AI920878 AA809614 BE932941 AI678261 C75308 AI148479 BE178174 W88513 BM013627
451043	MH1244_8		AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592865 AA978621 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BF255699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164
425996	138046_1		BM006551 AA367152 AW953705 AI631833 AW237429 AW027804 AA729038 BE503409 AI521935 BF739953 AA702982 AA557633 AA780065 AI218139 AW194264 D20120 AI082715 AI969980 BE857686 BE326711 AW953706 AI393749 AI383821 W67199 AI431759 AI796526 AI521794 AI796380 AW117545 AI749657 AI537634 N50122
427521	513212_1		AW973352 BF222929 AW016853 BF059130 AI651829 BE555176 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
444060	6315_1		AK055070 AK055612 AK000174 BG619808 BG108086 AI741949 AI004176 BF891936 BF378565 AW197163 BE856860 BE245124 AW674411 AA490531 AW674981 AA740788 AW247458 BF512523 AI521278 AA548759 AI802431 AW051682 AI628247 AI799606 AW088103 AA236549 AI191529 AW273168 AI168451 AW073812 AW090611 AW003593 AI215845 AI799616 AW474940 AA954927 BM193740 AW662704 AW090127

5	413497	1518002_1	AA969444 AI080438 AA552500 AW237538 AA481060 AI246378 AA565227 AA398921 AA207051 AA721378 BF438608 AI086295 AI886630
	430068	1177709_2	AA904112 AI864588 AW271985 AW078868 AA725342 BF326598 AA843572 AI082536 AA766664 AI453279 AA435673 AI619515 AA879080
	409208	10117_2	AA234592 AA890223 AA766824 BI259822 AA393631 AW968840 BE940639 T83865 BE762742 AW897470 W05809 N41323 T87376 R68544
10	422960	11862_2	H88711 BI087136
	434280	1474904_1	BE177661 H06215 BE144709 BE144829
	434442	111738_1	AA947566
15	410730	114639_1	AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843
	438089	22448_4	BM144372 AA989341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF881946
	425284	3834_5	BF090249 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119
20	422689	874209_1	AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260
	414405	112689_1	BE005398 AA628622 AA994155
	442495	928718_1	AA662701 AA633929 AA737415
25	450139	34017_1	BG427950 AA826016 AI903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823
			BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440
			AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664
30	406819	0_0	H91240 R60548 N41701
	424677	2518_37	BM476120 BE672181 AI697653 AA938187 AI280879 AW340123 AI912727 AI081775 AI089556 AI191349 AI871604 AI631607 AI890800 AI701917
	438980	917280_1	AW771624 AA663041 AI991576 AI160622 AA771763 BE089784 BE089788 AI222942 AW418516 AA329211 AI095736 BE550294 AA738345
35	451129	1495511_1	BE218683 BE670548 BG149505 BF061776 D19821 BE005786 BE178892 BE005728 BF841237 BE005648 R27634
	432666	144_7	AW954733 AA315006 AW856665
	418259	133853_1	AL047596 AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090696 AI927369 AI669226 AI369437 AI371075
40			AW612409 AI686711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 D81020 BF575223 AI356183 D79312 AI375558 H61111
			BG283489 BE090666 BE090664 BE090662 H26545
			AI184717 AW518883 AF121173
45			AK001838 AU135179 AU134241 AV651702 AV650032 AV651304 AV650101 AV651263 AV651888 AV651866 AA628554 AV651355 AV651174
			AV651172 AW856145 AU117599 AU135386 BG254665 AA166919 BG483981 AW809606 BG494194 AA622811 AI676156 AA687804 AI701729
			AU133725 AW961387 AU144387 AU151757 AA551031 BE675412 N34769 AA713483 AI890079 AI588918 AI361889 AI209020 AA668981 AI240990
50			AA741144 AA490899 AI200221 AW589574 W96201 BG154182 AV655159 AI328145 N36348 AI081357 N76715 AA693346 AA742488 AI269719
			AA897483 AI886459 AU155873 H04255 AW243986 AA557749 AI286227 R68691 R33453 AW388057
			AA908472
55			U09414 NM_003438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW609708
			AW502384 AA828822 AI982587
			BE072881 AI762181 BE072946
60			AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
			BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969
			BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563
65			AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317
			BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254
			W05240
70			BG119563 AW975776 BG498478 BE245304 AW450934 BF508792 AA599489 AA599477 AI805268 AA055489 AI128758 AA761425 AA731858
			AI302271 BE219432 AA687294 AA018972 AW629429 Z45675 AW961626 T30940 R34554 T84712 BG986694
			AI742311 AI025842 AA578843
75			AA075144
			AV711317 AI809938 AI808768 AI240593 AI915771
			AI432224 AW276890 AI499346 AA937014 AA653573 AI318525 AI246219 AA961591 AI270640
80			BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853
			AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424
			AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448
85			AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306
			AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522
			BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595
90			BI094458 BE706702 BG496559 BF248373 BG494800
			BE219720 BF475241 AI571723 BE219848 BI789268 AI224899 AA724864 AW771467 AA480255 AW845616 AI440295 H52800 BE218790 AI681575
			AW300064 AW262133 H21568 AI363015 AI884914 H86948
95			AW182329 AA613792 T05304 AW858385
			BG216963 BG164885 BG213710 BG204771 BG193014 BG197556 BG217481 BG198185 BG183594 BI596425 AA115605 AI589156 BF439839
			BG188832 AI359615 BG190473 AI024233 BF439574 AW118065 AI672797 AA610042 BG212008 AI204382 R70913 AA033534 AA781036 AI627278
100			AA307285 AA034218 BG482749 AW162429 BI602460 AA721969 AA476516 AA476416 AA903019 BF110864 AA307286 AA115471 AW964555
			AA423826 AA115129 AI419107
			AW088535 AI889321 AA954221 AI337552 R42581 AW194670 AA064862 AW001147 AA864374 AA630699 AW276176 AA676615 AA857965
105			AI625428 AA580792 AA582038 AA581668 AA658065 AA828156 AA857160 AA936103 AI149335 AA936925 AA581684 AA954198 AW238461
			AI281504 AI265812 AA583267 AW236162 AA876535 AW304286 AW474334 AI559415 AI589241 AI660952 AA641137 AI431696 AI688844
			AA552513 AA564954 AW090553 AI205612 AI245753 AA954883 AA947909 AI866014
110			AI890243
			AW971213 AA493925 AA493567 AA876839 AA934462
			T40644 AA136139 AA136026
115			BG425760 BF997600 N48516 W73454 BF816344 BF997601 AA488953
			AI433540 AA804981 AA728984
			BI918168 AW779760 N48674 BI735997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526
120			BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
			BC013728 BI084032 BF090365 BE410706 N36391 W80436 BF813124 R90857 R62778 H00591 H02329 AA355285 AK000826 BC008721
			BG744004 BG479141 BG823656 BG479061 AU121103 AU138176 BG702567 BI599840 BG422775 BG700944 BE280747 AU138529 BE269929
125			BG704110 AU123329 AU122058 AU138135 BG723106 BG722291 BG831041 BG705239 BE740517 BE207133 BE252867 AU139772 BG714385
			BF568538 BE304393 BF971755 BE267965 BE272012 AU135396 AU124535 BI551682 BG700612 AI815488 BG475195 BE388273 BE391517
			BM148991 BF929247 AV653435 AW250299 AW249189 BF093150 BF093173 AW205325 BF057101 BF000551 AI341108 AL162009 AK026136
130			BE907797 W73238 BI711467 BG926027 AI816428 AA837518 AI754405 BG179142 AA481485 AW023435 BE855747 AI885101 N52163 AI016096
			AI090204 BE677045 AI523320 AI126855 N26501 AA043680 AA976459 AI039590 AI937917 AI361000 W94866 AI375797 AI079801 AI168236
			AA599882 AA084368 AI342635 AI190294 N26093 AI085234 AI298169 BF939715 AI223164 H98704 BE218925 N29394 AI918735 N41520 AI147784
135			AI918796 AA854317 N22193 AA199850 AI149728 AA121263 AI051074 AA565116 AI097349 N22209 AA552917 N33151 D52422 BF477483
			AA476599 AA525787 AI279198 D53353 AA738063 AA558406 BI496334 AA999948 AA425847 BI496335 AA909624 BF197591 AW023259 AI652819
			T31424 AA088213 T31115 AI206650 AA976796 AI948989 AW248762 AA449265 AA290687 AI682521 AA310227 Z38743 AA935369 AW119141
140			BF941087 AI470657 AI349451 AW079338 D45665 N21640 T30071 AI446705 R60220 BE833481 R49680 R70049 R41223 R32402 R69984 R70111
			BM476906 BE293615 BE382443 BF155692 BE720538 BE931983 BE720594 BF085890 AA336953 BF081638 AA359915 AA384116 AA360142

5	BI667664 BG823235 BE315559 BE301958 BE891114 BG826267 BE253680 BG979094 AV722757 N67629 BG997927 BI915769 BG680692 R62777 BE251116 H56358 AW369586 BG677759 BI044604 R75787 BE770960 H69529 R69983 AA259238 R97827 AA310379 W01103 AI873384 AI.554578 BF038102 H87182 H87517 H01574 T52573 N28881 AA301397 T92375 R68401 AW800466 AI268172 BE876949 D54019 AI909769 AW798415 BI222383 AI393171 C15260 N26959 H17129 T53095 T52494 R68602 AI364765 BF687869 AI817035 AW105354 BE293820 H14206 BI093066 C14063 AL553439 BE255883 BE254088 AA428399 AW579360 AW579381 N53144 D60748 D54020 BG292106 H96705 D52423 T36174 D54161 R73016 D55021 BI857200 H83444 BI016954 D54163 R15563 BI818664 BE152207 BI048502 BF885667 BE613212 BE165773 BF149332 AW607045 BE305200		
	409019	32320_4	BM480413 N28908 H39792 BE240826 BE882093 BE240827 AW868637 BF739795 AA700834 AA765957 AA489668 AW968806 AW085196 AI093280 AI218457 AA063138 AI632958 AW515005 AI570530 Z41724 AA748789 AI696584 AA062544 AA773643 AA490285 AA761668 AA573621 R09670 R92814 M95678 NM_D04573 AL530754 AI439623 AW374413 BF898880 AW630959 BF875526 AW402206 BF818690 BF893068 AW504110 AW408049 BG002913 AL530753 AI524064 AW769231 AA464970 AA293723 AI095051 AI953375 AI982938 BM146050 AW575804 AA962489 AI655426 BM146046 T28538 BE241936 T89023 BI910963 AI416986 AI767111 AI422290 AW468260 BE676853 AI656771 AI961755 F04675 AA682826 BF376066 BM194382 AA912021 AW183098 BE676882 AI962227 AI591366 AA621765 AA293724 R51642 F10194 BI909727 BF892632 AW950600 AW950138 BG258587 BF892649 AI800647 BF892710 AA353176 BF894726 AA465038 BI048069 BI837749 BE244320 H18054 T74300 AW797026 AA926790 F32814 AW751282 AI933994 AA578823 T78372 BF899896 BF882808 BF974969 BG622121 AA631424 AA988296 AA631373 AW978773 AW298067 AA810101 AW194180 AA731645 AI690673 AA908548 AW972830 AA489820 AA527647 AA570362 BM469076 AA533027 AI127512 AI368802 AA533141 AA700560 AW576028 AI610851 AI435361 BM129172 AW474544 BM128899 AI814292 AW502039 AA531243 BF941858 AW502037 AA702337 AI419854 AA662755 AA934364 AI300510 AI291136 AA505263 AI144527 AI076919 AI633534 AI242473 AA938561 BG055372 AA512894 AI671356 AA962403 BF808010 AA663911 AA847056 AA513301 AA369069 AA377265 BG291206 AA402298 AA885766 AW801002 AA302290 AI305842 AW800873 AA302492 AA478427 AI817291 AW801104 AW801028 AA865744 BF155979 AI374743 AA478431 AI159846 AI369757 AI800672 BF435788 AA255451 AI937707 AW006198 AI280363 BF062434 AW801115 AI919181 F28413 W04214 AW152380 AW901567 AW901570 AA886371 AA384251 AI302846 BE701902 AA931606 H42673 R33703 AW901556 AA009816 AW901568 AW352200 AA256558 H15928 BI087170 AW800530 AA369068 N98562 H28652 N34644 H97650 H00956 W70039 AI142831 AA009817 F37136 N70289 AA531347 R72374 H27488 R66605 AW276131 AA740616 AA654854 AA229923 R36075 R36167 AI366546 BC022444 BC004138 NM_000970 BC020679 X69391 D17554 BC013863 BG779630 BG574189 BG571986 BG494603 BG575713 AV702244 AU145720 AI568177 BE350654 BG943995 AA730918 AA634024 AV744673 AI611573 AI613381 AI613403 AI250148 AW301759 AI312307 AI376488 BE139682 AV743357 AI371951 AI613376 AI613570 AI345719 AI312458 AI612697 AI334453 AW268747 AW268318 AI343026 AI335454 AI313096 AI308011 AW075176 AI348782 AI334479 AW268332 AI611433 AI371906 AI312459 AI371647 AI370051 AI335217 AI312262 AI610971 AI348798 AI613378 AI612698 AI348772 AI345434 AI345283 AI312292 AA775853 AI611363 AI345286 AI318305 BF054854 AI613384 AI348808 AI802857 AI609452 AI583301 AI349258 AI345645 AI345011 AI340442 AI335410 AI310907 BF055880 BF055774 BF055754 BF054712 AI583261 AI309664 BF054905 AI370092 AI349212 AI345583 AI334554 AI312242 BF055856 AI612686 AI611382 AI610952 AI345301 AI312235 AI610936 AI609836 AI340650 AI312472 BF054840 AI802838 AI345448 AI336508 AI313098 AI312293 AI312277 AI254912 AW302091 AW074788 AI611968 AI611948 AI583362 AI583284 AI583245 AI379398 AI371935 AI340564 AW301840 AI862239 AI612025 AI611869 AI609852 AI345449 AI312375 AI312318 AI311993 AI310895 BF057960 BE178604 AI802860 AI612115 AI611886 AI370059 AI313286 AI802856 AI611438 AI311987 AI802821 AI312997 BF054711 AI611889 AI376483 AI252445 AI611577 AI349139 BF054925 AI802840 AI583286 AI340739 AI612041 AI345196 BF054833 AI308909 AI611883 AI313275 BF477097 AI609466 AI348792 AI340468 BG944254 BG941457 AW302007 BG944413 BG941475 D58042 AA328428 BG429596 BE395392 BM424161 BF663310 AV727364 BM473884 BG531178 AA307591 BF965435 BG009500 AI376551 AA897445 T87714 BE564506 Z47727 BF028489 BI597545 AA152273 AA730753 W07504 AA406507 AA316220 AA424683 N35844 N72473 AA442109 W01788 AA747605 AA235894 N41438 AA382786 AI906934 AI906935 BF091197 N85572 N75678 AV758098 BE719745 BE719744 BE719735 AA639388 AA584945 AA776364 AA776365 AA865528 AI732997 AA977633 AA865518 AF075009 R63109 R63068 AK055270 BE348291 AI190289 AW612022 AI269506 AI266578 AI269675 AW271406 BE879851 BF574163 BI497126 AW903775 BI917368 AW150900 BF244813 H79201 BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548 AK057067 BF111915 AW249706 AI222199 AI887251 AI818753 AI244687 AW135782 BF476693 BF060935 AI197928 AW251092 AI685636 AI685630 BE673458 AA932894 AW205200 AA720784 BG236866 AI583152 BE677464 AW149338 AI926439 BG031285 BF915924 BG982583 BI060025 BG991393 BE830027 BE151985 BE152208 BE152002 BE818337 BE717581 BE818354 BE830030 AA377477 T51255 BF920761 BG170636 N90052 AI207197 BF773544 AW196462 AI207343 BF813684 BF928775 AA828585 AF070570 BF439282 BF109960 AI480268 AI038060 AW082339 BF516290 BE218214 AI469956 AA039955 BE644674 AI861871 AA766231 AA845840 W85716 AA676253 AI087188 AA022908 AW953178 T33195 BF594711 AA488969 R55652 D81245 D80778 D81560 AW960933 BF930897 BE698103 AA040024 BF515960 BE168475 AA453247 AI267601 R60894 R44223 T33194 AA114936 W31640 W38829 W39109 AA004849 H41952 W88634 BF031932 BM423354 AL041825 H29654 AI908178 W85754 AI905762 AA309860 C04540 AA340246 H84669 BM476605 BI545004 BI834636 BG112453 BI199049 BG112759 AA149846 H97925 AA306121 AA313204 W52451 AI734997 AA931168 AA429766 N47913 AA584321 BF940241 AI083648 AI089410 AI347705 AI343661 AI186232 AI889031 N98464 AI820039 AI459034 AV652512 AA622990 BE857200 AA932998 AA740573 AI826264 AA865683 AI344550 AI027349 AI056087 AA442777 AA603724 AA873347 AI056717 AI092185 AI032895 AA535689 BF806025 BF806061 BF805985 BF746099 BF746097 AI309259 AI597603 BF806066 AI090653 AI129205 AI248410 H72993 AW615341 BF805990 BF805982 AA993819 T34373 T35604 H56242 AA648145 T35907 BF808691 N94015 AV703438 BG774276 H82341 R76371 T65754 AA229658 AA229857 X79449 BC017853 AL121035 BF196384 AW119044 AI028023 AW451110 AI971911 AW015069 AI079170 AI376367 AI264113 AA829646 AA737579 AA449679 AA740864 NM_001111 U18121 AL567297 BG773801 BF973874 AV687104 AA527579 AA843525 BE706355 AI074589 AI523475 BE890249 AW406263 BE074258 AV729485 BF809610 BG058619 AA677244 BE179838 AA622264 AI460106 AA740411 AI499168 AI078223 AI682923 BE696559 AW375385 AA788739 BG984978 Z40874 T17054 F09669 AW844043 U10439 BI711870 AW245957 AU158567 AA679305 AA679316 W72510 AI346029 BG059762 AW251062 AA132373 AI925621 AI860230 AI340172 AW192891 AI707990 AI094937 AI042115 AI200901 BE328452 AA644678 AA551209 BE351065 AA970761 N68609 AW002028 AA160826 AI422774 AW873114 AW073597 AW664483 AI218710 AW020550 AW190607 AI984545 AI871921 AI333970 AI452887 AI818335 AA398655 AI554424 AI274187 BE460573 AW512940 AW241366 AI923954 AA576649 AW168294 AA813181 AA912168 AI049738 AW514073 AA548255 AI569630 BE710031 AA244182 AI341697 AA563904 AI537990 AW517908 AW172943 Z39498 AI750294 AW150414 AI253293 BE825720 T31860 AW150775 D20310 AA150892 AU133933 BE781148 AL038957 BF910979 AA352297 BG988142 AW372175 BF229106 AW866705 BE093482 BG990396 AI499917 AA054452 H05484 AI828502 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418 BF998473 T92021 BI021048 BM048783 AW501366 AW501342 AW501549 BE939021 BE707147 BE160974 BE305207 N49011 AA947119 AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 BI919250 BI253018 AW130996 BE074249 BE895428 BI034862 BE083277 BF952166 BE883520 BI057842 AA215702 AA215703 AA368006 BE006876 BE006655
10	433009	2142268_1	
	415995	2117_1	
15			
	434372	858779_1	
	436812	659779_1	
	406799	0_0	
20	430968	1237115_1	
	418905	517_1	
25			
30	406813	0_0	
	418876	121279_1	
	447197	2176805_1	
	457068	1196_1	
35			
40			
45	440638	371165_1	
	400281	9758_4	
	406781	0_0	
	440129	2607882_1	
50	438869	52134_1	
	419970	13569_1	
55	432586	6633_1	
	426395	22291_3	
60	445093	175963_1	
	438962	195763_1	
	425097	23175_2	
65	437386	5541_2	
70	418866	245947_1	
	400244	12188_1	
75			
80	418304	1093209_1	

438141 1173217_1 AA778849 AW946871 AW946782 AW946955
 455397 1163608_1 AW936332 AW936341
 413828 9453_1 BC011603 BG479117 AU124990 BG829759 AU143705 BG701663 BG699781 AU131718 BE515064 AU121812 BG898850 AL558461 BM151887
 AU128758 BM263692 AU099013 AI241350 U88316 AW058398 AW469340 BF683967 AI470140 AU150993 AA633376 AW150821 AA536142
 AU148749 AI620647 AU151769 AU153404 AW070666 AI457758 AU153077 N99966 AW050940 BG055674 AA506657 AW301529 AI918646
 AI611235 AI266081 AI334542 AW071277 AI312434 AW303114 AI436544 AI436466 R22972 AI472987 N77886 AW072883 AA318683 D19761
 AW050566 AI312433 AA328444 R72435 AA430721 AI142599 AA582290 AU148896 AA721233 AW628132 R93935 AA100710 BI520773 AI934172
 BG222461 H85359 AW074639 AA017117 BI026412 AL582142 AA443547 AA586793 AA777535 AA693844 AI018661 AA577422 AA522800
 BG222461 H85359 AW074639 AA017117 BI026412 AL582142 AA443547 AA586793 AA777535 AA693844 AI018661 AA577422 AA522800
 BF054818 AA102378 AA757993 AA687769 R55540 AA505784 BI820705 BI767939
 AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
 BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877458 AW877537 BE076866
 AW840571
 BC004324 NM_001020 BC007977 M60854 BM050628 BG829809 BE385504 BG744451 BI826914 BE440007 BI260656 BE395117 BE389334
 BE255792 BI194169 BI668218 BI194376 BG716213 BG714408 BE392513 AV722219 AW328077 BM424171 BI828267 AW958606 BG831252
 BE392943 BE394033 BI858915 BI668334 BE621019 BG706995 BE791985 BF967484 BI193635 BG761859 BM466537 BG747165 BG827488
 AI133550 BM011511 BI227282 BG489212 BG478388 BE727789 BI160880 BG831707 BG324692 BM470427 BI083889 BG831605 BG754114
 BG420536 BF308210 BE384213 BG832271 BG828032 BG481641 BF205675 BE899041 BE271558 BI193807 BI159866 BG473786 BG397178
 BI194428 BI117210 BG768326 BG759507 BF975645 BF343657 BM020598 BG831082 BG829943 BG829501 BF306557 BE562511 BM050145
 BM017978 BI193934 BI160764 BI160371 BG754991 BF973348 BF663234 BF032537 BE388168 BM009051 BI192794 BG831002 BG830459
 BG764737 BG761808 BG481705 BG104314 BM464565 BI261500 BG831857 BG831684 BG829852 BG765030 BG760419 BG760268 BG749762
 BG480900 BG419627 BG248771 BF975542 BM042233 BI161149 BG831302 BG830033 BG829626 BM050064 BI193014 BI161360 BG822729
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 BE395269 BG832027 BG831469 BG490895 BM413638 BG943529 BG831012 BG829471 BG686284 BG337575 BG336551 BF206677 BI258301
 BI160946 BG105893 BF183072 BM459542 BI193881 BG832043 BG831323 BI194545 BI160968 BG755930 BG706018 BE743865 BM465145
 BG831227 BG774290 BF683451 BE907161 BM045391 BI194396 BI161269 BG747091 BG546643 BF984863 BI160206 BI226402 BI226336
 AW328236 BG339458 BF972634 BE909808 BI160988 BI160251 BG828764 BG826860 BG758360 BF568228 BI818282 BI457127 BG831491
 BG759864 AI830010 BF568381 BE907238 BI161172 BI16773 BG827153 BG825088 BG335419 BG109404 AI929068 BE906354 BE408564
 BM045000 BG339617 BG282794 BG335767 BE907263 BF568921 BG829961 BG479305 BG260397 AI922228 BE301975 AW516055 BG480919
 BG480626 AW196817 BG336261 BE906157 BE395717 BE391427 BI192954 BG829757 BG476379 BE301536 BE394727 BE257695 BE905344
 AI433577 BE894416 BE886992 BE409223 BF034756 BE904077 BG830886 BE909153 BE907998 BE395767 AI871751 BE744523 BI192663
 BG831669 AI000225 BE743836 BE272515 AA628078 BM463802 BE393375 BE393033 AW170187 BE730961 BE395410 BE744572 BE392297
 BE391448 BE390780 BE388821 BE258477 BE905970 BE901567 BE988833 BE880326 BF726889 BE910504 BE390753 BE390131 AA650542
 BE744156 BE394125 BE742207 BE395265 BE392942 BE894336 BE378222 BE906926 BE904650 BE393704 BE620999 BE515162 BE378753
 BE272370 BE907458 BE612801 BE392484 BE907636 BE907353 BE910491 BE909796 BE905331 AW248173 AI683576 BE908826 BE620180
 BF037570 BE908312 BE615015 BE256977 BE746875 BE394133 BE391478 BE910068 BE907185 BE742109 AA995746 BE561195 BE908825
 BE906472 BE906509 BE906017 BE910442 BE514657 BI261969 BE741707 BE392216 BM042793 BF570283 BI262119 BE395707 BE378298
 AW327827 BE394422 BF569178 BE263240 AI700512 BG830290 BF569308 BF569156 BI194587 BE390831 BG745096 AI681675 BE395674
 AA136372 BE279892 AA442822 BE384898 AA313519 AI878866 AA305904 F33366 BE394852 F29153 F33618 AI133637 AA300009 F34063
 F29455 AU099691 AI905085 AI906656 AA343249 BE388691 AW404280 AA379888 F29022 BF089981 F31013 F24305
 BE271020 AI925430 AI806151 AW129911 AA828002 AW003539 BE042625 AI287859 AW778973 AI621173 AI991000 AA846016 AW150029
 AW169748 AA649945 AI358496 AI470921 BF434211 AW513748 AW451232 AI953739 AI249448 AI040580 AI655280 AI637976 AW194345
 AW611997 AI367197 BF064039 F29558 AI537342 BF593207 AW879538 AA973211 AI674328 AW879559 BF061961 AA481914 AA426532
 AA426653 AA480106 AW243290 BF513102 BF346057 AI763358 AW003726 AI139045 AI570748 AW237602 T57492 BE887212 AI969311
 AA133045 F23464 AA576416 T15590 AI650891 AI950958 AI983931 AW515101 AI650820 H81989 AA508473
 BF828833 AI968217 BI651409 AI760574 AI147562 AW001418 AI146791 AI650589 AI952939 AI432373 AI964094 AI963870 AI420438 AI336803
 AA809634 BF590826 AA741075 BI712639 AL134637 BM264338 AA527993 AI867208 AI439038 AI684987 AI631696 AI587126 AI637622 AI651931
 AI867525 AI783674 AI638281 AI825752 AI339197 AI653411 AI341372 AI673213 AI673191 AW779768 AI627934 AI921836 AI741634 AI382284
 AI741624 AI401569 AW190430 AW196390 AI829182 AI523816 AI760522 BE505014 AI917343 BG818909 AW009307 AA927544 AA825621
 AA829400 AA527307 AI887999 AI865022 AA885063 AA653458 AA483816 AA836167 AA505879 AA421004 AA252626 AI380678 AW196980
 AA649133 AI742276 AW015700 AA595019 AA877835 AI701658 AA729793 AA535004 AA926792 AA505113 AA603726 W68390 N90130 AA489461
 AA830462

TABLE 56C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402145	8018280	Plus	113086-114800
401091	9958240	Plus	94760-94898
401466	6682292	Plus	28748-29023
401113	9966541	Minus	19419-19959
406542	7711499	Plus	117335-118473
405086	8072509	Plus	73664-73841,74081-74217,74610-74779,7492
401846	7712190	Minus	82775-82823,82912-83022
404854	7143420	Plus	14260-14537
405266	4156171	Minus	63337-63552

TABLE 57A: 703 genes upregulated in testicular cancer relative to normal body tissues

Table 57A lists about 703 genes upregulated in testicular cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 5 Pred.Protdomains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1 95th percentile of testicular cancer Als divided by the 50th percentile of normal tissues Als, where the 10th percentile of all normal tissue Als was subtracted from both the numerator and denominator

10 Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Protdomains; R1

424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase); matrix metalloproteinase 9 (gelatinase B; 31.23
 440119; AA865455; Hs.125331; ESTs, Moderately similar to unknown [H.sapiens]; ESTs, Moderately similar to unknown [H.s; 27.37
 421241; X91817; Hs.102866; transketolase-like 1; transketolase-like 1; 26.89
 15 431840; AA534908; Hs.2860; POU domain, class 5, transcription factor 1; POU domain, class 5, transcription facto; 25.03
 435918; AF263538; Hs.86232; growth differentiation factor 3; growth differentiation factor 3; 19.88
 432666; AW204069; Hs.351118; ESTs, Weakly similar to unnamed protein product [H.sapiens]; ESTs, Weakly similar to unnamed protein; 17.74
 419556; U29615; Hs.91093; chitinase 1 (chitotriosidase); chitinase 1 (chitotriosidase); 17.64
 452838; U65011; Hs.30743; preferentially expressed antigen in melanoma; preferentially expressed antigen in mela; 17.06
 20 417886; AA214584; ; ESTs; ESTs; 15.95
 412265; AA101325; Hs.86154; hypothetical protein FLJ12457; hypothetical protein FLJ12457; 15.93
 425572; AB011076; Hs.158307; undifferentiated embryonic cell transcription factor 1; undifferentiated embryonic cell transcri; 15.82
 423905; AW579960; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 15.11
 25 419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; ubiquitin carrier protein E2-C; 15.08
 427584; BE410293; Hs.179718; v-myb avian myeloblastosis viral oncogene homolog-like 2; v-myb avian myeloblastosis viral oncogen; 14.17
 418696; AW959433; Hs.326290; hypothetical protein FLJ12581; hypothetical protein FLJ12581; 13.58
 416819; U77735; Hs.80205; pim-2 oncogene; pim-2 oncogene; 13.20
 414034; U89277; Hs.305985; early development regulator 1 (homolog of polyhomeotic 1); early development regulator 1 (homolog o; 12.93
 454077; AC005952; Hs.37062; insulin-like 3 (Leydig cell); insulin-like 3 (Leydig cell); 12.90
 30 432730; AI066520; Hs.131358; ESTs; ESTs; 12.84
 446293; AI420213; Hs.149722; LIM domain transcription factor LIM-1 (hLIM-1) mRNA; LIM domain transcription factor LIM-1 (h; 12.74
 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; calcium channel, voltage-dependent, alph; 12.46
 450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta 4; 12.42
 35 450719; AI096837; Hs.21349; ESTs, Weakly similar to R88B_HUMAN RAS-RELATED PROTEIN RAB-8B [H.sapiens]; ESTs, Weakly similar to R88B_HUMAN RAS-R; 12.26
 431462; AW583672; Hs.256311; granin-like neuroendocrine peptide precursor; granin-like neuroendocrine peptide precu; 11.96
 431354; BE046956; Hs.251673; DNA (cytosine-5)-methyltransferase 3 beta; DNA (cytosine-5)-methyltransferase 3 be; 11.91
 402199; ; Target Exon; Target Exon; 11.85
 424578; AK001973; Hs.150890; hypothetical protein; hypothetical protein; 11.81
 416350; AF188625; Hs.189507; phospholipase A2, group IID; phospholipase A2, group IID; 11.67
 40 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; hypothetical protein FLJ10430; 11.57
 410048; W76467; Hs.343874; proline oxidase homolog; proline oxidase homolog; 11.42
 442573; H93366; Hs.7567; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 11.42
 414812; X72755; Hs.77367; monokine induced by gamma interferon; monokine induced by gamma interferon; 11.38
 45 421917; AB028943; Hs.109445; KIAA1020 protein; KIAA1020 protein; 11.15
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-like; NALP2 protein; PYRIN-Containing APAF1-li; 10.92
 414683; S78296; Hs.76888; hypothetical protein MGC12702; hypothetical protein MGC12702; 10.91
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage elastase); matrix metalloproteinase 12 (macrophage ; 10.74
 433800; AI034361; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 10.68
 429120; AK001673; Hs.196530; hypothetical protein FLJ10811; hypothetical protein FLJ10811; 10.48
 50 444371; BE540274; Hs.239; forkhead box M1; forkhead box M1; 10.46
 441553; AA281219; Hs.121296; ESTs; ESTs; 10.37
 426534; U58096; Hs.2051; testis specific protein, Y-linked; testis specific protein, Y-linked; 10.28
 441878; AI801869; Hs.127982; ESTs; ESTs; 10.06
 432117; AL036195; Hs.2909; protamine 1; protamine 1; 10.01
 55 425427; AI652662; Hs.317432; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 9.97
 416201; AA467752; Hs.195161; ESTs; ESTs; 9.97
 410929; H47233; Hs.30643; ESTs; ESTs; 9.91
 427486; AA974433; Hs.362432; fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene); fibroblast growth factor 4 (heparin secr; 9.81
 60 427239; BE270447; Hs.356512; ubiquitin carrier protein; ubiquitin carrier protein; 9.68
 402680; ; Target Exon; Target Exon; 9.68
 409208; Y00093; Hs.172631; integrin, alpha X (antigen CD11C (p150), alpha polypeptide); integrin, alpha X (antigen CD11C (p150)); 9.46
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; chromosome 20 open reading frame 1; 9.42
 440207; AI371978; Hs.128326; ESTs; ESTs; 9.41
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; clone HQ0310 PRO0310p1; 9.41
 65 447534; AW953935; Hs.288655; ESTs; ESTs; 9.33
 442333; AI650877; Hs.129302; ESTs; ESTs; 9.28
 421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp434B0425 (from clone DKFZp434B0425); Homo sapiens mRNA; cDNA DKFZp434B0425 (f; 9.24
 423458; AI204212; Hs.351113; ESTs; ESTs; 9.23
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placental); cadherin 3, type 1, P-cadherin (placenta); 9.23
 70 422938; NM_001809; Hs.1594; centromere protein A (17kD); centromere protein A (17kD); 9.21
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 9.21
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); topoisomerase (DNA) II alpha (170kD); 9.18
 428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosophila)-like; similar to SALL1 (sal (Drosophila)-like; 9.17
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabotropic glutamate family GPCR; retinoic acid induced 3 (RAIG1); metabo; 9.11
 75 447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient, yeast, homolog)-like 2; MAD2 (mitotic arrest deficient, yeast, h; 9.11
 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 9.10
 449722; BE280074; Hs.23960; cyclin B1; cyclin B1; 8.86
 441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 8.86
 440983; M20681; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; solute carrier family 2 (facilitated glu; 8.86
 80 409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; BRCA1 associated RING domain 1; 8.83
 420367; AA259090; Hs.257028; ESTs; ESTs; 8.82
 415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1); mutS (E. coli) homolog 2 (colon cancer, ; 8.73
 418613; AA744529; Hs.85575; mitogen-activated protein kinase kinase kinase kinase kinase 1; mitogen-activated protein kinase kinase ; 8.71

- 417407; AA923278; Hs.290905; ESTs, Weakly similar to protease [H.sapiens]; ESTs, Weakly similar to protease [H.sapi]; 8.64
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 8.58
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-conjugating enzyme; HSPC150 protein similar to ubiquitin-con; 8.55
 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like (rabkinesin 6); RAB6 interacting, kinesin-like (rabkines); 8.52
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group 1, member 3; nuclear receptor subfamily 1, group 1, m; 8.51
 424800; AL035588; Hs.153203; MyoD family inhibitor; MyoD family inhibitor; 8.45
 447188; H65423; Hs.17631; hypothetical protein DKFZp434E2135; hypothetical protein DKFZp434E2135; 8.45
 430056; X97548; Hs.228059; KRAB-associated protein 1; KRAB-associated protein 1; 8.42
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor 2); midkine (neurite growth-promoting factor); 8.40
 430676; AF084866; Hs.372585; gb:Homo sapiens envelope protein RIC-3 (env) gene, complete cd; gb:Homo sapiens envelope protein RIC-3 (; 8.38
 420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.38
 406621; X57809; Hs.181125; immunoglobulin lambda locus; immunoglobulin lambda locus; 8.37
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; fructose-1,6-bisphosphatase 1; 8.25
 423198; M81933; Hs.1634; cell division cycle 25A; cell division cycle 25A; 8.19
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin, beta 2 (antigen CD18 (p95), ly; 8.17
 453968; AA847843; Hs.627111; High mobility group (nonhistone chromosomal) protein 4; High mobility group (nonhistone chromoso; 8.16
 453985; N44545; Hs.251865; ESTs; ESTs; 8.14
 451108; BE382701; Hs.25960; N-MYC oncogene; N-MYC oncogene; 8.10
 420347; AL033539; Hs.97124; Human DNA sequence from clone RP1-309H15 on chromosome 6p22.1-22.3 Contains a gene similar to HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)), ESTs, STGs, GSSs and a CpG Is; Human DNA sequence from clone RP1-309H15; 8.03
 415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.02
 425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; GSK-3 binding protein FRAT2; 7.90
 421016; AA504583; Hs.101047; transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47); transcription factor 3 (E2A immunoglobul; 7.89
 432407; AA221036; ; gb:z03f12.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ; mRNA sequence; gb:z03f12.r1 Stratagene NT2 neuronal pr; 7.83
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); neutrophil cytosolic factor 1 (47kD, chr; 7.80
 433228; F28212; Hs.14953; KIAA1491 protein; KIAA1491 protein; 7.73
 446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); nucleolar protein 1 (120kD); 7.71
 447350; AI375572; Hs.172634; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 7.71
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; nudix (nucleoside diphosphate linked moi; 7.71
 430253; AK001514; Hs.1572; hypothetical protein FLJ10652; hypothetical protein FLJ10652; 7.70
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1); ectonucleotide pyrophosphatase/phosphodi; 7.62
 443537; D13305; Hs.203; cholecystokinin B receptor; cholecystokinin B receptor; 7.57
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; interferon, gamma-inducible protein 30; 7.55
 410006; AW732308; Hs.57783; eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD); eukaryotic translation initiation factor; 7.53
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551 protein, partial cds; Homo sapiens mRNA for KIAA1551 protein, ; 7.52
 411975; AI916058; Hs.144583; 3'UTR of: dead ringer (Drosophila)-like 1; 3'UTR of: dead ringer (Drosophila)-like ; 7.50
 439864; AI720078; Hs.291997; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 7.47
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN cDNA 2700083B06 gene, clone MGC:4669, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 2700; 7.47
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; hypothetical protein FLJ14541; 7.47
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; protein tyrosine phosphatase, receptor t; 7.47
 407710; AW022727; Hs.23616; ESTs; ESTs; 7.45
 445093; AI207197; Hs.374149; ESTs; ESTs; 7.41
 418113; AI272141; Hs.83484; SRY (sex determining region Y)-box 4; SRY (sex determining region Y)-box 4; 7.39
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevisiae, homolog); CDC20 (cell division cycle 20, S. cerevi; 7.37
 429469; M64590; Hs.111801; glycine dehydrogenase (decarboxylating); glycine decarboxylase, glycine cleavage system protein P; glycine dehydrogenase (decarboxylating; ; 7.33
 422726; U11690; Hs.1572; faciogenital dysplasia (Aarskog-Scott syndrome); faciogenital dysplasia (Aarskog-Scott sy; 7.33
 430504; H52761; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 7.32
 448981; AI968719; Hs.195387; ESTs; ESTs; 7.28
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); FK506-binding protein 4 (59kD); 7.26
 435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; Homo sapiens mRNA; cDNA DKFZp761E13121 ; 7.25
 434414; AI798376; ; gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ; mRNA sequence; gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens; 7.24
 428977; AK001404; Hs.194698; cyclin B2; cyclin B2; 7.19
 434274; AA628539; Hs.57783; ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Moderately similar to ALU1_HUMAN A; 7.19
 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc f; Human DNA sequence from clone RP11-145L2; 7.16
 420524; AB010575; Hs.98547; amiloride-sensitive cation channel 3, testis; amiloride-sensitive cation channel 3, te; 7.15
 439053; BE244588; Hs.6456; chaperonin containing TCP1, subunit 2 (beta); chaperonin containing TCP1, subunit 2 (b; 7.14
 445076; AI206888; Hs.154131; ESTs; ESTs; 7.14
 448588; AI970276; Hs.156905; KIAA1676; KIAA1676; 7.13
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; hypothetical protein FLJ10339; 7.10
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E coli RecA homolog); RAD51 (S. cerevisiae) homolog (E coli Re; 7.04
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homolog (PIF1) mRNA, partial cds; Homo sapiens DNA helicase homolog (PIF1); 7.02
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; interferon-stimulated protein, 15 kDa; 7.02
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840937, mRNA, partial cds; Homo sapiens, clone IMAGE:3840937, mRNA.; 6.96
 416658; U03272; Hs.79432; fibrillin 2 (congenital contractural arachnodactyly); fibrillin 2 (congenital contractural ara; 6.92
 438450; AI050866; Hs.65853; nodal, mouse, homolog; nodal, mouse, homolog; 6.90
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); neutrophil cytosolic factor 2 (65kD, chr; 6.90
 444381; BE387335; Hs.283713; hypothetical protein BC014245; hypothetical protein BC014245; 6.89
 447582; BE293520; Hs.18910; prostate cancer overexpressed gene 1; prostate cancer overexpressed gene 1; 6.89
 424779; AL046851; Hs.153053; CD37 antigen; CD37 antigen; 6.89
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding protein; TYRO protein tyrosine kinase binding pro; 6.84
 427298; AA400495; ; ESTs; ESTs; 6.82
 414732; AW410976; Hs.77152; minichromosome maintenance deficient (S. cerevisiae) 7; minichromosome maintenance deficient (S.; 6.81
 424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; activated p21cdc42Hs kinase; 6.81
 426866; U02330; Hs.172816; neuregulin 1; neuregulin 1; 6.80
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CDC28 protein kinase 2; 6.80
 427521; AW973352; ; ESTs; ESTs; 6.75
 430397; AI924533; Hs.105607; bicarbonate transporter related protein 1; bicarbonate transporter related protein ; 6.75
 427719; AI393122; Hs.134726; ESTs; ESTs; 6.74

- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; thyroid hormone receptor interactor 13; 6.72
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; hypothetical protein FLJ12438; 6.71
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083 protein, partial cds; Homo sapiens mRNA for FLJ00083 protein, ; 6.70
 445363; NM_005993; Hs.12570; tubulin-specific chaperone d; tubulin-specific chaperone d; 6.70
 433701; AW445023; Hs.15155; ESTs; ESTs; 6.69
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lysyl oxidase-like 2; 6.63
 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen, B beta polypeptide; 6.62
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 6.59
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); protein kinase Chk2 (CHEK2); 6.58
 414821; M83835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Fc fragment of IgG, high affinity Ia, re; 6.58
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; acid phosphatase 5, tartrate resistant; 6.57
 414161; AA136106; Hs.184852; KIAA1553 protein; KIAA1553 protein; 6.57
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L0311; hypothetical protein DKFZp762L0311; 6.55
 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA, complete cds; Human RPL13-2 pseudogene mRNA, complete ; 6.55
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; Homo sapiens, Similar to complement comp; 6.55
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); baculoviral IAP repeat-containing 5 (sur; 6.51
 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin); minichromosome maintenance deficient (S.; 6.50
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; CD2 antigen (p50), sheep red blood cell; 6.49
 417911; AA333387; Hs.82916; chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing TCP1, subunit 6A (zeta 1); 6.44
 427747; AW411425; Hs.180655; serine/threonine kinase 12; serine/threonine kinase 12; 6.43
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; SMC4 (structural maintenance of chromoso; 6.42
 430280; AA361258; Hs.237868; interleukin 7 receptor; interleukin 7 receptor; 6.42
 432938; T27013; Hs.3132; steroidogenic acute regulatory protein; steroidogenic acute regulatory protein; 6.42
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; hypothetical protein FLJ10549; 6.40
 427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3_HUMAN TUBBY RELATED PROTEIN 3 [H.sapiens]; ESTs, Highly similar to TUL3_HUMAN TUBBY; 6.40
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; small nuclear ribonucleoprotein polypept; 6.39
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cys-X-Cys), member 10; small inducible cytokine subfamily B (Cy; 6.39
 441384; AA447849; Hs.288660; retinoic acid induced 3; retinoic acid induced 3; 6.38
 438915; AA280174; Hs.285681; Williams-Beuren syndrome chromosome region 14; Williams-Beuren syndrome chromosome regi; 6.34
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; hypothetical protein FLJ20333; 6.34
 451999; AW176401; Hs.27424; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase); DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; 6.31
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like 2 (bright and dead ringer); dead ringer (Drosophila)-like 2 (bright ; 6.31
 425274; BE281191; Hs.155462; minichromosome maintenance deficient (mis5, S. pombe) 6; minichromosome maintenance deficient (mi; 6.31
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350 transcription repressor protein YY1 [H.sapiens]; ESTs, Highly similar to A40350 transcrip; 6.30
 420507; AF093408; Hs.98397; A kinase (PRKA) anchor protein 3; A kinase (PRKA) anchor protein 3; 6.30
 415829; AW450198; Hs.163742; ESTs; ESTs; 6.28
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; Fc fragment of IgE, high affinity I, rec; 6.26
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil related protein; mitotic spindle coiled-coil related prot; 6.25
 457465; AW301344; Hs.122908; DNA replication factor; DNA replication factor; 6.25
 428918; AL036967; Hs.2324; protamine 2; protamine 2; 6.24
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; hypothetical protein FLJ10713; 6.19
 424415; NM_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase 2, (gamma, neuronal); 6.19
 407245; X90568; Hs.172004; titin; titin; 6.18
 458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (SOX17); SRY (sex determining region Y)-box 17 (S; 6.18
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cys-X-Cys), member 11; small inducible cytokine subfamily B (Cy; 6.16
 435099; AC004770; Hs.4756; flap structure-specific endonuclease 1; flap structure-specific endonuclease 1; 6.13
 424308; AW975531; Hs.154443; minichromosome maintenance deficient (S. cerevisiae) 4; minichromosome maintenance deficient (S.; 6.12
 430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; HOM-TES-85 tumor antigen; 6.10
 444823; BE262989; Hs.12045; putative protein; putative protein; 6.10
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; solute carrier family 7 (cationic amino ; 6.09
 402260; ; NM_001436; Homo sapiens fibrillarin (FBL), mRNA. transcript (F8A), mRNA.; NM_001436; Homo sapiens fibrillarin (FBL); 6.09
 441321; H17182; Hs.7771; B-cell associated protein; B-cell associated protein; 6.05
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like; CDC45 (cell division cycle 45, S.cerevis; 6.04
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); interferon, alpha-inducible protein (clo; 6.04
 402678; ; Target Exon; Target Exon; 6.03
 453884; AA355925; Hs.36232; KIAA0186 gene product; KIAA0186 gene product; 6.01
 439753; BE262233; Hs.7423; hypothetical protein from EUROIMAGE 2168212; hypothetical protein from EUROIMAGE 2168; 6.01
 420596; NM_002692; Hs.99185; polymerase (DNA directed), epsilon 2; polymerase (DNA directed), epsilon 2; 6.01
 420676; AI434780; Hs.4248; vav 2 oncogene; vav 2 oncogene; 6.00
 418756; AA252254; Hs.226949; ESTs; ESTs; 5.99
 454438; AA224053; Hs.172405; cell division cycle 27; cell division cycle 27; 5.98
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; jumonji (mouse) homolog; 5.98
 413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; glycyl-tRNA synthetase; 5.96
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lysozyme (renal amyloidosis); 5.95
 417777; AI823763; Hs.7055; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; ESTs, Weakly similar to I78885 serine/th; 5.94
 449569; AI656634; Hs.195389; ESTs; ESTs; 5.92
 436576; AI458213; Hs.77542; ESTs; ESTs; 5.90
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; Human melanoma-associated antigen p97 (m; 5.89
 420005; AW271106; Hs.133294; ESTs; ESTs; 5.89
 417208; S67773; Hs.81665; v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog; v-kit Hardy-Zuckerman 4 feline sarcoma v; 5.88
 403171; ; C2001472; gi|5809678|gb|AAB41848.2| (U64675) sperm membrane protein BS-63 [Homo sapiens]||; C2001472; gi|5809678|gb|AAB41848.2| (U64; 5.87
 448730; AB032983; Hs.21894; KIAA1157 protein; KIAA1157 protein; 5.87
 406137; ; NM_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA. VERSION NM_000178.1 GI; NM_000179; Homo sapiens mutS (E. coli) h; 5.85
 423787; AJ295745; Hs.236204; nuclear pore complex protein; nuclear pore complex protein; 5.85
 425126; N32759; Hs.172944; chorionic gonadotropin, beta polypeptide; chorionic gonadotropin, beta polypeptide; 5.84
 452796; AB011100; Hs.30656; KIAA0528 gene product; KIAA0528 gene product; 5.84
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); cyclin-dependent kinase inhibitor 3 (CDK; 5.80
 447359; NM_012093; Hs.18268; adenylate kinase 5; adenylate kinase 5; 5.79
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; putative G protein-coupled receptor; 5.78
 420297; AI628272; Hs.128757; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU1_HUMAN ALU S; 5.75
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila) homolog 2; enhancer of zeste (Drosophila) homolog 2; 5.75

- 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5_HUMAN LEUKEMIA ASSOCIATED PROTEIN 5 [H.sapiens]; ESTs, Weakly similar to LEU5_HUMAN LEUKE; 5.74
 436251; BE515065; Hs.296585; nucleolar protein (KKE/D repeat); nucleolar protein (KKE/D repeat); 5.73
 421535; AB002359; Hs.105478; phosphoribosylformylglycinamide synthase (FGAR amidotransferase); phosphoribosylformylglycinamide synthase; 5.71
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CDC28 protein kinase 1; 5.69
 425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; carbamoyl-phosphate synthetase 2, aspartate; 5.69
 401704; ; NM_021195; Homo sapiens claudin 6 (CLDN6), mRNA, VERSION NM_020982.1 GI; NM_021195; Homo sapiens claudin 6 (CLDN6); 5.66
 425358; AL079658; Hs.338207; FK506 binding protein 12-rapamycin associated protein 1; FK506 binding protein 12-rapamycin associated protein 1; 5.65
 402677; ; NM_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA, alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM_000478; Homo sapiens alkaline phosphatase; 5.64
 409264; NM_014937; Hs.52463; KIAA0966 protein; KIAA0966 protein; 5.63
 432185; AA221032; Hs.272838; hypothetical protein FLJ10494; hypothetical protein FLJ10494; 5.63
 409012; AL117435; Hs.49725; DKFZP434I216 protein; DKFZP434I216 protein; 5.63
 430252; AL638774; Hs.105328; testes development-related NYD-SP20; testes development-related NYD-SP20; 5.61
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeast homolog)-like; chromosome segregation 1 (yeast homolog); 5.61
 452816; AA131789; Hs.61509; ESTs; ESTs; 5.60
 402679; ; NM_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA, alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM_000478; Homo sapiens alkaline phosphatase; 5.59
 414291; AL289619; Hs.13040; G protein-coupled receptor 86; G protein-coupled receptor 86; 5.58
 453028; AB006532; Hs.31442; RecQ protein-like 4; RecQ protein-like 4; 5.58
 453905; NM_002314; Hs.36566; LIM domain kinase 1; LIM domain kinase 1; 5.56
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin-like 6 (mitotic centromere-associated kinesin); 5.55
 419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; solute carrier family 7 (cationic amino acid transporter, y system), member 7; 5.55
 446979; AL654443; Hs.197683; ESTs; ESTs; 5.54
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; lymphocyte-specific protein tyrosine kinase; 5.53
 418962; AA714835; Hs.271863; ESTs; ESTs; 5.53
 447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, complete cds; 5.52
 427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180)), lymphocyte function-associated antigen 1; alpha polypeptide; integrin, alpha L (antigen CD11A (p180)); 5.52
 449322; AL638616; Hs.196566; ESTs; ESTs; 5.51
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KIAA0175 gene product; 5.51
 415141; AA189099; Hs.268171; ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU7_HUMAN ALU S; 5.48
 454048; H05626; Hs.6921; ESTs; ESTs; 5.46
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; interleukin 1 receptor antagonist; 5.45
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 f1s, clone HEMBB1001304; Homo sapiens cDNA FLJ11980 f1s, clone HE; 5.44
 414334; AA824298; Hs.21331; hypothetical protein FLJ10036; hypothetical protein FLJ10036; 5.44
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; 5.44
 438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; major histocompatibility complex, class II, DQ alpha 1; 5.44
 427668; AA298760; Hs.180191; hypothetical protein FLJ14904; hypothetical protein FLJ14904; 5.43
 449437; AL702038; Hs.100057; Homo sapiens cDNA: FLJ22902 f1s, clone KAT05581; Homo sapiens cDNA: FLJ22902 f1s, clone K; 5.41
 453633; AA357001; Hs.34045; hypothetical protein FLJ20764; hypothetical protein FLJ20764; 5.40
 450746; D82673; Hs.278589; general transcription factor II, i; general transcription factor II, i; 5.40
 425966; NM_001761; Hs.1973; cyclin F; cyclin F; 5.39
 418134; AA397769; Hs.86617; ESTs; ESTs; 5.38
 432141; BE410964; Hs.272736; nuclear receptor binding protein; nuclear receptor binding protein; 5.37
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, member 3; nuclear receptor subfamily 1, group H, member 3; 5.36
 428329; AA426091; Hs.98453; ESTs, Moderately similar to R27328 2 [H.sapiens]; ESTs, Moderately similar to R27328 2 [H.sapiens]; 5.35
 406811; U82979; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; 5.34
 415819; AU077330; Hs.360791; transcription elongation factor A (SII), 1; transcription elongation factor A (SII), 1; 5.33
 448133; AA723157; Hs.73769; folate receptor 1 (adult); folate receptor 1 (adult); 5.33
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor 4 gamma, 2; eukaryotic translation initiation factor 4 gamma, 2; 5.32
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypeptide 1; 5.32
 429271; AF039850; Hs.198515; dead ringer (Drosophila)-like 1; dead ringer (Drosophila)-like 1; 5.32
 456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); 5.30
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; polo (Drosophila)-like kinase; 5.30
 422997; BE018212; Hs.122908; DNA replication factor; DNA replication factor; 5.29
 440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; 5.28
 418399; AF131781; Hs.84753; hypothetical protein FLJ12442; hypothetical protein FLJ12442; 5.26
 416178; AL808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; serologically defined breast cancer antigen NY-BR-81; 5.21
 450377; AB033091; Hs.355925; KIAA1265 protein; KIAA1265 protein; 5.20
 409670; AL368109; Hs.375604; KIAA1856 protein; KIAA1856 protein; 5.20
 429083; Y09397; Hs.227817; BCL2-related protein A1; BCL2-related protein A1; 5.20
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; chemokine (C-C motif) receptor 5; 5.20
 408908; BE296227; Hs.250822; serine/threonine kinase 15; serine/threonine kinase 15; 5.19
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); 5.19
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, member 3; 5.16
 437623; D63880; Hs.5719; chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-associated protein 1; 5.15
 448181; AF272833; Hs.279763; hypothetical protein FLJ10504; hypothetical protein FLJ10504; 5.15
 436540; BE397032; Hs.14468; hypothetical protein MGC14226; hypothetical protein MGC14226; 5.14
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; protein tyrosine phosphatase, receptor type, C; 5.14
 426752; X69490; Hs.172004; titin; titin; 5.13
 415007; BE244332; Hs.77770; adaptor-related protein complex 3, mu 2 subunit; adaptor-related protein complex 3, mu 2 subunit; 5.13
 400263; ; Hs.75309; Eos Control; Eos Control; 5.13
 437099; N77793; Hs.48659; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; 5.12
 427209; H06509; Hs.92423; KIAA1566 protein; KIAA1566 protein; 5.10
 407347; AA829847; ; gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1370413 3' similar to contains Alu repetitive element, mRNA sequence.; gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens; 5.10
 458933; AL638429; Hs.24763; RAN binding protein 1; RAN binding protein 1; 5.10
 450431; AW136797; Hs.266041; ESTs; ESTs; 5.09
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 5.08
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; protein tyrosine phosphatase, non-receptor type 6; 5.08
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Human T-cell receptor active alpha-chain; 5.05
 412723; AA648459; Hs.335951; hypothetical protein AF301222; hypothetical protein AF301222; 5.05

- 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 5.03
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; collagen, type XI, alpha 1; 5.03
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; Musashi (Drosophila) homolog 1; 5.02
 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog) 1; deleted in oral cancer (mouse, homolog) ; 5.02
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); karyopherin alpha 2 (RAG cohort 1, importin alpha 1); 5.00
 425237; U07695; Hs.155227; EphB4; EphB4; 5.00
 414809; A1434699; Hs.77356; transferrin receptor (p90, CD71); transferrin receptor (p90, CD71); 4.99
 402145; ; Target Exon; Target Exon; 4.99
 432126; AA865239; Hs.37196; ESTs; ESTs; 4.99
 408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 4.98
 419525; T79257; Hs.1259; asialoglycoprotein receptor 2; asialoglycoprotein receptor 2; 4.97
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; ligase I, DNA, ATP-dependent; 4.97
 427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis, clone NT2RP1000112; Homo sapiens cDNA FLJ10417 fis, clone NT; 4.96
 457313; AF047002; Hs.241520; transcriptional coactivator; transcriptional coactivator; 4.96
 448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; signal transducer and activator of trans; 4.94
 426427; M86699; Hs.169840; TTK protein kinase; TTK protein kinase; 4.91
 440129; AA865818; Hs.369523; ESTs, Weakly similar to S71886 Ste20-like protein kinase [H.sapiens]; ESTs, Weakly similar to S71886 Ste20-lik; 4.91
 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; budding uninhibited by benzimidazoles 1 ; 4.90
 435602; AF217515; Hs.283532; uncharacterized bone marrow protein BM039; uncharacterized bone marrow protein BM03; 4.89
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; chemokine (C-C motif) receptor 1; 4.88
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; hypothetical protein FLJ12538 similar to; 4.88
 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; thyroid hormone receptor coactivating pr; 4.87
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIG51) mRNA, complete cds; Homo sapiens cysteine knot protein (ZSIG; 4.87
 421350; AW301608; Hs.278188; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene; 4.87
 409093; BE243834; Hs.50441; CGI-04 protein; CGI-04 protein; 4.86
 424304; NM_001395; Hs.144879; dual specificity phosphatase 9; dual specificity phosphatase 9; 4.86
 437696; Z83844; Hs.5790; hypothetical protein dJ37E16.5; hypothetical protein dJ37E16.5; 4.86
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; solute carrier family 23 (nucleobase tra; 4.84
 416445; AL043004; Hs.79337; KIAA0135 protein; KIAA0135 protein; 4.83
 448939; BE267795; Hs.22595; hypothetical protein FLJ10637; hypothetical protein FLJ10637; 4.82
 413566; AW604451; Hs.285814; sprouty (Drosophila) homolog 4; sprouty (Drosophila) homolog 4; 4.82
 424081; NM_006413; Hs.139120; ribonuclease P (30kD); ribonuclease P (30kD); 4.81
 425474; Z48054; Hs.158084; peroxisome receptor 1; peroxisome receptor 1; 4.81
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); macrophage migration inhibitory factor (; 4.81
 422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapiens cDNA, mRNA sequence; gb:RC3-CT0297-290100-013-d03 CT0297 Homo; 4.80
 409101; NM_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide binding protein (G pr; 4.79
 412760; AW379030; Hs.41324; ESTs; ESTs; 4.79
 447250; A1878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; protein phosphatase 1G (formerly 2C), ma; 4.79
 429345; R11141; Hs.199695; hypothetical protein; hypothetical protein; 4.78
 448950; AF288687; Hs.9275; CGI-152 protein; CGI-152 protein; 4.78
 412926; A1879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; macrophage myristoylated alanine-rich C ; 4.78
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; heat shock 90kD protein 1, beta; 4.76
 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 4.76
 421905; A1660247; Hs.32699; ESTs, Weakly similar to LIV-1 protein [H.sapiens]; ESTs, Weakly similar to LIV-1 protein [H]; 4.75
 413880; A1660842; Hs.110915; interleukin 22 receptor; interleukin 22 receptor; 4.75
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2 (NEK2); NIMA (never in mitosis gene a)-related k; 4.74
 418355; L42563; Hs.1165; ATPase, H⁺ transporting, nongastric, alpha polypeptide; ATPase, H⁺ transporting, nongastric, alp; 4.74
 435905; AW997484; Hs.5003; KIAA0456 protein; KIAA0456 protein; 4.74
 428024; Z29067; Hs.2236; NIMA (never in mitosis gene a)-related kinase 3; NIMA (never in mitosis gene a)-related k; 4.74
 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; protein kinase C substrate 80K-H; 4.72
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ryanodine receptor 1 (skeletal); 4.72
 437296; AA350994; Hs.20281; KIAA1700; KIAA1700; 4.70
 450142; AW207469; Hs.24485; chondroitin sulfate proteoglycan 6 (bamacan); chondroitin sulfate proteoglycan 6 (bama; 4.70
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism); fibroblast growth factor receptor 3 (ach; 4.69
 449475; A1348027; Hs.129826; hypothetical protein PP1057; hypothetical protein PP1057; 4.69
 420062; AW411096; Hs.94785; TGF(beta)-induced transcription factor 2; TGF(beta)-induced transcription factor 2; 4.69
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1; cytochrome P450, subfamily XXVIIIB (25-hy; 4.69
 436856; A1469355; Hs.127310; ESTs; ESTs; 4.68
 406937; U14622; ; gb:Human transketolase-like protein gene, partial cds.; gb:Human transketolase-like protein gene; 4.67
 411296; BE207307; Hs.10114; growth suppressor 1; growth suppressor 1; 4.67
 426726; AA488915; Hs.171955; trophinin associated protein (lastin); trophinin associated protein (lastin); 4.67
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; protein kinase, AMP-activated, beta 2 no; 4.67
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; melanoma cell adhesion molecule; 4.66
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; hypothetical protein FLJ20371; 4.65
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; complement component 1, q subcomponent, ; 4.65
 441595; AW206035; Hs.356457; ESTs; ESTs; 4.64
 423419; R55336; Hs.23539; ESTs; ESTs; 4.64
 415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SMase) activation associated factor; neutral sphingomyelinase (N-SMase) activ; 4.63
 435045; BE297155; Hs.143698; ESTs; ESTs; 4.62
 424441; X14850; Hs.147097; H2A histone family, member X; H2A histone family, member X; 4.62
 414972; BE263782; Hs.77695; KIAA0008 gene product; KIAA0008 gene product; 4.62
 436685; W28661; Hs.5288; Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245); Homo sapiens mRNA; cDNA DKFZp434M245 (fr; 4.62
 449515; A1653378; Hs.302012; ESTs; ESTs; 4.61
 425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; fibroblast growth factor receptor 4; 4.61
 420027; AF009746; Hs.94395; ATP-binding cassette, sub-family D (ALD), member 4; ATP-binding cassette, sub-family D (ALD); 4.61
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; Down syndrome critical region gene 2; 4.61
 413441; A1929374; Hs.75367; Src-like-adaptor; Src-like-adaptor; 4.60
 456847; A1360456; Hs.86088; ESTs; ESTs; 4.58
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; thymidine kinase 1, soluble; 4.57
 426935; NM_000088; Hs.172928; collagen, type I, alpha 1; collagen, type I, alpha 1; 4.57
 428782; X12830; Hs.193400; interleukin 6 receptor; interleukin 6 receptor; 4.56
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; splicing factor, arginine/serine-rich 5; 4.56
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; similar to vaccinia virus HindIII K4L ORF; 4.55

- 443068; A1188710; Hs.374480; ESTs; ESTs; 4.55
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; neuronal cell adhesion molecule; 4.54
 453227; AW135862; Hs.243991; ESTs; ESTs; 4.52
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; Homo sapiens cDNA FLJ13655 fis, clone PL; 4.51
 422565; BE259035; Hs.118400; singed (Drosophila)-like (sea urchin fascin homolog like); singed (Drosophila)-like (sea urchin fas); 4.51
 453613; F06838; Hs.374476; ESTs; ESTs; 4.50
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); stress-induced-phosphoprotein 1 (Hsp70/H; 4.50
 412507; L36645; Hs.73964; EphA4; EphA4; 4.50
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; hemopoietic cell kinase; 4.49
 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); ubiquitin-conjugating enzyme E2N (homolo; 4.49
 406547; ; Target Exon; Target Exon; 4.49
 443216; W80487; Hs.324521; hypothetical protein DC50; hypothetical protein DC50; 4.48
 417497; AVW402482; Hs.82212; CD53 antigen; CD53 antigen; 4.47
 448595; AB014544; Hs.21572; KIAA0644 gene product; KIAA0644 gene product; 4.47
 445350; AF052112; Hs.12540; lysophospholipase I; lysophospholipase I; 4.46
 446236; NM_006293; Hs.301; TYRO3 protein tyrosine kinase; TYRO3 protein tyrosine kinase; 4.46
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; smoothened (Drosophila) homolog; 4.46
 420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TIT3 complex); CD3Z antigen, zeta polypeptide (TIT3 com; 4.46
 413426; U88837; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; GCN1 (general control of amino-acid synt; 4.44
 421819; NM_013403; Hs.108665; zinedin; zinedin; 4.44
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; melanoma differentiation associated prot; 4.44
 428995; AW004975; Hs.194716; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; MAD (mothers against decapentaplegic, Dr; 4.43
 434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; ESTs, Highly similar to A35661 DNA excis; 4.43
 418295; AW970043; Hs.238039; hypothetical protein FLJ11090; hypothetical protein FLJ11090; 4.42
 409243; AB037761; Hs.51743; KIAA1340 protein; KIAA1340 protein; 4.42
 437103; AW139408; Hs.152940; ESTs; ESTs; 4.42
 413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic acid transporters), member 1; solute carrier family 16 (monocarboxylic; 4.42
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 4.40
 424078; AB006625; Hs.139033; paternally expressed 3; paternally expressed 3; 4.39
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; HMT1 (hnRNP methyltransferase, S. cerevi; 4.37
 410134; U68140; Hs.58927; nuclear VCP-like; nuclear VCP-like; 4.36
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; membrane-spanning 4-domains, subfamily A; 4.35
 400440; X83957; Hs.83870; nebulin; nebulin; 4.35
 437218; AL117497; Hs.58185; ESTs, Weakly similar to T42727 proliferation potential-related protein - mouse [M.musculus]; ESTs, Weakly similar to T42727 prolifera; 4.34
 430478; NM_014349; Hs.241535; apolipoprotein L, 3; apolipoprotein L, 3; 4.34
 432744; AA988835; Hs.38664; ESTs; ESTs; 4.33
 423173; AA442655; Hs.124942; protein phosphatase 2A 48 kDa regulatory subunit; protein phosphatase 2A 48 kDa regulatory; 4.33
 415995; NM_004573; Hs.355888; phospholipase C, beta 2; phospholipase C, beta 2; 4.33
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; hypothetical protein FLJ13912; 4.30
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A (sperm receptor); zona pellucida glycoprotein 3A (sperm re; 4.30
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; tumor necrosis factor receptor superfami; 4.29
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; Human proteinase activated receptor-2 mR; 4.29
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); Fc fragment of IgG, low affinity IIb, r; 4.29
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; pyruvate dehydrogenase phosphatase; 4.29
 412314; AA825247; Hs.356084; downstream of: G protein-coupled receptor 27 (GPR27) (SREB1); downstream of: G protein-coupled recepto; 4.28
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; protein tyrosine phosphatase, receptor t; 4.28
 426108; AA622037; Hs.166468; programmed cell death 5; programmed cell death 5; 4.28
 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); integrin, alpha M (complement component ; 4.27
 437908; A1082424; Hs.351043; ESTs; ESTs; 4.27
 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; map kinase phosphatase-like protein MK-S; 4.27
 429002; AW248439; Hs.2340; junction plakoglobin; junction plakoglobin; 4.26
 439334; A1148976; Hs.112062; ESTs; ESTs; 4.26
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan receptor 2; receptor tyrosine kinase-like orphan rec; 4.25
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; interleukin 2 receptor, beta; 4.25
 453648; W21493; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 4.24
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 4.24
 447528; A1612027; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 4.23
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; solute carrier family 37 (glycerol-3-pho; 4.22
 449810; AB008681; Hs.23994; activin A receptor, type IIB; activin A receptor, type IIB; 4.22
 447198; D61523; Hs.283435; ESTs; ESTs; 4.22
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); CD79A antigen (immunoglobulin-associated; 4.22
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 145kD; inositol polyphosphate-5-phosphatase, 14; 4.22
 422605; H16646; Hs.118666; hypothetical protein PP591; hypothetical protein PP591; 4.21
 444535; AF011466; Hs.122575; EDG-4 (endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4); EDG-4(endothelial differentiation, lys; 4.21
 417088; M54915; Hs.81170; pim-1 oncogene; pim-1 oncogene; 4.20
 421707; NM_014921; Hs.107054; lectomedin-2; lectomedin-2; 4.20
 408717; AF045458; Hs.47061; unc-51 (C. elegans)-like kinase 1; unc-51 (C. elegans)-like kinase 1; 4.20
 438485; W57578; Hs.378718; RAB7, member RAS oncogene family; RAB7, member RAS oncogene family; 4.19
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; PTK7 protein tyrosine kinase 7; 4.18
 418755; Y14443; Hs.88219; zinc finger protein 200; zinc finger protein 200; 4.18
 417212; AW952823; Hs.351547; NS1-binding protein; NS1-binding protein; 4.17
 413686; A1469213; Hs.71404; ESTs; ESTs; 4.17
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); diacylglycerol kinase, zeta (104kD); 4.16
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); chemokine (C-X-C motif), receptor 4 (fus; 4.16
 408482; NM_000676; Hs.45743; adenosine A2b receptor; adenosine A2b receptor; 4.16
 422391; D63479; Hs.115907; diacylglycerol kinase, delta (130kD); diacylglycerol kinase, delta (130kD); 4.15
 409421; AA199883; Hs.67624; ESTs; ESTs; 4.15
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; A kinase (PRKA) anchor protein 1; 4.14
 415198; AW009480; Hs.943; natural killer cell transcript 4; natural killer cell transcript 4; 4.14
 424685; W21223; Hs.151734; nuclear transport factor 2 (placental protein 15); nuclear transport factor 2 (placental pr; 4.13

428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; cell division cycle 2, G1 to S and G2 to; 4.13
 423728; AW891294; Hs.132136; solute carrier family 4, sodium bicarbonate cotransporter, member 8; solute carrier family 4, sodium bicarbon; 4.13
 433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; Ts translation elongation factor, mitoch; 4.13
 420253; A1656055; Hs.96200; neighbor of A-kinase anchoring protein 95; neighbor of A-kinase anchoring protein 9; 4.12
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; DNA segment on chromosome 12 (unique) 24; 4.12
 400205; ; Hs.81848; NM_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA. (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; NM_006265; Homo sapiens RAD21 (S. pombe); 4.12
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; protein kinase, DNA-activated, catalytic; 4.11
 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Homo sapiens clone 23783 mRNA sequence; 4.10
 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothetical protein Y50E8A.g - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31611 hypotheti; 4.10
 432512; NM_003284; Hs.3017; transition protein 1 (during histone to protamine replacement); transition protein 1 (during histone to; 4.10
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; DNA segment on chromosome 19 (unique) 11; 4.09
 423804; AW403448; Hs.1706; interferon-stimulated transcription factor 3, gamma (48kD); interferon-stimulated transcription fact; 4.09
 413745; AW247252; Hs.75514; nucleoside phosphorylase; nucleoside phosphorylase; 4.09
 442091; AW770493; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; guanine nucleotide binding protein (G pr; 4.09
 425003; AF119046; Hs.154149; apurinic/aprimidinic endonuclease(APEX nuclease)-like 2 protein; apurinic/aprimidinic endonuclease(APEX ; 4.08
 421859; AA356620; Hs.108947; KIAA0050 gene product; KIAA0050 gene product; 4.08
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-receptor type 12; protein tyrosine phosphatase, non-recept; 4.08
 452069; AB028949; Hs.183994; KIAA1026 protein; KIAA1026 protein; 4.08
 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; potassium voltage-gated channel, shaker; 4.07
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; solute carrier family 16 (monocarboxylic; 4.07
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; Homo sapiens cDNA FLJ12169 fis, clone MA; 4.07
 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe combined immunodeficiency); interleukin 2 receptor, gamma (severe co; 4.06
 446791; A1632278; Hs.195922; ESTs; ESTs; 4.06
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; protein phosphatase 4 (formerly X), cata; 4.06
 431194; D43704; Hs.250712; calcium channel, voltage-dependent, beta 3 subunit; calcium channel, voltage-dependent, beta; 4.06
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); phosphoinositide-3-kinase, regulatory su; 4.06
 425923; NM_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, delta polypeptide; phosphoinositide-3-kinase, catalytic, de; 4.05
 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; dipeptidylpeptidase VI; 4.04
 446272; BE268912; Hs.14601; hemalopoietic cell-specific Lyn substrate 1; hemalopoietic cell-specific Lyn substrat; 4.04
 439176; A1446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; ESTs, Weakly similar to B28096 line-1 pr; 4.04
 417880; BE241559; Hs.82848; selectin L (lymphocyte adhesion molecule 1); selectin L (lymphocyte adhesion molecule; 4.04
 410068; A1633888; Hs.58435; FYN-binding protein (FYN-120/130); FYN-binding protein (FYN-120/130); 4.03
 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; hypothetical protein FLJ20596; 4.03
 427716; L38951; Hs.180446; karyopherin (importin) beta 1; karyopherin (importin) beta 1; 4.03
 451050; AW937420; Hs.351869; ESTs; ESTs; 4.02
 449667; AB023227; Hs.23860; KIAA1010 protein; KIAA1010 protein; 4.02
 448499; BE613280; Hs.77550; p53-regulated DDA3; p53-regulated DDA3; 4.01
 437527; A1241019; Hs.145644; ESTs; ESTs; 4.01
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase; methylene tetrahydrofolate dehydrogenase; 4.00
 451931; AK000208; Hs.27267; Homo sapiens cDNA FLJ20201 fis, clone COLF1210; Homo sapiens cDNA FLJ20201 fis, clone CO; 4.00
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor 1 gamma; eukaryotic translation elongation factor; 4.00
 409581; U66243; Hs.55039; mitogen-activated protein kinase 12; mitogen-activated protein kinase 12; 3.99
 433577; AW007080; Hs.284192; ESTs; ESTs; 3.99
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); platelet-activating factor acetylhydrola; 3.99
 418629; BE247550; Hs.88859; growth factor receptor-bound protein 7; growth factor receptor-bound protein 7; 3.99
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin, gamma 1; 3.98
 402398; ; ; C19000263.gi|3108023|gb|AAC15755.1| [Homo sapiens]||66335; C19000263.gi|3108023|gb|AAC15755.1| (AC0; 3.97
 408414; A1114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell ; 3.97
 415012; NM_004383; Hs.77793; c-src tyrosine kinase; c-src tyrosine kinase; 3.97
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kinase); deoxythymidylate kinase (thymidylate kin; 3.95
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; solute carrier family 25 (mitochondrial ; 3.95
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine protease; caspase 8, apoptosis-related cysteine pr; 3.95
 430770; AA765694; Hs.123296; ESTs; ESTs; 3.94
 442994; A1026718; Hs.16954; ESTs; ESTs; 3.94
 420333; A1001383; Hs.97084; lymphocyte antigen 94 (mouse) homolog (activating NK-receptor; NK-p46); lymphocyte antigen 94 (mouse) homolog (a; 3.94
 438456; AA913381; Hs.279763; ESTs; ESTs; 3.94
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; non-metastatic cells 1, protein (NM23A) ; 3.93
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; cyclin-dependent kinase 4; 3.93
 424829; NM_002507; Hs.1827; nerve growth factor receptor (TNFR superfamily, member 16); nerve growth factor receptor (TNFR super; 3.93
 447574; AF162666; Hs.18895; tousel-like kinase 1; tousel-like kinase 1; 3.93
 425797; AF002986; Hs.159545; platelet activating receptor homolog; platelet activating receptor homolog; 3.93
 421910; NM_014586; Hs.109437; hormonally upregulated neu tumor-associated kinase; hormonally upregulated neu tumor-associat; 3.92
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; IMP (inosine monophosphate) dehydrogenas; 3.92
 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis, clone NT2RP4002075; Homo sapiens cDNA FLJ13221 fis, clone NT; 3.92
 400262; ; Hs.75309; Eos Control; Eos Control; 3.90
 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 3.90
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; phosphoserine phosphatase-like; 3.90
 435206; A1432364; Hs.160594; ESTs; ESTs; 3.90
 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; paired immunoglobulin-like receptor beta; 3.90
 413627; BE182082; Hs.246973; intron of Bicaudal D homolog 1; intron of Bicaudal D homolog 1; 3.90
 426265; AA421069; Hs.97896; ESTs; ESTs; 3.89
 451063; AW163702; Hs.25911; HLA-B associated transcript-2; HLA-B associated transcript-2; 3.89
 407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial cds; gb:Human nebulin mRNA, partial cds; 3.89
 437239; AW503395; Hs.5541; ATPase, Ca transporting, ubiquitous; ATPase, Ca transporting, ubiquitous; 3.88
 400261; ; Hs.1802; Eos Control; Eos Control; 3.88
 450447; AF212223; Hs.25010; hypothetical protein P15-2; hypothetical protein P15-2; 3.88
 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamyl gamma-semialdehyde synthetase); pyrroline-5-carboxylate synthetase (glut; 3.87
 414251; AL042306; Hs.97689; VASA protein; VASA protein; 3.87
 417767; BE242241; Hs.82542; acyloxyacyl hydrolase (neutrophil); acyloxyacyl hydrolase (neutrophil); 3.87
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor, beta polypeptide; platelet-derived growth factor receptor; 3.87

444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; solute carrier family 7 (cationic amino ; 3.86
 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; MKP-1 like protein tyrosine phosphatase; 3.86
 427022; AW245839; Hs.173255; small nuclear ribonucleoprotein polypeptide A; small nuclear ribonucleoprotein polypept; 3.86
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.86
 408056; AA312329; Hs.42331; ephrin-A4; ephrin-A4; 3.86
 410552; X66945; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 3.85
 450778; U81375; Hs.25450; solute carrier family 29 (nucleoside transporters), member 1; solute carrier family 29 (nucleoside tra; 3.85
 418978; T85295; Hs.268606; ESTs; ESTs; 3.84
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); cyclin-dependent kinase 5, regulatory su; 3.84
 442980; AA857025; Hs.8878; kinesin-like 1; kinesin-like 1; 3.84
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; interleukin 10 receptor, alpha; 3.84
 434689; AF154115; Hs.4076; CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1; CTD (carboxy-terminal domain, RNA polyme; 3.83
 432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; karyopherin beta 2b, transportin; 3.83
 415684; D59356; Hs.374480; sorbitol dehydrogenase; sorbitol dehydrogenase; 3.83
 451598; N29102; Hs.79658; ESTs; ESTs; 3.82
 449433; AI672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-binding protein 5 [H.sapiens]; ESTs, Weakly similar to S26650 DNA-bind; 3.82
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.81
 435160; AB002374; Hs.4791; KIAA0376 protein; KIAA0376 protein; 3.80
 443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, Williams-Beuren syndrome); elastin (supravalvular aortic stenosis, ; 3.80
 422753; AI928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); small nuclear ribonucleoprotein D3 polyp; 3.79
 421508; NM_004833; Hs.105115; absent in melanoma 2; absent in melanoma 2; 3.79
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; phosphatidylserine synthase 1; 3.79
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone LNG15735; Homo sapiens cDNA: FLJ23602 fis, clone L; 3.79
 421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; suppressor of var1 (S.cerevisiae) 3-like; 3.79
 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; frizzled (Drosophila) homolog 8; 3.79
 411125; AA151647; Hs.88877; cytochrome b-245, alpha polypeptide; cytochrome b-245, alpha polypeptide; 3.78
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; dual specificity phosphatase 4; 3.78
 425354; U62027; Hs.155935; complement component 3a receptor 1; complement component 3a receptor 1; 3.78
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, member 6; immunoglobulin superfamily, member 6; 3.78
 429687; AI675749; Hs.211608; nucleoporin 153kD; nucleoporin 153kD; 3.77
 414177; AI351355; Hs.356303; uncharacterized hypothalamus protein HARP11; uncharacterized hypothalamus protein HAR; 3.77
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; dual specificity phosphatase 5; 3.77
 445817; NM_003642; Hs.13340; histone acetyltransferase 1; histone acetyltransferase 1; 3.77
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, complete cds; Homo sapiens, clone MGC:15203, mRNA, com; 3.76
 412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); APEX nuclease (multifunctional DNA repai; 3.76
 413011; AW068115; Hs.821; biglycan; biglycan; 3.76
 428157; AI738719; Hs.198427; hexokinase 2; hexokinase 2; 3.76
 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor, alpha polypeptide); integrin, alpha 5 (fibronectin receptor,; 3.75
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; melanoma antigen, family D, 1; 3.75
 405484; ; C3002124*.gi|12737280[ref]XP_006682.2| keratin 18 [Homo sapiens][6633; C3002124*.gi|12737280[ref]XP_006682.2| k; 3.75
 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; splicing factor 3b, subunit 4, 49kD; 3.75
 432460; H12912; Hs.274691; adenylate kinase 3; adenylate kinase 3; 3.75
 428816; AA004986; Hs.193855; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; ATP-binding cassette, sub-family C (CFTR; 3.74
 431884; AA521246; Hs.210792; ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar
 to ALU8_HUMAN ALU S; 3.74
 453329; T97205; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell ; 3.74
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; solute carrier family 2 (facilitated glu; 3.74
 438330; AW450572; Hs.257316; ESTs; ESTs; 3.74
 419911; L15301; Hs.1276; BN51 (BHK21) temperature sensitivity complementing; BN51 (BHK21) temperature sensitivity com; 3.74
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; mitogen-activated protein kinase-activat; 3.73
 442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; ESTs, Weakly similar to I38022 hypotheti; 3.73
 451295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene ; 3.73
 410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Homo sapiens clone 24675 mRNA sequence; 3.73
 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; intercellular adhesion molecule 1 (CD54); 3.72
 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; solute carrier family 31 (copper transpo; 3.71
 423523; AW299828; Hs.193580; ESTs; ESTs; 3.71
 413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like 1; inositol polyphosphate phosphatase-like ; 3.71
 448336; R53848; Hs.44976; ESTs; ESTs; 3.70
 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; arachidonate 15-lipoxygenase, second typ; 3.70
 416087; AF045184; Hs.79008; SKI-INTERACTING PROTEIN; SKI-INTERACTING PROTEIN; 3.70
 442200; AW590572; Hs.235768; ESTs; ESTs; 3.70
 414280; BE410769; Hs.75873; zyxin; zyxin; 3.69
 409354; N68188; Hs.159472; Homo sapiens cDNA: FLJ22224 fis, clone HRC01703; Homo sapiens cDNA: FLJ22224 fis, clone H; 3.69
 415276; U88666; Hs.78353; SFRS protein kinase 2; SFRS protein kinase 2; 3.69
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA; leucine-rich repeat-containing G protein; 3.69
 446522; NM_003876; Hs.15196; putative receptor protein; putative receptor protein; 3.69
 422785; AI824114; Hs.289088; heat shock 90kD protein 1, alpha; heat shock 90kD protein 1, alpha; 3.68
 401083; ; NM_016582*.Homo sapiens peptide transporter 3 (LOC51296), mRNA. VERSION NM_016579.1 GI; NM_016582*.Homo sapiens peptide transpo; 3.68
 413048; M93221; Hs.75182; mannose receptor, C type 1; mannose receptor, C type 1; 3.68
 452690; AI536070; Hs.15085; ESTs; ESTs; 3.68
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar
 to ALU2_HUMAN ALU S; 3.68
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase; membrane-associated tyrosine- and threon; 3.68
 428579; NM_005756; Hs.184942; G protein-coupled receptor 64; G protein-coupled receptor 64; 3.68
 446430; AA346837; Hs.15075; hypothetical protein DKFZp434E2216; hypothetical protein DKFZp434E2216; 3.66
 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains the NIFS gene for
 cysteine desulfurase, two genes for novel proteins and the gene for the; Human DNA sequence from clone RP11-353C1; 3.66
 416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; Protein kinase C-binding protein NELL2; 3.65
 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 0610;
 3.65
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; wee1 (S. pombe) homolog; 3.65
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; ESTs, Weakly similar to S65657 alpha-1C-; 3.65
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN20), member 2; ATP-binding cassette, sub-family F (GCN2; 3.65

451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ATP-binding cassette, sub-family A (ABC1); 3.65
 414774; X02419; Hs.77274; plasminogen activator, urokinase; plasminogen activator, urokinase; 3.65
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin, beta 1; 3.65
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; hepatocyte growth factor-regulated tyrosine kinase substrate; 3.64
 437669; AI358105; Hs.123184; ESTs, Weakly similar to match to ESTs AA667999 [H.sapiens]; ESTs, Weakly similar to match to ESTs AA; 3.64
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); mannose-6-phosphate receptor (cation dep); 3.64
 444388; AB033058; Hs.11101; KIAA1232 protein; KIAA1232 protein; 3.64
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; CCAAT-box-binding transcription factor; 3.63
 451484; AV648896; Hs.283771; hypothetical protein; hypothetical protein; 3.63
 444613; H29627; Hs.79092; hypothetical protein FLJ14427; hypothetical protein FLJ14427; 3.63
 447495; AV401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); programmed cell death 8 (apoptosis-induc); 3.62
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; CDC2-related protein kinase 7; 3.62
 424732; D80001; Hs.152629; KIAA0179 protein; KIAA0179 protein; 3.62
 411165; NM_000169; Hs.69089; galactosidase, alpha; galactosidase, alpha; 3.62
 422112; BE540240; Hs.111783; Lsm1 protein; Lsm1 protein; 3.62
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); Homo sapiens mRNA; cDNA DKFZp434M229 (fr; 3.61
 438795; AA825792; Hs.377119; gb:od84b11.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone, mRNA sequence; gb:od84b11.s1 NCL_CGAP_Ov2 Homo sapiens; 3.61
 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; Homo sapiens, clone IMAGE:3457003, mRNA; 3.61
 407797; AK000524; Hs.39850; hypothetical protein FLJ20517; hypothetical protein FLJ20517; 3.60
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); collagen, type VII, alpha 1 (epidermolys; 3.60
 444985; AI677737; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 3.60
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM_023929); zinc finger protein RINZF (NM_023929); 3.59
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; hypothetical protein FLJ22865; 3.59
 415020; BE249915; Hs.293533; Human DNA sequence from clone RP11-127L20 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains the gene for a novel
 glutathione-S-transferase and five novel genes; Human DNA sequence from clone RP11-127L2; 3.59
 415149; X12451; Hs.78056; cathepsin L; cathepsin L; 3.57
 458715; AK000973; Hs.1706; hypothetical protein FLJ10111; hypothetical protein FLJ10111; 3.57
 423576; NM_000383; Hs.129829; autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy); autoimmune regulator (autoimmune polyen; 3.57
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; cytokine receptor-like molecule 9; 3.57
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; hypothetical protein MGC12959; 3.57
 404976; ; NM_014323*; Homo sapiens zinc finger protein 278 (ZNF278), transcript variant 1, mRNA; NM_014323*; Homo sapiens zinc finger prot; 3.57
 449656; AA002008; Hs.188633; ESTs; ESTs; 3.56
 413795; AL040178; Hs.142003; ESTs; ESTs; 3.56
 406859; AI581134; Hs.181357; laminin receptor 1 (67kD, ribosomal protein SA); laminin receptor 1 (67kD, ribosomal prot; 3.56
 411030; BE387193; Hs.67896; 7-60 protein; 7-60 protein; 3.56
 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; ESTs, Weakly similar to dJ963K23.2 [H.sa; 3.56
 424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs)
 syndrome, spastic paraplegia 1); L1 cell adhesion molecule (hydrocephalus; 3.55
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; solute carrier family 1 (glial high affi; 3.55
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible Ikbap kinase; IKK-related kinase epsilon; inducible Ik; 3.55
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); uridine monophosphate synthetase (orotat; 3.55
 450931; N25156; Hs.25648; tumor necrosis factor receptor superfamily, member 5; tumor necrosis factor receptor superfam; 3.55
 425836; AW955696; Hs.90960; ESTs; ESTs; 3.54
 441054; AA913591; Hs.126480; ESTs; ESTs; 3.54
 440592; AL137268; Hs.7285; KIAA0759 protein; KIAA0759 protein; 3.54
 458946; AA009716; Hs.42311; ESTs; ESTs; 3.53
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; dipeptidylpeptidase III; 3.53
 421662; NM_014141; Hs.106552; cell recognition molecule Caspr2; cell recognition molecule Caspr2; 3.53
 422732; AA577455; Hs.24937; transformer-2 alpha (htra-2 alpha); transformer-2 alpha (htra-2 alpha); 3.53
 424870; T15545; Hs.244624; ESTs; ESTs; 3.52
 442794; AI744130; Hs.356753; hypothetical protein MGC2975; hypothetical protein MGC2975; 3.52
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); protein C receptor, endothelial (EPCR); 3.51
 419971; AA400027; Hs.296234; ESTs, Weakly similar to T31613 hypothetical protein Y50E8A.1 - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31613 hypotheti; 3.51
 410257; BE244044; Hs.61469; hypothetical protein; hypothetical protein; 3.51
 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerevisiae ARD1; N-acetyltransferase, homolog of S. cerev; 3.51
 421921; H83363; Hs.355993; translocase of inner mitochondrial membrane 10 (yeast) homolog; translocase of inner mitochondrial membr; 3.50
 454128; AL031259; Hs.367900; programmed cell death 2; programmed cell death 2; 3.50
 434049; AA501430; Hs.5771; amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2; amyotrophic lateral sclerosis 2 (juvenil; 3.50
 453641; AA444140; Hs.90960; ESTs; ESTs; 3.50
 429592; AB029041; Hs.209646; KIAA1118 protein; KIAA1118 protein; 3.49
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211_HUMAN ZINC FINGER PROTEIN 211 [H.sapiens]; ESTs, Weakly similar to Z211_HUMAN ZINC; 3.47
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; RAD54 (S.cerevisiae)-like; 3.44
 413372; H55532; Hs.349695; tubulin, alpha 2; tubulin, alpha 2; 3.07
 437224; AL117628; Hs.97808; ESTs; ESTs; 2.77
 430439; AL133561; ; DKFZP434B061 protein; DKFZP434B061 protein; 2.76
 435897; AF269223; Hs.128322; t-complex 11 (a murine tcp homolog); t-complex 11 (a murine tcp homolog); 2.53
 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383 chromosome segregation protein smc1 [H.sapiens]; ESTs, Weakly similar to I54383 chromosom; 2.46
 412026; AA383618; Hs.73073; testis-specific ankyrin motif containing protein; testis-specific ankyrin motif containing; 2.35
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; hypothetical protein FLJ10251; 2.33
 426627; AF012359; Hs.195685; ESTs; ESTs; 2.12
 438983; AF065884; Hs.20029; proacrosin binding protein sp32 precursor; proacrosin binding protein sp32 precursor; 2.07
 425709; AA383076; Hs.159274; outer dense fibre of sperm tails 1; outer dense fibre of sperm tails 1; 1.99
 433724; AI827749; Hs.144924; serine/threonine protein kinase SSTK; serine/threonine protein kinase SSTK; 1.68
 420710; NM_007009; Hs.99875; zona pellucida binding protein; zona pellucida binding protein; 1.54

TABLE 57B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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417886 1031334_1 AA210987 D57294 AA214584 AA207006 D56572
 432407 MH1429_12 BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104
 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279
 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849
 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859
 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
 434414 35978_1 AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422
 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298
 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175
 BF854337
 427298 115241_1 AA933717 BF061897 AW628327 AA641788 AA400495
 427521 513212_1 AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165
 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
 407347 810943_1 T23514 AI655785
 430439 6750_2 AL133561 AL117481 AL122069 AW439292 AI968826 AL041090

TABLE 57C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402199	8576116	Minus	84187-84744
402680	8113438	Plus	137634-137768, 139702-139893, 140475-14059
402260	3399665	Minus	113765-113910, 115653-115765, 116808-11694
402678	8113438	Plus	37395-37514, 37866-37981
403171	9838164	Minus	74502-74703
406137	9166422	Minus	30487-31058
401704	3097841	Plus	24712-25374
402677	8113438	Plus	22135-22309, 23063-23238
402679	8113438	Plus	132079-132216
402145	8018280	Plus	113086-114800
406547	7711513	Minus	172780-174358
402398	4092817	Minus	24019-24973
405484	5922025	Plus	199214-199579, 199672-199920, 200262-20049
401083	3242744	Plus	33192-33360
404976	3419864	Minus	139625-140632

TABLE 58A: 434 genes upregulated in bladder cancer relative to normal body tissues

Table 58A lists about 434 genes upregulated in bladder cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1: 90th percentile of bladder tumor AIs divided by the 50th percentile of normal tissue AIs

Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prod.Domains; R1

430630; AW269920; Hs.2621; cystatin A (steffin A); cystatin;TM=M;; 35.25
 422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExtB;TM=Y;SS=M; 33.25
 414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets, ; phoslip;TM=M;SS=Y; 31.68
 415192; D17793; Hs.78183; aldo-keto reductase family 1, member C3 ; aldo_ket_red;TM=M;; 31.04
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 28.50
 439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep_L_domain, Furin-like, pkinase, Recep_L_domain, Peptidase_M24; 27.43
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;SS=M; 25.98
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT,none; 25.38
 418818; AA228899; Hs.101307; Homo sapiens HUT11 protein mRNA, partial; UT,none; 25.28
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisolv,HATPase_c;SS=M; 23.58
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; ig, pkinase;TM=Y;SS=M; 21.24
 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1;TM=Y;SS=M; 20.45
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 19.78
 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL3;TM=M; 18.90
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M;; 18.75
 410687; U24389; Hs.65436; lysyl oxidase-like 1; LysylOxidase;SS=M; 18.63
 444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypothetli; Collagen;TM=M;SS=M; 18.60
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd_glycop;TM=Y;SS=M; 18.55
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M;; 18.25

- 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic); PKI;SS=M; 17.73
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; Ig;TM=Y;SS=M; 17.68
 450746; D82673; Hs.278589; general transcription factor II, i; none;SH3,PX; 17.12
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M; 16.88
 420981; L40904; Hs.100724; peroxisome proliferative activated recep; hormone_rec,zf-C4;TM=M; 16.78
 439941; A1392640; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y; 16.75
 431846; BE019924; Hs.271580; uropod 1B; transmembrane4;TM=Y;SS=M; 16.56
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys.Ig.FAD_Synth,Ich_C,kinase;SS=M; 16.43
 414883; AA926960; ; CDC28 protein kinase 1; CKS; 16.20
 438091; AW373062; ; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 15.80
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH_Lb.Lipase_GDSL;TM=M; 15.70
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,kinase;TM=M; 15.63
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 15.45
 434293; NM_004445; Hs.3796; EphB6; EPH_Lbd,fn3,kinase,SAM;TM=Y;SS=M; 15.43
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule); EGF,lectin_c,sushi;TM=M;SS=M; 15.28
 443991; NM_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 15.10
 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; ig;TM=Y;SS=M; 14.90
 432306; Y18207; Hs.303090; protein phosphatase 1, regulatory (inhib); CBM_21;TM=M; 14.80
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M; 14.73
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 14.58
 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; Ig,Isohd,Ribosomal_L6,F-box;TM=Y;SS=M; 14.55
 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M; 14.53
 446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 14.35
 429556; AW139399; Hs.98988; ESTs; none;TM=M; 14.18
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand;SS=M; 14.13
 429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-recept; Y_phosphatase,Band_41,PDZ;SS=M; 13.90
 426657; NM_015865; Hs.171731; solute carrier family 14 (urea transport; UT;TM=Y; 13.83
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 13.80
 400843; ; NM_003105*; Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 13.78
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M; 13.38
 432314; AA533447; Hs.312989; ESTs; Xlink,none; 13.25
 413109; AW389845; Hs.110855; ESTs; PHO4,none; 13.15
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,pkinase;TM=M; 13.13
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M; 12.93
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,kinase,Recep_L_domain,Furin-like,kinase,Recep_L_domain,Peptidase_M24; 12.43
 440249; A1246590; Hs.249175; ESTs; TatD_DNase,pkinase,death,none; 12.38
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 12.38
 404942; U30825; ; splicing factor, arginine/serine-rich 9; CD36;TM=Y;SS=M; 12.03
 439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 11.93
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fis, clone NT; Aa_trans,none; 11.88
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,Ich_C,CH,AlP3;TM=M; 11.88
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 4; rrm,hormone_rec,zf-C4,sugar_tr; 11.85
 433470; AW960564; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.80
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding,THF_DHG_C,THF_DHG_C,THF_DHG_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M; 11.69
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 11.50
 426761; A1015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586I2022 (f; none;TM=Y;SS=M; 11.48
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 11.38
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 11.23
 436729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.18
 409960; BE261944; Hs.339673; hexokinase 1; none,none; 11.02
 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3,PDZ,Guanylate_kin;TM=M; 10.78
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; coflin_ADF;SS=M; 10.63
 427654; AA410183; Hs.137475; ESTs; ion_trans,vwc,IGFBP,isp_1; 10.58
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 10.53
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (f; SH3,PH,RhoGEF;TM=M; 10.53
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone K; none,none; 10.52
 436856; A1469355; Hs.127310; ESTs; pkinase,rrm;TM=M; 10.48
 451035; AU076785; Hs.430; plasmin 1 (I isoform); efhand,CH,Adaptin_N;SS=M; 10.38
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin_B,EGF,PSI;TM=Y;SS=M; 10.35
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 10.34
 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD_DAPIN;NA; 10.25
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 10.18
 437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365012.1 [H.s.a; GPS,7tm_2;TM=Y; 10.13
 400752; ; NM_003105*; Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 10.08
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPc;TM=M; 10.05
 426728; NM_007118; Hs.171957; triple functional domain (PTPRF interact; SH3,Ig,pkinase,PH,spectrin,RhoGEF;TM=M; 10.05
 400496; ; ENSP00000224716*; GTP-binding protein SAR; none;TM=Y; 10.01
 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3,PDZ,Guanylate_kin;TM=M; 10.00
 404568; ; NM_022071*; Homo sapiens hypothetical pro; SH2;TM=M; 10.00
 444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 9.93
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand,kazal,arf,ras,7tm_1;TM=M; 9.90
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2,SH3;TM=M; 9.90
 424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,WD40,IRK;TM=M; 9.88
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; pkinase;TM=M; 9.85
 439223; AW238299; Hs.260618; UL16 binding protein 2; ldl_recept_a,PKD,MHC_I;TM=M;SS=Y; 9.83
 429238; NM_002849; Hs.198288; protein tyrosine phosphatase, receptor t; Y_phosphatase;TM=Y;SS=M; 9.80
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y_phosphatase;TM=M; 9.73
 452239; AW379378; Hs.170121; protein tyrosine phosphatase, receptor t; none,none; 9.73
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M; 9.72
 403912; ; C5000394*; gij12737280refXP_006682.2l k; none;TM=M; 9.70
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 9.70

- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xc; pkinase;TM=M;; 9.68
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor I; kinesin,fn3,Y_phosphatase;TM=M;; 9.63
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;; 9.63
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3_P14_kinase,FAT,FATC;TM=M;; 9.55
 430259; BE550182; Hs.127826; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 9.50
 428520; AA331901; Hs.184736; hypothetical protein FLJ10097; none;TM=M;; 9.50
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;; 9.50
 448913; AA194422; Hs.22564; myosin VI; rrm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-
 C2H2,PHD,BTB,TfIIIS,AT_hook,SAM;TM=M;; 9.50
 414911; NM_000107; Hs.77602; damage-specific DNA binding protein 2 (4; WD40,homeobox,LIM;TM=M;; 9.48
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene ; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 9.45
 402328; ; Target Exon; pkinase;TM=M;; 9.44
 443710; A1928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha,none; 9.42
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;; 9.42
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase,PRK,Thymidylate_kin;SS=M; 9.40
 418827; BE327311; Hs.47166; HT021; none;TM=M;; 9.40
 440675; AW005054; Hs.47883; ESTs, Weakly similar to KCC1_HUMAN CALCI; pkinase,none; 9.35
 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;SS=M; 9.28
 410668; BE379794; Hs.65403; hypothetical protein; death,TNFR_c6;TM=Y;SS=M; 9.25
 430024; A1808780; Hs.227730; integrin, alpha 6; integrin_A,FG-GAP;TM=Y;SS=M; 9.23
 452696; A1826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanlylate_kin,PDZ,SH3; 9.13
 434263; N34895; Hs.44648; ESTs; ig,none; 9.13
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell ; Ribosomal_S14,ank,pkinase,death,none; 9.10
 429332; AF030403; Hs.199263; Ste-20 related kinase; pkinase,metalthio;TM=M;SS=M; 9.08
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,integrin_B;SS=M; 9.08
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22_Claudin,none; 9.07
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 8.98
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;; 8.93
 438000; A1825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M;; 8.90
 446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.90
 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.88
 437056; A1147061; ; gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S; none,spectrin,SH3,PH,CH; 8.78
 445496; AB007860; Hs.12802; development and differentiation enhancin; SH3,ank,PH,ArfGap;TM=M;; 8.78
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 8.75
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 8.70
 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank;; 8.68
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 8.65
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept; Y_phosphatase;SS=M; 8.65
 430397; A1924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;; 8.64
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M;; 8.60
 442994; A102718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 8.60
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M;; 8.60
 455439; AW945484; Hs.184252; ESTs, Weakly similar to ALU8_HUMAN ALU S; none,7tm_1; 8.55
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 ; TIMP,pkinase,DAG_PE-bind,RBD; 8.43
 417035; AA192455; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA se; none,none; 8.40
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 8.39
 448209; AW160489; Hs.20709; tetraspan 5; transmembrane4;TM=Y;SS=M; 8.33
 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none,none; 8.33
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2;TM=M;; 8.31
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm_1;TM=Y;SS=M; 8.30
 445633; A1453386; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK,none; 8.28
 446719; W39500; Hs.301872; hypothetical protein MGC4840; AAA,SKI;TM=M;; 8.23
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none,none; 8.20
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, fo; ig,pkinase;TM=Y;SS=M; 8.18
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none,none; 8.15
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS,zf-C2H2,SET; 8.15
 417386; AL037228; Hs.82043; D123 gene product; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 8.13
 431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 8.10
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none;TM=M;SS=M; 8.09
 425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;; 8.08
 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin receptor; FG-GAP,integrin_A,none; 8.05
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg;TM=M;SS=M; 8.03
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase;SS=M; 8.03
 404891; ; Target Exon; none,none; 7.95
 414278; AA330116; Hs.77273; Human glucose transporter pseudogene; none,none; 7.93
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 7.93
 433211; H11850; Hs.12808; MARK; pkinase,UBA,KA1;SS=M; 7.91
 438485; W57578; Hs.237955; RAB7, member RAS oncogene family; pkinase,ABC1,none; 7.90
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 7.90
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase tra; xan_ur_permease,RA; 7.88
 427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase (c-erb-b2; Furin-like,pkinase,Recep_L_domain,YLP;TM=Y;SS=M; 7.86
 405036; ; NM_021628; Homo sapiens arachidonate lip; lipoxygenase,complex1_49Kd,PLAT;TM=M;; 7.83
 418529; AW005895; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 8.73
 431912; A1660552; Hs.76549; ESTs, Weakly similar to A56154 Abl subst; none,Acyl-CoA_dh,Acyl-CoA_dh_M,Acyl-CoA_dh_N; 7.80
 432981; NM_002733; Hs.3136; protein kinase, AMP-activated, gamma 1 n; CBS,Aa_trans;TM=M;; 7.78
 422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo; Sec7,PH,ANF_receptor,Ig_chan,WD40,IRK; 7.78
 446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonin; CNH,DAG_PE-bind,PH,Involucrin,M;TM=M;; 7.78
 431183; NM_006855; Hs.250699; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept;TM=M;SS=M; 7.78
 400845; ; NM_003105; Homo sapiens sortilin-related; EGF,fn3,Idl_recept_a,Idl_recept_b,granulin,BNR;TM=Y;SS=M; 7.73
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 7.73
 437192; AW975786; Hs.75355; ubiquitin-conjugating enzyme E2N (homolo; UQ_con_Y_phosphatase,SH2; 7.70
 403212; ; NM_019595; Homo sapiens intersectin 2 (IT; SH3,efhand,C2,PH,RhoGEF;TM=M;; 7.70
 441190; H09073; Hs.25046; ESTs; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,none; 7.68

409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 7.68
 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene; SH2,SH3,kinase;SS=M; 7.65
 447898; AW969638; Hs.112318; 6.2 kd protein; none,none; 7.65
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;SS=M; 7.63
 401927; ; C17000914; gi|8394367|ref|NP_058549.1|s; none; 7.60
 407347; AA829847; ; gb:od40d07.s1 NCL_CGAP_GCB1 Homo sapiens; RhoGAP,SH2,kinase,POLO_box,none; 7.58
 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3,none; 7.57
 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; kinase,ubiquitin,Enterotoxin_A,PHO4,kinase,ubiquitin; 7.55
 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, ty; none,none; 7.55
 421489; A1922821; Hs.32433; ESTs; none,PI-PLC-X,PI-PLC-Y,C2; 7.53
 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 7.53
 431605; AW972407; Hs.124370; gb:EST384498 MAGE resequences, MAGL Homo; adenylatekinase,SRP54;TM=M; 7.50
 430570; A1417881; Hs.292464; ESTs; 7tm_2,Fz,Frizzled,none; 7.50
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 7.48
 420676; A1434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind,none; 7.48
 444252; R21135; Hs.54985; ESTs; none,none; 7.47
 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3_PI4_kinase;TM=M; 7.47
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M; 7.45
 418546; AA224827; ; gb:nc32g04.s1 NCL_CGAP_Pr2 Homo sapiens; vwa,integrin_A,FG-GAP,none; 7.45
 437860; AA333063; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 7.43
 452007; AA426234; Hs.34906; ESTs, Weakly similar to T17210 hypotheti; none,kinase; 7.40
 432407; AA221036; ; gb:zr0312.r1 Stratagene NT2 neuronal pr; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rila,abhydrolase,TGF-beta,DUF139,TPR,DSPC,tsp_1,Ribosomal_S21,rvp;TM=M; 7.40
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,kinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M; 7.40
 421429; NM_014922; Hs.104305; death effector filament-forming Ced-4-li; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC;NA;NA; 7.38
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone_rec,zf-C4;SS=M; 7.38
 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y; 7.38
 422813; AV656571; Hs.121068; transmembrane 4 superfamily member 6; transmembrane4;TM=Y;SS=M; 7.32
 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 (; none,spectrin,SH3,PH,CH; 7.25
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,kinase;TM=M; 7.24
 444745; AF117754; Hs.11861; thyroid hormone receptor-associated prot; none;TM=M; 7.23
 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; kinase,PBD;TM=M; 7.19
 407591; NM_000910; Hs.37125; neuropeptide Y receptor Y2; 7tm_1;TM=Y; 7.18
 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 7.18
 450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M; 7.18
 403344; ; NM_000341; Homo sapiens solute carrier fa; alpha-amylase;TM=Y; 7.15
 427268; X78520; Hs.174139; chloride channel 3; CBS,voltage_CLC;TM=Y; 7.14
 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 7.14
 404875; ; NM_022819; Homo sapiens phospholipase A2; phoslip;SS=M; 7.11
 433618; AA602539; Hs.345494; ESTs; G-alpha_A_deaminase; 7.10
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 7.08
 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9;TM=M;SS=M; 7.05
 426655; AL049589; Hs.171723; neuronal cell death-related protein; TFIID-31;TM=M; 7.05
 423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 7.03
 400211; ; NM_003899; Homo sapiens PAK-interacting ; SH3,PH,RhoGEF,Terpene_synth;TM=M; 7.03
 438150; AA037534; Hs.342874; transforming growth factor, beta recepto; zona_pellucida,none; 6.93
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit, ; proteasome;TM=M; 6.93
 405275; AB028989; ; mitogen-activated protein kinase 8 inter; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 6.93
 415392; Z44067; Hs.10957; ESTs; PIP5K,none; 6.89
 429355; AW973253; Hs.292689; ESTs; kinase,bZIP,Armadillo_seg,none; 6.88
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic; ; C2,PLA2_B;TM=M; 6.85
 427832; AF038362; Hs.180930; TBP-associated factor 172; SNF2_N,helicase_C,Armadillo_seg,HEAT;TM=M; 6.83
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M; 6.80
 400158; ; ENSP00000244302; cDNA FLJ11591 fis, clone; Sm;SS=M; 6.78
 401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_prot,ion_trans,PAC,PAS,none; 6.78
 400844; ; NM_003105; Homo sapiens sortilin-related; EGF,fn3,ldl_recept_L,ldl_recept_L,granulin,BNR;TM=Y;SS=M; 6.73
 457238; U07358; Hs.211601; mitogen-activated protein kinase kinase ; kinase; 6.73
 404440; ; NM_021048; Homo sapiens melanoma antigen, ; MAGE;TM=M; 6.73
 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kina; Ets,SAM_PNT;TM=M; 6.70
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Pribosyltran,OMPdecase;TM=M; 6.70
 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 6.65
 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin;SS=M; 6.64
 408638; AW451353; Hs.173328; ESTs; B56,none; 6.63
 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 6.61
 401057; BE563196; ; eukaryotic translation elongation factor; ion_trans,IQ;TM=Y; 6.60
 446526; H89616; Hs.296290; Homo sapiens cDNA FLJ13357 fis, clone PL; none,none; 6.60
 400528; ; NM_020975; Homo sapiens ret proto-oncoge; cadherin,kinase;TM=Y;SS=M; 6.58
 418562; R60659; Hs.124831; CGI-67 protein; none,Skp1,AAA; 6.57
 453826; AL138129; ; gb:DKFZp547F152_r1 547 (synonym: hibr1) ; PK,PK_C,none; 6.55
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC_tran,GTP_EFTU,ABC_membrane,none; 6.54
 415088; A1077288; Hs.296323; serum/glucocorticoid regulated kinase; none,none; 6.50
 453489; AA300067; Hs.33032; hypothetical protein DKFZp434N185; F5_F8_type_C,kinase,Ets,F5_F8_type_C,kinase,Ets; 6.47
 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm,NTF2;TM=M; 6.46
 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M; 6.46
 441712; AW391927; Hs.7946; KIAA1288 protein; AIP3;TM=M; 6.44
 414557; AA340111; Hs.100009; acyl-Coenzyme A oxidase 1, palmitoyl; kinase,7tm_1; 6.43
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M; 6.43
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 6.40
 438941; AF075047; Hs.31864; ESTs; Ca_channel_B,SH3,arf,none; 6.40
 441466; AW673081; Hs.54828; ESTs; kinase,zf-C2H2,KRAB,none; 6.33
 438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypotheti; lipoxygenase,PLAT,none; 6.33
 433255; A1274270; Hs.96840; KIAA1527 protein; MHCK_EF2_kinase;TM=M;SS=M; 6.33
 427801; AW979155; Hs.298275; amino acid transporter 2; Aa_trans;TM=M;SS=M; 6.32

- 407970; AW403814; Hs.41714; BCL2-associated athanogene; ubiquitin,BAG,Tropomyosin;; 6.30
 438464; AA669735; Hs.324743; protein phosphatase 4 regulatory subunit; none,none; 6.30
 453977; AA886006; Hs.250427; ESTs; pkinase,P2X_receptor,E1-E2_ATPase,Hydrolase; 6.30
 412491; W31589; Hs.73957; RAB5A, member RAS oncogene family; ras,arf,PP2C;TM=M;; 6.30
 413235; BE243445; Hs.75248; topoisomerase (DNA) II beta (180kD); DNA_gyraseB,DNA_topoisolV,HATPase_c,DNA_gyraseB,DNA_topoisolV,HATPase_c; 6.29
 404342;; C7002192:g[17299207]gb|AA54404.1| (AE0; none;TM=M;; 6.27
 409274; NM_003930; Hs.52644; SKAP55 homologue; SH3,PH;SS=M; 6.25
 419693; AA133749; Hs.301350; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 6.23
 405429;; Target Exon; Y_phosphatase,none; 6.23
 404975; AL042279;; uncharacterized hypothalamus protein HT0; kringle;TM=Y;SS=M; 6.20
 452929; AW954938; Hs.172816; neuregulin 1; Neuregulin,EGF,ig,Neuregulin,EGF,ig; 6.18
 446883; AW452756; Hs.16364; hypothetical protein FLJ10955; DEAD,helicase_C,rm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPc,Isp_1,Ribosomal_S21,rvp;TM=M;; 6.18
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M;; 6.15
 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y;; 6.15
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none,none; 6.14
 447727; AI421079;; tumor necrosis factor receptor superfam; none,synaplobrevin; 6.13
 401536;; NM_002530*:Homo sapiens neurotrophic tyr; ig,pkinase,LRR,LRRNT,LRRCT;TM=M;SS=M; 6.11
 444317; A1140566; Hs.143436; ESTs, Weakly similar to PLHU plasmin [H.; PAN,kringle,trypsin,PI-PLC-X,C2,SH2,PH,SH3,PI-PLC-Y,PAN; 6.10
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR_LY6,ET,PLA2_inh;SS=M; 6.08
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;; 6.08
 450107; AI873287; Hs.257812; ESTs; ICE_p20,DED;TM=M;; 6.05
 418175; AW967054; Hs.206312; ESTs, Weakly similar to I38022 hypotheti; zf-C2H2,BTB,K_tetra,Syntaxin,none; 6.05
 408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC_tran,ABC_membrane,PRK,Bac_export_3;TM=Y;; 6.05
 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema,PSI,integrin_B;TM=Y;; 6.03
 427625; AF008216; Hs.285013; putative human HLA class II associated p; none,none; 6.03
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.03
 446650; AB016625; Hs.15813; solute carrier family 22 (organic cation; sugar_tr;TM=Y;SS=M; 6.03
 405102;; C15001220:g[4469558]gb|AAD21311.1| (AF; DAG_PE-bind,PH,RhoGEF,DC1;SS=M; 6.03
 400121;; Eos Control; SH3,PH,RhoGEF,Terpene_synth;TM=M;; 6.03
 415327; H22769;; gb:ym54c02.r1 Soares infant brain 1N1B H; SH3,PDZ,Guanylate_kin;SS=M; 6.03
 404148;; NM_002944*:Homo sapiens v-ros avian UR2; fn3,pkinase,DUF139;TM=Y;SS=M; 6.03
 405531;; Target Exon; PDZ,CARD,Guanylate_kin;TM=M;; 6.00
 433363; AA584829; Hs.275163; non-metastatic cells 2, protein (NM23B); NDK,none; 6.00
 427270; H47921; Hs.174139; chloride channel 3; voltage_CLC,CBS,none; 5.99
 423774; L39064; Hs.1702; interleukin 9 receptor; none;TM=M;SS=M; 5.98
 424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked; pkinase,TBC; 5.98
 411040; AF007393; Hs.177574; protein-kinase, interferon-inducible dou; HLH;TM=M;; 5.95
 423422; AC005175; Hs.128425; NY-REN-24 antigen; Sulfotransfer,7tm_1,none; 5.88
 453902; BE502341; Hs.3402; ESTs; none,none; 5.88
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y;; 5.86
 436154; AA764950; Hs.119898; ESTs; ehband,DAG_PE-bind,DAGKa,PHD,DAGKc,PSI,none; 5.85
 455358; AW902641;; gb:QV3-NN1024-100500-181-d08 NN1024 Homo; Sulfatase,Somatomedin_B,Phosphodiester,none; 5.83
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol_BP,pkinase;TM=M;; 5.82
 452547; AA335295; Hs.74120; adipose specific 2; LEA;TM=M;; 5.82
 415204; T27434;; gb:hbc2294 Human pancreatic islet Homo s; Na_Ca_Ex,Calx-beta,none; 5.80
 435563; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;; 5.78
 456097; C15702; Hs.288028; ESTs, Moderately similar to I54374 gene; dsrm,FKBP; 5.78
 422445; M23114; Hs.1526; ATPase, Ca transporting, cardiac muscle; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase;TM=Y;; 5.77
 436246; AW450963; Hs.119991; ESTs; none,DNA_gyraseB,DNA_topoisolV,HATPase_c; 5.75
 422953; AA488860; Hs.245043; hypothetical protein FLJ14297; ABC_tran,PRK;TM=Y;SS=M; 5.75
 425854; AA749190;; ESTs; RhoGAP,SH2,pkinase,POLO_box,none; 5.74
 424160; T74062;; gb:yc81f01.r1 Soares Infant brain 1N1B H; ROK,none; 5.70
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 5.69
 437613; R19892; Hs.10267; MIL1 protein; none,none; 5.68
 410820; BE391493; Hs.16475; Human DNA sequence from clone RP5-852M4; TBC;SS=M; 5.68
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD;TM=M;; 5.66
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M;; 5.63
 406930; U04691;; gb:Human olfactory receptor (OR17-219) g; none;TM=Y;SS=M; 5.60
 401044;; Target Exon; none,ICE_p20,ICE_p10,CARD,Peptidase_M1; 5.56
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 5.55
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RR; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_Pi4_kinase,FAT,FATC,Bola,RUN;TM=M;; 5.53
 426248; T18988; Hs.293668; ESTs; pkinase,none; 5.50
 418426; NM_003804; Hs.296327; receptor (TNFRSF)-interacting serine-thr; pkinase,death;TM=M;; 5.43
 417086; AA194446;; ESTs, Weakly similar to S55024 nebulin; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 5.43
 447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupl; 7tm_1,SH2;TM=Y;SS=M; 5.40
 412247; AF022375; Hs.73793; vascular endothelial growth factor; PDGF;SS=M; 5.40
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, com; pkinase,TBC,Rhodanese;TM=M;; 5.38
 419355; AA428520; Hs.90061; progesterone binding protein; heme_1;TM=Y;SS=M; 5.35
 411188; BE161168;; gb:PM0-HT0425-170100-002-a10 HT0425 Homo; adenylatekinase,none; 5.35
 422461; NM_003417; Hs.117077; zinc finger protein 264; zf-C2H2,KRAB,TFIIS;TM=M;; 5.28
 426348; BE466586; Hs.17433; hypothetical protein FLJ20967; none,none; 5.25
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;; 5.23
 429592; AB029041; Hs.209646; KIAA1118 protein; Troponin,Exo_endo_phos,IQ;TM=M;; 5.22
 434821; AA159111; Hs.284281; Human putative ribosomal protein S1 mRNA; ER_lumen_recept,Ribosomal_L11,Ribosomal_L11_N;TM=Y;SS=M; 5.21
 434368; AW519020; Hs.73893; dopamine receptor D2; pkinase,SH3,none; 5.15
 405586;; NM_000299:Homo sapiens plakophilin 1 (ec; Armadillo_seg;TM=M;; 5.13
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylatekinase,none; 5.12
 407443; AF227138;; gb:Homo sapiens candidate taste receptor; none;TM=Y;SS=M; 5.11
 416817; AA398045; Hs.104679; ESTs; Furin-like,pkinase,Recep_L_domain,fn3,none; 5.10
 401886;; NM_021783:Homo sapiens XEDAR (XEDAR), mR; TNFR_c6;TM=M;SS=M; 5.08
 410314; AW860708; Hs.18851; hypothetical protein FLJ10875; myb_DNA-binding,PAH,BAH,bromodomain,PHD,SET;TM=M;; 5.08

- 401579; AL031447; ; Homo sapiens, clone IMAGE:4053044, mRNA; ; Neur_chan_LBD, Neur_chan_memb, none; 5.05
 445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-; PABP,rm, pkinase, 14-3-3; 5.05
 417529; AA203634; ; gb:zx58b09.r1 Soares_fetal_liver_spleen_; pkinase,UBA,KA1,none; 5.03
 417527; AA203524; ; gb:zx56e10.r1 Soares_fetal_liver_spleen_; SH3;SS=M; 4.98
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; pfb;TM=M; 4.96
 431321; AW136372; Hs.1852; acid phosphatase, prostate; acid_phosphat,none; 4.93
 404298; ; C6001238*gi121715|sp|P26697|GTA3_CHICK; none,GST_C,GST_N,pkinase; 4.85
 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299322, mRNA; ; none;TM=M; 4.82
 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y; 4.73
 422366; T83882; Hs.97927; ESTs; pkinase,none; 4.64
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase;TM=M; 4.48
 426925; NM_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fis, clone H; Esterase,enolase,Peptidase_S9;TM=M; 4.45
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1;TM=Y;SS=M; 4.40
 400749; ; NM_003105; Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.38
 425721; AC002115; Hs.159309; uroplakin 1A; transmembrane4;TM=Y;SS=M; 4.33
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ldl_recept_a,PKD,MHC_I;TM=M;SS=Y; 4.31
 400751; ; NM_003105; Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.18
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;SS=M; 3.90
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc transport; none,none; 3.88
 458760; AI498631; Hs.111334; ferritin, light polypeptide; cystatin,ferritin,histone,HCO3_cotransp,SH3,RhoGAP,xan_ur_permease,FCH;SS=M; 3.85
 441218; BE327561; Hs.202345; ESTs; none,WD40,E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase; 3.78
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death,ZU5;SS=M; 3.76
 451385; AA017656; ; gb:ze39h01.r1 Soares retina N2b4HR Homo; Atrophin-1,enolase,Atrophin-1,Y_phosphatase,SH2,fibrinogen_C,TIM; 3.60
 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M; 3.30
 409582; R27430; Hs.271565; ESTs; none,Neur_chan_LBD,Neur_chan_memb; 3.28
 441155; AW161008; Hs.7719; GABA(A) receptor-associated protein; MAP1_LC3;SS=M; 3.23
 436740; AW975133; ; gb:EST387239 MAGE resequences, MAGN Homo; none,EPH_lbd,fn3,pkinase,SAM; 3.20
 418319; AW611703; Hs.190173; ESTs, Weakly similar to A46010 X-linked; ; none,IRK; 3.20
 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (f; none;NA;NA; 3.13
 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit; none,none; 3.10
 400846; ; sortilin-related receptor, L(DLR class); EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 3.09
 422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (fr; none,Na_H_Exchange; 3.03
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 3.02
 424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK,none; 2.98
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member; death,TNFR_c6;TM=Y;SS=M; 2.93
 401279; ; C13000351*gi2494033|sp|Q64398|KGDG_MES; none,none; 2.88
 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth fa; Sema,pkinase,TIG,PSI,none; 2.83
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, s; IRK;TM=Y; 2.80
 453619; H87648; Hs.33922; Homo sapiens, clone MGC:9084, mRNA, comp; pkinase;TM=M; 2.75
 441699; AW511126; Hs.127572; ESTs; none,Aa_trans; 2.73
 458781; AI444821; Hs.63085; ESTs, Weakly similar to MPP3_HUMAN MAGUK; SH3,PDZ,Guanylate_kin,L27;TM=M; 2.73
 446913; AA430650; Hs.16529; transmembrane 4 superfamily member (tet; transmembrane4;TM=Y;SS=M; 2.70
 453487; R31770; Hs.56562; ESTs; 7tm_1,none; 2.68
 421279; AW664878; Hs.106645; ESTs; pkinase,none; 2.68
 419720; AA249131; Hs.337778; hypothetical protein FLJ11068; none,none; 2.65
 452345; AA293279; Hs.29173; hypothetical protein FLJ20515; DSPc;TM=M; 2.63
 422247; U18244; Hs.113602; solute carrier family 1 (high affinity a; SDF;TM=Y; 2.62
 425212; AW962253; Hs.171618; ESTs; pkinase,none; 2.60
 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 2.58
 423629; AW021173; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone H; voltage_CLC,CBS,none; 2.55
 456737; BE247203; Hs.124831; CGI-67 protein; abhydrolase_2;TM=M;SS=M; 2.53
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm_1;TM=Y;SS=M; 2.53
 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fis, clone Y7; none,none; 2.50
 448324; AI571356; Hs.34174; ESTs, Moderately similar to ALU8_HUMAN A; ICE_p20,CARD,ICE_p10,none; 2.50
 402256; ; Target Exon; pkinase,UBA,none; 2.43
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HE; GDI,7tm_1,none; 2.40
 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypotheti; none,spectrin,SH3,PH,CH; 2.40
 420634; S42457; Hs.1323; cyclic nucleotide gated channel alpha 1; cNMP_binding,ion_trans;TM=Y; 2.35
 419630; W57756; ; gb:zd20g10.r1 Soares_fetal_heart_NbHH19W; zf-C3HC4,none; 2.35
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1;TM=Y;SS=M; 2.35
 400704; ; Target Exon; lig_chan,SBP_bac_3,ANF_receptor;TM=Y;SS=M; 2.33
 400149; ; Eos Control; acid_phosphat;TM=Y;SS=M; 2.30
 459327; AW149706; Hs.7859; gb:xf41d02.x1 NCL_CGAP_Brn50 Homo sapien; PHD,PWWP,SET,pkinase,jg; 2.30
 452220; BE158006; Hs.212296; ESTs; integrin_A,FG-GAP,none; 2.25
 416690; H84078; Hs.108551; ESTs; pkinase,none; 2.23
 408354; AI382803; Hs.159235; ESTs; none,none; 2.23
 452203; X57522; ; transporter 1, ATP-binding cassette, sub; ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 2.21
 405093; ; C12001101*gi7522643|pir|T32733 AMPA g; none,none; 2.20
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M; 2.20
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none,none; 2.18
 417185; NM_002484; Hs.81469; nucleotide binding protein 1 (E.coli Min; ParA,fer4_Niif,ArsA_ATPase;TM=M; 2.18
 433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none,PHO4; 2.18
 413627; BE182082; Hs.246973; ESTs; Armadillo_seg,IBB;TM=M; 2.18
 407415; AF073328; ; gb:Homo sapiens tetracycline transporter-; none,none; 2.15
 450592; AI701555; Hs.202562; ESTs; pkinase,none; 2.15
 428767; AI421972; Hs.98802; ESTs, Moderately similar to T14342 NSD1; none,pkinase,jg; 2.15
 429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm,BAG;SS=M; 2.15
 419122; AI401360; Hs.44410; ESTs; ABC_tran,ABC_membrane,none; 2.10
 446420; AW015693; Hs.135614; ESTs; ion_trans,none; 2.05
 420076; AA827860; Hs.293717; ESTs; DUF59,pkinase; 2.05
 409416; AW388359; Hs.10667; ESTs; transmembrane4;TM=Y;SS=M; 2.03
 428766; AA477989; Hs.98800; ESTs; TPR,7tm_1; 2.03
 427001; NM_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphoryl; pkinase;TM=M; 2.03

453709; AL119133; ; protein kinase C substrate 80K-H; none,histone; 2.03
 423341; AW242394; Hs.108660; ESTs; none,none; 2.00
 456772; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.88
 427786; BE407863; Hs.256871; ESTs; none,FG-GAP,7tm_1; 1.65
 423508; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.00
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00

TABLE 58B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

414883 8371_2 AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AA772418
 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239
 AI339996 AA701623 AI139549 AI36880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA459292
 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715
 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
 438091 22448_1 AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE395919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184
 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689
 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370
 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698
 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445
 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770
 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391
 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468
 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210
 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791
 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796
 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033
 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186
 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA040570 AI075878 W38161 AI972739
 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827
 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817
 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693
 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453
 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301
 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398
 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071
 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414
 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525
 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645
 BF843900 AW806193 AA502832 AA649494 AI568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380
 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088966 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927
 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995
 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206
 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242
 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442
 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866
 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151
 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BE811337 BF593847 BG055071
 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895
 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185
 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799
 BF702221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446
 BI879003 BE088925 BE088854 AA921353 R21800 AA011222 T97525
 436729 6624_1 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796
 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033
 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186
 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA040570 AI075878 W38161 AI972739
 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827
 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817
 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693
 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453
 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301
 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398
 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071
 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414
 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525
 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645
 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380
 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088966 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927
 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995
 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206
 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242
 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442
 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866
 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151
 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BE811337 BF593847 BG055071
 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895

			AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
5	437056 422940 409745	428504_3 58443_1 MH1944_5	AW976398 AI147061 AA765223 AA743380 AI803927 BC012771 BG397153 BF366196 AA337277 AA319285 AW843252 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
10	407347 418546 432407	810943_1 242836_1 MH1429_12	T23514 AI655785 T59708 AA224827 T59843 BE156903 BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
15			L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449639 R73300 NM_004624 AI797007 BE045643 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138 NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AI535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876
20	423387 400211	2612_2 3532_1	AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030
25			BC000486 BC001930 U15008 NM_004597 BG326561 AV761269 BF212132 BG113313 BI838038 BG944198 BG255198 BG164334 BM013507 AV682717 BF028761 BG755489 BG030141 BG105489 BE440103 BF727449 BM454228 BG912181 BM015197 BG395995 AI126579 AW248204 BI857394 BI857319 BG944205 BG323958 BI092930 AV756576 AA280959 BF033078 BE539360 AW247174 BG107836 BE796975 BG170920 AI148142 AI092009 AI336349 AV713409 BF685591 BE616029 AV713166 BE909458 BE743868 BM018218 AI340153 BE792567 BE206806 AI159916 AI184271 BE208585 BI862286 C18760 BG219364 AI122677 BE207297 BF754798 AA314384 BE873951 BG207294 AI148198 AI336189 AI141094 AI308985 BF220098 AI143289 BE856397 AA644001 BE675402 AJ346708 AI052809 AI140082 BF081542 AI342428 AI479625 AA278456 AI750163 BE707501 BG944510 AA314616 AA315774 BF630721 BE738404 AA814194 AA477195 AA932107 F36858 AA363159 BE865458 AA354147 AW904224 AI055855 AA380365 F28474 D59140 AA341946 AA993339 AA323350 F24344 AA774436 BG942061 AA636015 AA852919 T31486 F36334 BG943190 T30319 BG943153 BG941836 T32569 T31160 AA311749 BE710086 BE709911 W23826 BG941639 BF769034 AA026407 AA229555 AV756340 AV714380 AI138129 BG003205 AL138179 BI021773 BE064231
30	400158	2166_1	AL520734 BI666852 BF870571 BF945361 BF945354 AI770086 BI861138 AI421079 AL043200 BG683612 AW946265 NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AI535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030
35	453826 447727 400121	366136_1 10123_14 3532_1	BM048470 BG983877 N92089 Z43545 F05783 R35182 H22769 H71928 H63921 R94394 AW195830 AA630220 F02030 R60760 R08204 H71929 BE464731 R62568 H63520 H77840 AL515501 F01971 T71768 N55275 AA883505 AW606824 AA704682 N74193 W57593 AW753776 H60439 AI076352 R31485 BE160931 AW130730 BE160869 AW580256 AW902073 BE702158 AW382079 N76884 BF431013 H38156 AV648937 H80573 AW902569 AW902557 AW902654 AW902641 AW902650 AW902741 AW902644 Z25288 R85077 F00323 D82802 T27434 BF184345 AA364846 BI494468 AA775693 BF195801 AA749190 AI480223 BE327332 AI470017 AW628345 AI917472 AI972264 AI375571 AI652583 AI656167 AI983110 BE550378 AW015085 BE552318 AI631475 AI433447 AA534540 AI865480 AI468119 BF110875 AW512059 W58721 AA827482 R59357
40			AW370493 AA923304 AI660828 AA502611 BI017370 AA039704 W65393 BE938514 W65295 BF919626 BI759440 BI838879 AA336207 F12441 BF171187 BE185031 T74062 AW904410 AA280078 BF919629 AK056605 AK056969 AW380724 AA195950 F21243 Z17422 AA176595 AA176955 AA194350 BC005933 BC017866 AA196396 Z24810 AA181361 AA193115 AA086465 F25194 F30130 AA180013 AJ346143 F20589 F20620 F29371 F32439 F25153 F32146 F26110 F28506 F25307 F27533 F20375 F32370 AA653078 BF574897 Z24852 F00172 T30560 AW449825 AI620346 BG986374 BE706521 C02691 AI596834 F31902 F26078 AA670099 BF475555 F30818 F37524 AJ346558 F28050 F17933 F31637 C03413 AI092152 AA180743 AA085730 F21998 F20854 F18944 F31180 F37937 F37738 AA193162 Z17344 AA192546 AW821260 BE162466 BE161168 AA203634 AA203524 W88451 AA019761 AA017656 AA017374 AW975133 AA805813 AA729943 BF223647 AA204668 AA256086 BF574707 W57756 AA249070 BI906494 AA248011 BC003160 NM_001610 X12548 BG386685 BI760866 BI559619 BG323829 AU135543 BI834101 AU142120 AU124511 AU124889 AL558171 AU117286 BI824000 BG386610 BI753285 BI223475 AU134828 BM126369 BE206493 BF751498 AI544274 AY007137 BI828921 BE870130 BF771242 BI835451 BI765655 BI820955 BI223344 BG015924 BI759894 AL527413 BF310588 N31870 N23974 BE514914 T48863 AW860257 BF334625 AA883860 AU144168 AA442562 AU159491 AU148353 AA564123 AU148667 AI377256 AW664004 AI871712 AI141486 AI332351 AI339094 BE206109 AW519033 AI817729 AI332490 AI149455 AI857411 AI763154 AI751608 AI377222 AI081956 AW664229 AI275872 AW168546 AA975270 AI367408 AI687729 AI269164 AW105344 BM193081 BE550930 AI082116 AA854691 AI056249 AI221062 AI290113 D51818 AA732409 BG055125 N85878 AU156121
45			
50			
55	415327	9792_2	
60	455358 415204 425854	1160035_1 1865508_1 2638_3	
65	424160 417086	5320_3 1154_2	
70			
75	411188 417529 417527 451385 436740 419630 400149	1072487_1 3302462_1 2431831_1 85022_1 1239008_1 37310_5 16458_1	
80			

BF093671 AA053070 T28548 AL570460 BI006862 BI007207 AA373620 W95069 AA629136 AA708164 AI014886 AW168697 D51623 AA577168
 AI094208 AA028946 AA975078 R16815 BG151132 AI276297 D51676
 BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519
 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470
 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429
 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404
 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220
 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184
 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619
 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256
 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601
 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
 AK057669 AK054977 AL519747 BE893744 BM313248 BG913430 H80793 BF813504 N36311 N39276 H95973 BF791919 BE739392 BE144239
 AA074615 AI291059 AI681053 AA702355 BF439899 AW055166 AI096957 BF223853 AL119659 AI692209 BM312961 AI669297 BE466252 AI292024
 AA402764 AI214620 AA765312 BF380770 AA442682 AL519746 AW295039 AI037878 AW473433 AI499437 AI401618 AI130831 AA427406 AI042138
 BG272488 AI828769 AI828764 AI189390 W84635 AA398496 AA761672 AA699520 AI200406 N68093 AI143913 AA993133 AA613306 AI050971
 AA661905 AA722687 AI749977 AA829345 BG057324 BF001339 AA910169 AA765133 AI360722 AI701849 AI365083 H95974 AI830377 AI12866
 AI370491 BE858907 N62185 AA705746 BE379632 W93803 AI440333 AW367670 AW367640 N77131 BF993216 AI858263 W52329 N68106 R83113
 R85153 BE380058 AA082537 AA729731 W23495 W31190 BF995236 BF968827 BF355168 N24508 AA215711 BF170735 AA280395 BE738851
 AW367707 AA630879 AA428420 R76236 BG567847 N25931 AA173568 AI073567 AA004957 AI539585 N95093 H99798 H95072 H96853 AA215712
 AA034214 R85096 H82051 H80794 R44954 AA278972 H68352 H68346 R94750 R89010 R67951 H65817 N24891 AA173731 AI693577 BE181027
 AA709461 BE181002 W60239 BF987598 BF995279 H17483 R76237 AL119133 BF964815 AW663315 H65903 H17591 R20167 AA310039 R58734
 R58506

TABLE 58C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807
404942	7382153	Plus	92095-92252
400752	7331445	Minus	36215-36461
400496	9743564	Plus	41515-41695
404568	9966995	Minus	92893-93116
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
402328	4464283	Minus	13758-13922,14558-14752
404891	7329392	Plus	84974-85125
405036	7543748	Minus	121957-122129
400845	9188605	Plus	34428-34612
403212	7630897	Minus	156037-156210
401927	3873185	Minus	112000-112137

Table 59A lists about 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03
 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 8.2. The "average" prostate cancer level was set to the
 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 50th percentile amongst non-malignant tissues. In order to remove gene-specific
 background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the
 ratio was evaluated.

TABLE 59A: ABOUT 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	108.1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	102.5
420923	AF097021	Hs.273321	differentially expressed in hematopoietic	90.5
416854	H40164	Hs.80296	Purkinje cell protein 4	79.8
425075	AA506324	Hs.1852	acid phosphatase, prostate	71.6
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	70.6
434666	AF151103	Hs.112259	T cell receptor gamma locus	69.1
419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	66.4
413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	66.4
420154	AI093155	Hs.95420	JM27 protein	63.9
428336	AA503115	Hs.183752	microseminoprotein, beta-	61.4
400287	S39329	Hs.181350	kallikrein 2, prostatic	59.7
416602	NM_006159	Hs.79389	nel (chicken)-like 2	54.6
428398	AI249368	Hs.98558	ESTs	54.6
432441	AW292425	Hs.163484	ESTs	54.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	54.2
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	54.2
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	53.7

	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	49.6
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	48.0
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	46.8
5	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	45.0
	427674	NM_003528	Hs.2178	H2B histone family, member Q	44.9
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	44.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	44.5
	415314	N88802	Hs.5422	glycoprotein M6B	43.2
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	41.9
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	41.1
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	40.5
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	39.5
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	39.3
15	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	39.0
	447726	AL137638	Hs.19368	matrilin 2	38.6
	426174	AA547959	Hs.115838	ESTs	38.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	38.0
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	37.5
20	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	37.0
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	35.5
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	35.1
	453096	AW294631	Hs.11325	ESTs	35.1
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	34.9
25	427665	AF134803	Hs.180141	cofilin 2 (muscle)	34.9
	415539	AI733881	Hs.72472	BMP-R1B	34.9
	428411	AW291464	Hs.10338	ESTs	34.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	34.3
	401424			NM_001172:Homo sapiens arginase, type II	34.0
30	452114	N22687	Hs.8236	ESTs	34.0
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	33.8
	448045	AJ297436	Hs.20166	prostate stem cell antigen	33.1
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	32.9
	432101	AI918950	Hs.123642	EphA3	32.7
35	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	32.4
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg),	32.4
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	32.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	32.3
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	31.9
40	408380	AF123050	Hs.44532	diubiquitin	31.6
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	31.4
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.3
	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	31.2
	408001	AA046458	Hs.95296	ESTs	30.8
45	440274	R24595	Hs.7122	scrapie responsive protein 1	30.7
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	30.3
	442993	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1	30.2
	433404	T32982	Hs.102720	ESTs	29.6
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	29.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	29.3
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	29.2
	418827	BE327311	Hs.47166	HT021	29.0
	410330	AW023630	Hs.46786	ESTs	28.6
	450377	AB033091	Hs.74313	KIAA1265 protein	28.6
55	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	28.5
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	28.2
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	27.7
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	27.7
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	27.6
60	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.4
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	27.4
	407202	N58172	Hs.109370	ESTs	27.4
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	27.4
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	27.3
65	403047			NM_005656*:Homo sapiens transmembrane pr	27.2
	407709	AA456135	Hs.23023	ESTs	27.0
	433444	AW975324	Hs.129816	ESTs	26.8
	415989	AI267700	Hs.317584	ESTs	26.8
	430539	AK001489	Hs.242894	ADP-ribosylation factor-like 1	26.5
70	408221	AA912183	Hs.47447	ESTs	26.5
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	26.4
	437179	AA393508	Hs.300642	serologically defined colon cancer antig	26.4
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	26.2
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	26.2
75	400292	AA250737	Hs.72472	BMP-R1B	26.0
	433647	AA603367	Hs.222294	ESTs	26.0
	429220	AW207206	Hs.136319	ESTs	25.8
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	25.6
	448106	AI800470	Hs.171941	ESTs	25.5
80	415992	C05837	Hs.145807	hypothetical protein FLJ13593	25.5
	452792	AB037765	Hs.30652	KIAA1344 protein	25.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	25.2
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	24.9
	418961	AW967646	Hs.23023	ESTs	24.8

	451027	AW519204	Hs.40808	ESTs	24.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	24.5
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	24.4
5	418396	AI765805	Hs.26691	ESTs	24.1
	412088	AI689496	Hs.108932	ESTs	24.1
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	24.0
	411644	H92064	Hs.278626	Arg/Abl-interacting protein ArgBP2	24.0
10	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	23.9
	433466	AA508353	Hs.105314	relaxin 1 (H1)	23.7
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	23.6
	440995	T57773	Hs.10263	ESTs	23.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	23.2
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	23.1
15	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	22.9
	440260	AI972867	Hs.7130	copine IV	22.5
	443622	AI911527	Hs.11805	ESTs	22.2
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	22.0
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	21.9
20	450642	R39773	Hs.7130	copine IV	21.9
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	21.8
	435981	H74319	Hs.188620	ESTs	21.8
	450693	AW450461	Hs.203965	ESTs	21.7
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.7
25	423242	AL039402	Hs.125783	DEME-6 protein	21.7
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	21.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	21.5
	404210			NM_005936:Homo sapiens myeloid/lymphoid	21.5
	417622	AW298163	Hs.82318	WAS protein family, member 3	21.5
30	419526	AI821895	Hs.193481	ESTs	21.5
	442799	AI564739	Hs.68505	ESTs	21.4
	424846	AU077324	Hs.1832	neuropeptide Y	21.3
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	21.3
	429922	Z97630	Hs.226117	H1 histone family, member 0	21.3
35	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	21.3
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	21.2
	431474	AL133990	Hs.190642	ESTs	21.2
	430887	N66801	Hs.260287	KIAA1841 protein	21.1
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	21.1
40	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	21.1
	445133	AW157646	Hs.153506	ESTs	21.0
	421513	X00949	Hs.105314	relaxin 1 (H1)	21.0
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	20.8
	446795	AI797713	Hs.156471	ESTs	20.7
45	440774	AI420511	Hs.127832	ESTs	20.7
	407168	R45175	Hs.117183	ESTs	20.6
	417511	AL049176	Hs.82223	chordin-like	20.6
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	20.6
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	20.6
50	411800	N39342	Hs.103042	microtubule-associated protein 1B	20.5
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	20.5
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.5
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	20.5
	424897	D63216	Hs.153684	frizzled-related protein	20.5
55	430280	AA361258	Hs.237868	interleukin 7 receptor	20.4
	401197			ENSP00000229263*:HSPC213.	20.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	20.3
	429918	AW873986	Hs.119383	ESTs	20.2
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	20.2
60	453469	AB014533	Hs.33010	KIAA0633 protein	20.2
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	20.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	20.0
	419440	AB020689	Hs.90419	KIAA0882 protein	20.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.9
65	441690	R81733	Hs.33106	ESTs	19.9
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	19.8
	423044	AA320829	Hs.97266	protocadherin 18	19.8
	410929	H47233	Hs.30643	ESTs	19.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	19.7
70	431556	AF016028	Hs.183428	sarcospan (Kras oncogene-associated gene	19.6
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	19.6
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	19.6
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	19.5
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	19.4
75	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	19.4
	430187	AI799909	Hs.158989	ESTs	19.3
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	19.3
	434423	NM_006769	Hs.3844	LIM domain only 4	19.2
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	19.1
80	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	19.0
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	18.9
	436032	AA150797	Hs.109276	latexin protein	18.9
	431548	AI834273	Hs.9711	novel protein	18.9
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	18.9

	445929	AI089660	Hs.323401	dpy-30-like protein	18.8
	453160	AI263307	Hs.239884	H2B histone family, member L	18.8
	439897	NM_015310	Hs.6763	KIAA0942 protein	18.8
5	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	18.8
	434987	AW975114	Hs.293273	ESTs	18.7
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	18.7
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	18.7
	418819	AA228776	Hs.191721	ESTs	18.7
10	450831	R37974	Hs.25255	ESTs	18.7
	415691	AW963979	Hs.24723	ESTs	18.7
	417124	BE122762	Hs.25338	ESTs	18.7
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	18.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	18.5
15	410099	AA081630	Hs.169387	KIAA0036 gene product	18.5
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	18.5
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	18.5
	436420	AA443966	Hs.31595	ESTs	18.4
20	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	18.4
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	18.3
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	18.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	18.2
	437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	18.2
	439569	AW602166	Hs.222399	CEGP1 protein	18.1
25	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	18.1
	424682	AW604804	Hs.151717	KIAA0437 protein	18.0
	432435	BE218886	Hs.282070	ESTs	17.9
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	17.8
30	431121	AW971157		gb:EST383245 MAGE resequences, MAGL Homo	17.8
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	17.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	17.7
	440703	AI137653	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	17.7
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	17.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	17.6
35	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	17.5
	430487	D87742	Hs.241552	KIAA0268 protein	17.4
	419355	AA428520	Hs.90061	progesterone binding protein	17.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	17.3
	423943	AF163570	Hs.135756	polymerase (DNA directed) kappa	17.3
40	434217	AW014795	Hs.23349	ESTs	17.3
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	17.2
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	17.2
	430177	AW969233	Hs.302746	MSTP028 protein	17.2
	432473	AI202703	Hs.152414	ESTs	17.1
45	421823	N40850	Hs.28625	ESTs	17.1
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	17.0
	420092	AA814043	Hs.88045	ESTs	17.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	17.0
	417426	NM_002291	Hs.82124	laminin, beta 1	17.0
50	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	17.0
	401747			Homo sapiens keratin 17 (KRT17)	17.0
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	17.0
	442369	AI565071	Hs.159983	ESTs	16.9
55	432966	AA650114	Hs.325198	ESTs	16.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	16.8
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	16.8
	443745	AB039670	Hs.9728	ALEX1 protein	16.8
	438899	AF085833	Hs.135624	ESTs	16.8
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	16.8
60	442064	AI422867	Hs.88594	ESTs	16.8
	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	16.5
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocan	16.4
	443801	AW206942	Hs.253594	ESTs	16.3
	437536	X91221	Hs.144465	ESTs	16.3
65	409196	NM_001874	Hs.334873	carboxypeptidase M	16.3
	438337	AK002058	Hs.6166	hypothetical protein FLJ11196	16.3
	416239	AL038450	Hs.48948	ESTs	16.3
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	16.2
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	16.2
70	409060	AI815867	Hs.50130	necdin (mouse) homolog	16.1
	442571	C06338	Hs.165464	ESTs	16.1
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	16.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	16.0
	450164	AI239923	Hs.30098	ESTs	16.0
75	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	16.0
	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	16.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	16.0
	436024	AI800041	Hs.190555	ESTs	16.0
	412652	AI801777	Hs.6774	ESTs	16.0
80	456516	BE172704	Hs.222746	KIAA1610 protein	16.0
	452576	AB023177	Hs.29900	KIAA0960 protein	15.9
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	15.9
	434792	AA649253	Hs.132458	ESTs	15.9
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	15.9

	442787	W93048	Hs.250723	hypothetical protein MGC2747	15.9
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	15.9
	402812			NM_004930*:Homo sapiens capping protein	15.8
5	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	15.8
	413597	AW302885	Hs.117183	ESTs	15.7
	439677	R82331	Hs.164599	ESTs	15.7
	432527	AW975028	Hs.102754	ESTs	15.7
	413654	AA331881	Hs.75454	peroxiredoxin 3	15.7
10	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	15.7
	426501	AW043782	Hs.293616	ESTs	15.7
	435056	AW023337	Hs.5422	glycoprotein M6B	15.7
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	15.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	15.6
	434988	AI418055	Hs.161160	ESTs	15.6
15	435380	AA679001	Hs.192221	ESTs	15.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	15.6
	446377	AW014022	Hs.170953	ESTs	15.5
20	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	15.5
	415672	N53097	Hs.193579	ESTs	15.5
	450325	AI935962	Hs.26289	ESTs	15.5
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	15.4
	443674	AI081330	Hs.145008	ESTs	15.4
25	415263	AA948033	Hs.130853	ESTs	15.4
	442081	AA401863	Hs.22380	ESTs	15.3
	415788	AW628686	Hs.78851	KIAA0217 protein	15.3
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	15.3
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	15.3
30	418693	AI750878	Hs.87409	thrombospondin 1	15.3
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	15.3
	443180	R15875	Hs.258576	claudin 12	15.2
	432437	W07088	Hs.293685	ESTs	15.2
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	15.2
35	446091	AW022192	Hs.200197	ESTs	15.2
	409341	AI963376	Hs.12532	chromosome 1 open reading frame 21	15.2
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	15.1
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	15.1
	453698	AA037615	Hs.42746	ESTs	15.1
40	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	15.1
	427707	NM_005578	Hs.180398	LIM domain-containing preferred transloc	15.1
	453308	AW959731	Hs.323099	ESTs	15.1
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	15.1
	433927	AI557019	Hs.116467	small nuclear protein PRAC	15.0
45	443162	T49951	Hs.9029	DKFZP434G032 protein	15.0
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	15.0
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	15.0
	443912	R37257	Hs.184780	ESTs	15.0
	410297	AA148710	Hs.79914	lumican	15.0
50	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	14.9
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	14.9
	451652	AA018968	Hs.133536	ESTs	14.9
	406038	Y14443	Hs.88219	zinc finger protein 200	14.8
55	408784	AW971350	Hs.63386	ESTs	14.8
	453510	AI699482	Hs.42151	ESTs	14.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	14.8
	433908	AW298141	Hs.157975	ESTs	14.8
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	14.8
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	14.8
60	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	14.7
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	14.7
	447752	M73700	Hs.105938	lactotransferrin	14.7
	426044	AA502490	Hs.336695	ESTs	14.7
	403362			NM_001615*:Homo sapiens actin, gamma 2,	14.7
65	427982	NM_016156	Hs.181326	KIAA1073 protein	14.7
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	14.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	14.7
	433226	AW503733	Hs.9414	KIAA1488 protein	14.6
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	14.6
70	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	14.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.6
	409264	NM_014937	Hs.52463	KIAA0966 protein	14.6
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	14.5
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proli	14.5
75	410339	AI916499	Hs.298258	ESTs	14.5
	431992	NM_002742	Hs.2891	protein kinase C, mu	14.5
	424432	AB037821	Hs.146858	protocadherin 10	14.5
	431933	AI187057	Hs.132554	ESTs	14.5
	440749	W22335	Hs.7392	hypothetical protein MGC3199	14.5
80	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	14.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	14.5
	407021	U52077		gb:Human mariner1 transposase gene, comp	14.5
	413786	AW613780	Hs.13500	ESTs	14.5
	437866	AA156781	Hs.74170	metallothionein 1E (functional)	14.5

	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	14.4
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	14.4
	443280	AA299688	Hs.24183	ESTs	14.4
5	416836	D54745	Hs.80247	cholecystokinin	14.4
	436860	H12751	Hs.5327	PRO1914 protein	14.3
	425174	D87450	Hs.154978	KIAA0261 protein	14.3
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	14.3
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	14.3
10	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule)	14.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	14.2
	437718	AI927288	Hs.196779	ESTs	14.2
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeldt-Jakob)	14.2
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta)	14.2
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	14.2
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl)	14.2
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	14.1
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	14.1
20	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	14.0
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	14.0
	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	14.0
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	14.0
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	13.9
	418848	AI820961	Hs.193465	ESTs	13.9
25	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	13.9
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	13.9
	443967	AW294013	Hs.200942	ESTs	13.9
	424775	AB014540	Hs.153026	SWAP-70 protein	13.9
	411190	AA306342	Hs.69171	protein kinase C-like 2	13.9
30	447384	AI377221	Hs.40528	ESTs	13.9
	444880	AW118683	Hs.154150	ESTs	13.9
	433409	AI278802	Hs.25661	ESTs	13.9
	423201	NM_000163	Hs.125180	growth hormone receptor	13.9
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	13.9
35	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	13.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	13.8
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	13.8
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	13.8
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	13.8
40	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	13.8
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	13.8
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR)	13.8
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	13.8
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	13.7
45	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	13.7
	428054	AI948688	Hs.266619	ESTs	13.7
	444636	T96667	Hs.17877	ESTs	13.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.7
50	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	13.7
	452260	AA453208	Hs.28726	RAB9, member RAS oncogene family	13.7
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	13.7
	450316	W84446	Hs.226434	hypothetical protein MGC4643	13.7
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	13.7
	443634	H73972	Hs.134460	ESTs	13.7
55	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	13.7
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	13.7
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	13.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	13.6
	416795	AI497778	Hs.20509	HBV pX associated protein-8	13.6
60	410001	AB041036	Hs.57771	kallikrein 11	13.6
	452242	R50956	Hs.159993	glycosyltransferase	13.6
	413231	D87461	Hs.75244	BCL2-like 2	13.6
	404641			NM_021965*:Homo sapiens phosphoglucomuta	13.6
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfami	13.6
65	414279	AW021691	Hs.101067	GCN5 (general control of amino-acid synt	13.6
	411573	AB029000	Hs.70823	KIAA1077 protein	13.5
	417632	R20855	Hs.5422	glycoprotein M6B	13.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	13.5
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	13.5
70	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	13.5
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!!	13.5
	418663	AK001100	Hs.41690	desmocollin 3	13.5
	452277	AL049013	Hs.28783	KIAA1223 protein	13.5
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	13.5
75	447082	T85314	Hs.42644	thioredoxin-like	13.5
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	13.4
	415443	T07353	Hs.7948	ESTs	13.4
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.4
	442113	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypotheti	13.3
80	433517	AW022133	Hs.189838	ESTs	13.3
	430829	AW451999	Hs.194024	ESTs	13.3
	453111	AB014598	Hs.31720	hephaestin	13.3
	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (13.3
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	13.3

5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	13.3
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	13.3
	437323	AA371145	Hs.226627	leptin receptor	13.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.2
	433037	NM_014158	Hs.279938	HSPC067 protein	13.2
10	407938	AA905097	Hs.85050	phospholamban	13.2
	400860			Target Exon	13.2
	411031	W37943	Hs.34892	KIAA1323 protein	13.2
	436797	AA731491	Hs.336454	hypothetical protein MGC14879	13.2
	409277	T05558	Hs.156880	ESTs	13.2
15	434036	AI659131	Hs.197733	hypothetical protein MGC2849	13.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.2
	450755	AA010984	Hs.159464	ESTs	13.1
	450649	NM_001429	Hs.25272	E1A binding protein p300	13.1
	408495	W68796	Hs.237731	ESTs	13.1
20	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	13.1
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	13.1
	416987	D86957	Hs.80712	KIAA0202 protein	13.0
	453006	AI362575	Hs.167133	ESTs	13.0
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	13.0
25	415752	BE314524	Hs.78776	putative transmembrane protein	13.0
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	13.0
	417318	AW953937	Hs.12891	ESTs	13.0
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	12.9
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	12.9
30	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	12.9
	428218	AA424266	Hs.123642	EphA3	12.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	12.9
	448779	BE042877	Hs.177135	ESTs	12.8
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	12.8
35	417315	AI080042	Hs.336901	ribosomal protein S24	12.8
	429697	AW296451	Hs.24605	ESTs	12.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	12.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	12.8
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	12.8
40	424806	AA382523	Hs.105689	MSTP031 protein	12.7
	442343	AA992480	Hs.129874	ESTs	12.7
	432244	AI669973	Hs.200574	ESTs	12.7
	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	12.7
	452512	AW363486	Hs.337635	ESTs	12.7
45	415079	R43179	Hs.22895	hypothetical protein FLJ23548	12.7
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	12.7
	411067	AI681006	Hs.71721	ESTs	12.7
	442501	AA315267	Hs.23128	ESTs	12.7
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	12.7
50	437052	AA861697	Hs.120591	ESTs	12.7
	433234	AB040928	Hs.65366	KIAA1495 protein	12.6
	453830	AA534296	Hs.20953	ESTs	12.6
	409995	AW960597	Hs.30164	ESTs	12.6
	414290	AI568801	Hs.71721	ESTs	12.6
55	417248	AA329449	Hs.247302	twisted gastrulation	12.6
	418624	AI734080	Hs.104211	ESTs	12.6
	412654	AI093480	Hs.29263	hypothetical protein FLJ11896	12.6
	450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp434D0215 (f	12.6
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.5
60	427078	AI676062	Hs.111902	ESTs	12.5
	420838	AW118210	Hs.5244	ESTs	12.5
	449784	AW161319	Hs.12915	ESTs	12.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	12.5
	415276	U88666	Hs.78353	SFRS protein kinase 2	12.5
65	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	12.5
	400301	X03635	Hs.1657	estrogen receptor 1	12.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	12.5
	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced transl	12.5
	420345	AW295230	Hs.25231	ESTs	12.4
70	432205	AI806583	Hs.125291	ESTs	12.4
	451893	AW192083	Hs.290855	ESTs	12.4
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	12.4
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	12.4
	404642			NM_021965":Homo sapiens phosphoglucomuta	12.4
75	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	12.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	12.4
	420871	AA702972	Hs.65300	ESTs	12.4
	448072	AI459306	Hs.24908	ESTs	12.4
	441269	AW015206	Hs.178784	ESTs	12.3
80	427761	AA412205	Hs.140996	ESTs	12.3
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	12.3
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	12.3
	436521	AW203986	Hs.213003	ESTs	12.3
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	12.3
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	12.2
	453994	BE180964	Hs.165590	ribosomal protein S13	12.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	12.2

	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	12.2
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	12.2
	400880			NM_000611*:Homo sapiens CD59 antigen p18	12.2
5	425920	AL049977	Hs.162209	claudin 8	12.2
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	12.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	12.1
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	12.1
	452994	AW962597	Hs.31305	KIAA1547 protein	12.1
10	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	12.1
	437124	AA554458	Hs.197751	KIAA0666 protein	12.1
	411450	H49619	Hs.127301	ESTs	12.1
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	12.1
	449625	NM_014253	Hs.23796	odz (odd Oz/ten-m, Drosophila) homolog 1	12.1
15	419459	AW291128	Hs.278422	DKFZP586G1122 protein	12.1
	426252	BE176980	Hs.28917	ESTs	12.1
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	12.1
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	12.0
	435047	AA454985	Hs.54973	cadherin-like protein VR20	12.0
20	417625	U59305	Hs.44708	Ser-Thr protein kinase related to the my	12.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	12.0
	443646	AI085198	Hs.164226	ESTs	12.0
	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	12.0
	443837	AI984625	Hs.9884	spindle pole body protein	12.0
25	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	12.0
	424232	AB015982	Hs.143460	protein kinase C, nu	11.9
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	11.9
	446874	AW968304	Hs.56156	ESTs	11.9
	454119	BE549773	Hs.40510	uncoupling protein 4	11.9
30	436746	AA730045	Hs.187866	ESTs	11.9
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	11.9
	416508	R39769	Hs.206088	ESTs, Moderately similar to ALU8_HUMAN A	11.8
	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	11.8
	413991	H44725	Hs.42683	ESTs	11.8
35	431645	AF078849	Hs.266483	dynein light chain-A	11.8
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.8
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	11.8
	412977	AA125910	Hs.191461	ESTs	11.8
40	426981	AL044675	Hs.173081	KIAA0530 protein	11.8
	410853	H04588	Hs.30469	ESTs	11.7
	444670	H58373	Hs.332938	hypothetical protein MGC5370	11.7
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	11.7
	434398	AA121098	Hs.3838	serum-inducible kinase	11.7
45	438032	BE045624	Hs.152992	ESTs	11.7
	433212	BE218049	Hs.121820	ESTs	11.6
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	11.6
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	11.6
	430929	AA489166	Hs.156933	ESTs	11.6
50	423782	AI472209	Hs.323117	ESTs	11.6
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.6
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	11.6
	430200	BE613337	Hs.234896	geminin	11.5
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.5
55	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	11.5
	422805	AA436989	Hs.121017	H2A histone family, member A	11.5
	422538	NM_006441	Hs.118131	5,10-methylnetetrahydrofolate synthetase	11.5
	412677	AW029608	Hs.17384	ESTs	11.5
	421896	N62293	Hs.45107	ESTs	11.5
60	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	11.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	11.5
	415293	R49462	Hs.106541	ESTs	11.5
	443161	AI038316		gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_	11.5
	420185	AL044056	Hs.158047	ESTs	11.5
65	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	11.5
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp556B213 (fr	11.5
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	11.5
	449919	AI674685	Hs.200141	ESTs	11.5
	414844	AA296874	Hs.77494	deoxyguanosine kinase	11.5
70	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	11.4
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	11.4
	407786	AA687538	Hs.38972	tetraspan 1	11.4
	414407	AA147026	Hs.76704	ESTs	11.4
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	11.4
	456804	AI421645	Hs.139851	caveolin 2	11.4
75	422546	AB007969	Hs.301478	KIAA0500 protein	11.4
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	11.4
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	11.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.4
80	433577	AW007080	Hs.8817	ESTs	11.4
	453935	AI633770	Hs.42572	ESTs	11.4
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	11.4
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.3
	448766	AI473827	Hs.31793	ESTs	11.3

5	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	11.3
	410108	AA081659	Hs.318775	OSBP-related protein 6	11.3
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	11.3
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	11.3
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	11.3
10	414212	AA136569	Hs.10848	KIAA0187 gene product	11.3
	401519			C15000476*:gil12737279[ref]XP_012163.1]	11.3
	458509	AA654650	Hs.282906	ESTs	11.2
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	11.2
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.2
15	436758	AW977167	Hs.155272	ESTs	11.2
	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	11.2
	434715	BE005346	Hs.116410	ESTs	11.2
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	11.2
	428342	AI739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	11.2
20	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	11.2
	430519	AF129534	Hs.49210	F-box only protein 4	11.2
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	11.1
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	11.1
	434158	T86534	Hs.14372	ESTs	11.1
25	414341	D80004	Hs.75909	KIAA0182 protein	11.1
	414650	AA150435	Hs.72063	ESTs	11.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	11.1
	437575	AW954355	Hs.36529	hypothetical protein MGC11242	11.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	11.1
30	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	11.1
	452598	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	11.0
	438379	N23018	Hs.171391	C-terminal binding protein 2	11.0
	433230	AW136134	Hs.220277	ESTs	11.0
35	412622	AW664708	Hs.171959	ESTs	11.0
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	11.0
	434349	NM_015678	Hs.3821	neurobeachin	11.0
	430261	AA305127	Hs.237225	hypothetical protein HT023	11.0
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	11.0
40	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	11.0
	442082	R41823	Hs.7413	ESTs	11.0
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	11.0
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	11.0
	450244	AA007534	Hs.125062	ESTs	11.0
45	417169	R13550	Hs.246773	ESTs	11.0
	421481	AW391972	Hs.104696	KIAA1324 protein	10.9
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	10.9
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	10.9
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.9
50	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	10.9
	433658	L03678	Hs.156110	immunoglobulin kappa constant	10.9
	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	10.9
	441540	C01367	Hs.127128	ESTs	10.9
	431154	AW971228	Hs.290259	ESTs, Weakly similar to I38022 hypotheti	10.9
55	416777	AF146760	Hs.79844	DKFZP564M1416 protein	10.9
	439556	AI623752	Hs.163603	ESTs	10.9
	428280	H05541	Hs.183428	sarcospan (Kras oncogene-associated gene	10.8
	453942	AW190920	Hs.19928	hypothetical protein SP329	10.8
	447982	H22953	Hs.137551	ESTs	10.8
60	422779	AA317036	Hs.118787	transforming growth factor, beta-induced	10.8
	447595	AW379130	Hs.18953	phosphodiesterase 9A	10.8
	427115	AW972853	Hs.112237	ESTs	10.8
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	10.8
	419326	W94915	Hs.42419	ESTs	10.8
65	435163	AA668884	Hs.19155	ESTs	10.8
	417578	T91443	Hs.193963	ESTs	10.8
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	10.8
	450206	AI796450	Hs.201600	ESTs	10.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	10.8
70	421977	W94197	Hs.110165	ribosomal protein L26 homolog	10.8
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	10.8
	408243	Y00787	Hs.624	interleukin 8	10.8
	439492	AF086310	Hs.103159	ESTs	10.8
	413492	D87470	Hs.75400	KIAA0280 protein	10.8
75	436962	AW377314	Hs.5364	DKFZP564I052 protein	10.8
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	10.8
	422583	AA410506	Hs.27973	KIAA0874 protein	10.8
	417665	AW852858	Hs.22862	ESTs	10.7
	433285	AW975944	Hs.237396	ESTs	10.7
80	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	10.7
	424878	H57111	Hs.221132	ESTs	10.7
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	10.7
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	10.7
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	10.7
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	10.7
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	10.7
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	10.7

	433923	AI823453	Hs.146625	ESTs	10.7
	418196	AI745649	Hs.26549	KIAA1708 protein	10.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	10.7
5	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	10.7
	429350	AI754634	Hs.131987	ESTs	10.7
	418601	AA279490	Hs.86368	calmegin	10.6
	437267	AW511443	Hs.258110	ESTs	10.6
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	10.6
10	421982	AF206019	Hs.110347	REV1 (yeast homolog)- like	10.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	10.6
	418662	AI801098	Hs.151500	ESTs	10.6
	449685	AW296669	Hs.66095	ESTs	10.6
	441111	AI806867	Hs.126594	ESTs	10.6
15	436671	AW137159	Hs.146151	ESTs	10.6
	447974	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	10.6
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.6
	424562	AI420859	Hs.150557	basic transcription element binding prot	10.6
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	10.6
20	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.6
	439584	AA838114	Hs.221612	ESTs	10.6
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	10.6
	420929	AI694143	Hs.296251	programmed cell death 4	10.6
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.6
25	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	10.6
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	10.6
	424433	H04607	Hs.9218	ESTs	10.6
	420230	AL034344	Hs.284186	forkhead box C1	10.6
	419441	AW023731	Hs.274368	MSTP032 protein	10.6
30	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	10.6
	451900	AB023199	Hs.27207	KIAA0982 protein	10.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	10.6
	439999	AA115811	Hs.6838	ras homolog gene family, member E	10.5
	424368	AB037766	Hs.146085	KIAA1345 protein	10.5
35	402076			C5002020*:gij1082876[pir]S55467 tropomy	10.5
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.5
	445041	T64183	Hs.282982	solute carrier	10.5
	428927	AA441837	Hs.90250	ESTs	10.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulaio	10.5
40	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	10.5
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	10.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	10.5
	438913	AI380429	Hs.172445	ESTs	10.5
	443684	AI681307	Hs.55098	ESTs	10.5
45	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	10.5
	421040	AA715026	Hs.135280	ESTs	10.5
	425277	NM_001241	Hs.155478	cyclin T2	10.5
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	10.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.5
50	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	10.5
	419972	AL041465	Hs.182982	golgin-87	10.5
	416182	NM_004354	Hs.79069	cyclin G2	10.4
	418365	AW014345	Hs.161690	ESTs	10.4
	452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	10.4
55	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	10.4
	446716	AA436575	Hs.16602	ESTs	10.4
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	10.4
	433023	AW864793	Hs.87409	thrombospondin 1	10.4
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	10.4
60	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	10.4
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	10.4
	443228	W24781	Hs.293798	KIAA1710 protein	10.4
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	10.4
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	10.4
65	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	10.4
	428728	NM_016625	Hs.191381	hypothetical protein	10.4
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	10.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	10.3
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	10.3
70	411359	H86088	Hs.22635	ESTs	10.3
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	10.3
	412262	W26406	Hs.295923	seven in absentia (Drosophila) homolog 1	10.3
	419875	AA853410	Hs.93557	proenkephalin	10.3
	414422	AA147224	Hs.337232	Homeo box A13	10.3
75	426581	AB040956	Hs.135890	KIAA1523 protein	10.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	10.3
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheli	10.3
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	10.3
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	10.3
80	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	10.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	10.3
	451593	AF151879	Hs.26706	CGI-121 protein	10.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	10.3
	438157	AW137011	Hs.49576	ESTs	10.3

	443181	AI039201	Hs.283316	ESTs	10.3
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	10.2
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	10.2
5	446553	AB021179	Hs.15299	HMBa-inducible	10.2
	418278	AI088489	Hs.83937	hypothetical protein	10.2
	419791	AI579909	Hs.105104	ESTs	10.2
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	10.2
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	10.2
10	445564	AB028957	Hs.12896	KIAA1034 protein	10.2
	435021	AA922192	Hs.54709	ESTs	10.2
	457498	AI732230	Hs.191737	ESTs	10.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	10.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	10.2
	446162	AI631319	Hs.63841	hypothetical protein DKFZp434E2318	10.2
15	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	10.2
	427393	AB029018	Hs.177635	KIAA1095 protein	10.1
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	10.1
	437743	AI383497	Hs.131811	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
20	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	10.1
	448172	N75276	Hs.135904	ESTs	10.1
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	10.1
	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATI	10.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	10.1
25	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.1
	410150	AW382942	Hs.6774	ESTs	10.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	10.1
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	10.1
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	10.1
30	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	10.1
	423681	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	10.1
	450205	AI219748	Hs.11356	ESTs	10.1
	408374	AW025430	Hs.155591	forkhead box F1	10.0
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	10.0
35	432589	AL135725	Hs.131708	ESTs	10.0
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	10.0
	411997	AW673478	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	10.0
	419672	AA465113	Hs.23853	ESTs, Weakly similar to A34615 profilagg	10.0
	444564	AI167877	Hs.143716	ESTs	10.0
40	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	10.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	10.0
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	10.0
	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	10.0
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	10.0
45	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	10.0
	442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.0
	418884	AA230228	Hs.59197	ESTs	10.0
	444821	AA053564	Hs.12040	STE20-like kinase	9.9
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	9.9
50	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	9.9
	453127	AI696671	Hs.294110	ESTs	9.9
	435706	W31254	Hs.7045	GL004 protein	9.9
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	9.9
55	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	9.9
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	9.9
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	9.9
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9.9
	432887	AI926047	Hs.162859	ESTs	9.9
	430291	AV660345	Hs.238126	CGI-49 protein	9.9
60	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	9.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	9.9
	428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	9.9
	441054	AA913591	Hs.126480	ESTs	9.9
	415875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	9.9
65	453078	AF053551	Hs.31584	metaxin 2	9.8
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	9.8
	446720	AI439136	Hs.140546	ESTs	9.8
	418475	AI858732	Hs.30443	sentrin/SUMO-specific protease	9.8
	417708	N74392	Hs.50495	ESTs	9.8
70	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	9.8
	420568	F09247	Hs.247735	protocadherin alpha 10	9.8
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	9.8
	453548	AL079983	Hs.116774	integrin, alpha 1	9.8
	427308	D26067	Hs.174905	KIAA0033 protein	9.8
75	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	9.8
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	9.8
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	9.8
	413174	AA723564	Hs.191343	ESTs	9.8
	443250	AI041530	Hs.132107	ESTs	9.8
80	451957	AF796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	9.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	9.8
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	9.8
	427635	BE397988	Hs.179982	tumor protein p53-binding protein	9.8
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	9.8

	439091	AA830144	Hs.135613	ESTs, Moderately similar to I38022 hypot	9.8
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	9.7
	432426	AW973152	Hs.31050	ESTs	9.7
	404571			NM_015902*:Homo sapiens progesteron induce	9.7
5	444427	H25094	Hs.293663	ESTs, Moderately similar to I38022 hypot	9.7
	439183	AW970600	Hs.303261	ESTs	9.7
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	9.7
	432689	AB018320	Hs.278626	Arg/Abl-interacting protein ArgBP2	9.7
10	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.7
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	9.7
	412324	AW978439	Hs.69504	ESTs	9.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	9.7
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	9.7
15	417171	BE613486	Hs.81412	lipin 1	9.7
	421709	AA159394	Hs.107056	CED-6 protein	9.7
	415156	X84908	Hs.78060	phosphorylase kinase, beta	9.7
	436446	AW016809	Hs.323795	ESTs	9.7
	447482	AB033059	Hs.18705	KIAA1233 protein	9.7
20	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	9.7
	429525	N92540	Hs.205353	ecolnucleoside triphosphate diphosphohyd	9.7
	409190	AU076536	Hs.50984	sarcoma amplified sequence	9.6
	419111	AA234172	Hs.137418	ESTs	9.6
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	9.6
25	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class III), chi	9.6
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.6
	419241	AA523939	Hs.165258	ESTs	9.6
	409752	AW963990		gb:EST376063 MAGE resequences, MAGH Homo	9.6
	453894	AW937825	Hs.56847	Homo sapiens cDNA FLJ12874 fis, clone NT	9.6
30	439671	AW162840	Hs.6641	kinesin family member 5C	9.6
	407230	AA157857	Hs.182265	keratin 19	9.6
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	9.6
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	9.6
	434263	N34895	Hs.44648	ESTs	9.6
35	412766	BE544475	Hs.54347	ESTs	9.6
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	9.6
	443970	AI280341	Hs.166571	ESTs	9.6
	424534	D87682	Hs.150275	KIAA0241 protein	9.6
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.6
40	447889	AW469180	Hs.170651	ESTs	9.5
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	9.5
	433165	AA578904	Hs.292437	ESTs	9.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	9.5
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	9.5
45	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	9.5
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	9.5
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	9.5
	432682	AI376400	Hs.159588	ESTs	9.5
	435803	Z44194	Hs.4994	transducer of ERBB2, 2	9.5
50	437444	H46008	Hs.31518	ESTs	9.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	9.5
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	9.5
	449226	AB002365	Hs.23311	KIAA0367 protein	9.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	9.4
55	420969	AI636310	Hs.28310	ESTs	9.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	9.4
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	9.4
	420805	L10333	Hs.99947	reticulon 1	9.4
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	9.4
60	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	9.4
	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	9.4
	425657	T89839	Hs.119471	ESTs	9.4
	428250	AW809208	Hs.183297	DKFZP566F2124 protein	9.4
	453293	AA382267	Hs.10653	ESTs	9.4
65	412446	AI768015	Hs.92127	ESTs	9.4
	441102	AA973905	Hs.331328	intermediate filament protein syncoilin	9.4
	421689	N87820	Hs.106826	KIAA1696 protein	9.4
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	9.4
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	9.4
70	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	9.4
	441499	AW298235	Hs.101689	ESTs	9.4
	420184	AA188408	Hs.95665	hypothetical protein	9.4
	420061	AW024937	Hs.29410	ESTs	9.4
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.4
75	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.3
	450580	N40087	Hs.15248	ESTs	9.3
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	9.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	9.3
	412639	AW961284	Hs.296235	ESTs	9.3
80	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	9.3
	446131	NM_000929	Hs.290	phospholipase A2, group V	9.3
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	9.3
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.3
	425139	AW630488	Hs.325820	protease, serine, 23	9.3

5	448807	AI571940	Hs.7549	ESTs	9.3
	412505	AA974491	Hs.21734	ESTs	9.3
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	9.3
	445704	AI493742	Hs.165210	ESTs, Moderately similar to I38022 hypot	9.3
	402855			NM_001839*:Homo sapiens calponin 3, acid	9.3
	428465	AW970976	Hs.293653	ESTs	9.3
	422564	AI148006	Hs.222120	ESTs	9.3
	430027	AB023197	Hs.227743	KIAA0980 protein	9.2
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.2
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	9.2
	433862	D86960	Hs.3610	KIAA0205 gene product	9.2
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	9.2
	401558			ENSP00000220478*:SECRETOGRANIN III.	9.2
15	428634	AA811845	Hs.106290	Kelch motif containing protein	9.2
	437678	AA829860	Hs.122834	ESTs	9.2
	416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.2
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	9.2
20	431187	AW971146	Hs.293187	ESTs	9.2
	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	9.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	9.1
	430669	AW969657	Hs.291029	ESTs	9.1
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	9.1
25	448822	BE149845	Hs.289038	hypothetical protein MGC4126	9.1
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	9.1
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (9.1
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	9.1
	434361	AF129755	Hs.117772	ESTs	9.1
30	443247	BE614387	Hs.333893	c-Myc target JPO1	9.1
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	9.1
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	9.1
	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	9.1
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	9.1
35	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	9.1
	418821	AA436002	Hs.183161	ESTs	9.1
	427213	AW007211	Hs.16131	hypothetical protein FLJ12876	9.1
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	9.1
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	9.1
40	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	9.1
	447033	AI357412	Hs.157601	ESTs	9.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	9.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	9.0
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	9.0
45	444984	H15474	Hs.132898	fatty acid desaturase 1	9.0
	445674	BE410347	Hs.13063	transcription factor CA150	9.0
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	9.0
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	9.0
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	9.0
50	432161	AK000400	Hs.292807	ESTs, Weakly similar to envelope [H.sapi	9.0
	405523			C8001409*:gil7441226 pir S31212 collage	9.0
	416662	T25853	Hs.7538	ESTs	9.0
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	9.0
55	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	9.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	9.0
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	8.9
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	8.9
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.9
	413554	AA319146	Hs.75426	secrelogranin II (chromogranin C)	8.9
60	414917	C04863	Hs.47191	ESTs	8.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	8.9
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	8.9
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	8.9
	424683	N87519	Hs.27196	ESTs	8.9
65	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	8.9
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	8.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	8.9
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	8.9
	441079	AW150697	Hs.107418	ESTs	8.9
70	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	8.9
	431316	AA502663	Hs.145037	ESTs	8.9
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	8.9
	433628	AI821784	Hs.188578	ESTs	8.9
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	8.9
75	453344	BE349075	Hs.44571	ESTs	8.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	8.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	8.9
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	8.9
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	8.9
80	433213	AW665130	Hs.137190	ESTs	8.9
	451573	AW130351	Hs.243549	ESTs	8.9
	408393	AW015318	Hs.23165	ESTs	8.8
	434725	AK000796	Hs.4104	hypothetical protein	8.8
	418876	AA740616		gb:ny97f11.s1 NCL_CGAP_GCB1 Homo sapiens	8.8

	444558	AW181975	Hs.165892	ESTs	8.8
	417355	D13168	Hs.82002	endothelin receptor type B	8.8
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	8.8
5	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	8.8
	424956	AW198103	Hs.158154	ESTs, Weakly similar to granule cell mar	8.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	8.8
	444647	H14718	Hs.11506	Human clone 23589 mRNA sequence	8.8
	444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!!	8.8
10	409643	AW450866	Hs.257359	ESTs	8.8
	428647	AA830050	Hs.124344	ESTs	8.8
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	8.8
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	8.8
	425465	L18964	Hs.1904	protein kinase C, iota	8.8
15	424113	AI743880	Hs.12876	ESTs	8.8
	459324	AW080953		gb:xc28c12.x1 NCL_CGAP_Co18 Homo sapiens	8.8
	451684	AF216751	Hs.26813	CDA14	8.8
	451244	AW008798	Hs.267448	hypothetical protein FLJ20039	8.8
	439170	AA332365	Hs.165539	ESTs, Weakly similar to I38022 hypothe	8.8
20	424238	AA337401	Hs.137635	ESTs	8.8
	449686	AW072813	Hs.270868	ESTs, Moderately similar to ALUA_HUMAN A	8.8
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	8.8
	410870	U81599	Hs.66731	homeo box B13	8.8
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	8.8
25	429831	AA564489	Hs.137526	ESTs	8.8
	453468	W00712	Hs.32990	DKFZP566F084 protein	8.8
	428340	AF261088	Hs.154721	aconitase 1, soluble	8.8
	453345	AA302862	Hs.90063	neurocalcin delta	8.8
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	8.8
30	440486	BE243513	Hs.7212	hypothetical protein PP1044	8.7
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	8.7
	408949	AF189011	Hs.49163	putative ribonuclease III	8.7
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
35	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.7
	408242	AA251594	Hs.43913	PIBF1 gene product	8.7
	430848	AW021726		gb:df27e02.y1 Morton Fetal Cochlea Homo	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypothe	8.7
40	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	8.7
	425913	AA365799	Hs.50785	SEC22, vesicle trafficking protein (S. c	8.7
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	8.7
	427723	AI355260	Hs.279789	histone deacetylase 3	8.7
	441683	BE564214	Hs.102946	ESTs	8.7
45	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	8.7
	428259	AA424793	Hs.24144	ESTs	8.7
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	8.7
	420041	AB005142	Hs.94592	klotho	8.7
	432432	AA541323	Hs.115831	ESTs	8.7
50	452335	AW188944	Hs.61272	ESTs	8.7
	412673	AL042957	Hs.31845	ESTs	8.7
	430335	D80007	Hs.239499	KIAA0185 protein	8.7
	419904	AA974411	Hs.18672	ESTs	8.6
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	8.6
55	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	8.6
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.6
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	8.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	8.6
	419647	AA348947	Hs.91816	hypothetical protein	8.6
60	425907	AA365752	Hs.155965	ESTs	8.6
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	8.6
	424434	H87028	Hs.146861	hypothetical protein FLJ20580	8.6
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	8.6
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	8.6
65	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.6
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	8.6
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	8.6
	441790	AW294909	Hs.132208	ESTs	8.6
	441124	T97717	Hs.119563	ESTs	8.6
70	438160	AA779332	Hs.122671	ESTs	8.6
	433264	D85782	Hs.3229	cysteine dioxygenase, type I	8.6
	434851	AA806164	Hs.116502	ESTs	8.6
	420608	BE548277	Hs.103104	ESTs	8.6
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	8.6
75	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	8.5
	454058	AI273419	Hs.135146	hypothetical protein FLJ13984	8.5
	435614	R09718	Hs.20403	ESTs	8.5
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	8.5
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	8.5
80	447894	AW204253	Hs.21912	ESTs	8.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	8.5
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	8.5
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	8.5
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	8.5

5	434747	AA837085	Hs.220585	ESTs	8.5
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	8.5
	450813	AI739625	Hs.203376	ESTs	8.5
	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.5
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	8.5
	440840	AW629666	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	8.5
	407891	AA486620	Hs.41135	endomucin-2	8.5
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	8.5
10	432620	AA777749	Hs.5978	LIM domain only 7	8.5
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	8.5
	408170	AW204516	Hs.31835	ESTs	8.5
	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	8.5
	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	8.5
15	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	8.5
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	8.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	8.4
	418120	AA213437	Hs.192249	ESTs	8.4
	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	8.4
20	432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	8.4
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	8.4
	434384	AA631910	Hs.162849	ESTs	8.4
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	8.4
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	8.4
25	421622	AB037748	Hs.106204	KIAA1327 protein	8.4
	431160	AW971174	Hs.324330	ESTs	8.4
	449567	AI990790	Hs.188614	ESTs	8.4
	411088	BE247593	Hs.145053	ESTs	8.4
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	8.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.3
30	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	8.3
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	8.3
	438440	AA807228	Hs.225161	ESTs	8.3
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	8.3
35	422295	AF051151	Hs.114408	tol-like receptor 5	8.3
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	8.3
	425242	D13635	Hs.155287	KIAA0010 gene product	8.3
	432769	AA620814	Hs.144959	ESTs	8.3
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.3
40	427229	AI799751	Hs.5635	ESTs	8.3
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	8.3
	403149			NM_001450:Homo sapiens four and a half L	8.3
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	8.3
	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
45	436476	AA326108	Hs.33829	bHLH protein DEC2	8.3
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	8.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	8.3
	453121	AI968264	Hs.232286	ESTs	8.3
	420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp434O0921 (f	8.3
50	426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	8.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	8.2
	425707	AF115402	Hs.11713	E74-like factor 5 (els domain transcript	8.2
	440080	AW051597	Hs.143707	ESTs	8.2
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.2
55	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	8.2
	432695	D63480	Hs.278634	KIAA0146 protein	8.2
	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	8.2
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	8.2
	418051	AW192535	Hs.19479	ESTs	8.2
60	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	8.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!	8.2
	417958	AA767382	Hs.193417	ESTs	8.2
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	8.2
	430468	NM_004673	Hs.241519	angiotensin-like 1	8.2
65	407802	D84145	Hs.39913	novel RGD-containing protein	8.2
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.2
	414138	AA135884	Hs.3772	ESTs	8.2
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	8.2
	408267	AW380525	Hs.32675	tubulin-specific chaperone e	8.2
70	429692	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypotheti	8.2
	408108	AI580492	Hs.42743	hypothetical protein	8.2
	408418	AW963897	Hs.44743	KIAA1435 protein	8.2
	430334	AI824719	Hs.328700	ESTs	8.2
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	8.2

TABLE 59B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
409385	112523_1	AA071267 T65940 T64515 AA071334

409752 115301_1 AW963990 AA078196 AW749482 AA077468 BE151571 AA376917
 411479 1247077_1 AW848047 AW848202 AW848631 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
 AW848214
 5 411667 1253334_1 BE160198 AW935898 T11520 AW935930 AW856073 AW861034
 416913 163001_1 AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
 418866 179788_1 T65754 AA229857 AA229658
 418876 179960_1 AA740616 AA654854 AA229923
 419536 185688_1 AA603305 AA244095 AA244183
 10 419544 185760_2 AI909154 AA526337 AA244193 AI909153
 423800 232161_1 AA331156 AA331157 AA331155
 426413 266650_1 AA377823 AW954494 AI022688
 429163 300543_1 AA884766 AW974271 AA592975 AA447312
 430848 324621_1 AW021726 AA487752 AA488085
 15 431121 328275_1 AW971157 AA492575 AA492520
 432189 342819_1 AA527941 AI810608 AI620190 AA635266
 432600 350959_1 AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
 434415 385931_1 BE177494 AW276909 AA632849
 434579 38916_1 T55958 T57205 AF147346
 20 439518 47334_1 W76326 AF086341 W72300
 443161 561305_1 AI038316 AI344631 AI261653
 447974 745643_1 R76886 AI453674 R77049

TABLE 59C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400860	9757499	Minus	151830-152104,152649-152744
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
402076	8117410	Plus	128316-128627
402812	6010110	Plus	25026-25091,25844-25920
402855	9662953	Minus	59763-59909
403047	3540153	Minus	59793-59968
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
403149	9799833	Plus	25034-25185
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404571	7249169	Minus	112450-112648
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

Table 60A lists about 1166 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 60A: ABOUT 1166 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	56.6
419526	AI821895	Hs.193481	ESTs	56.2
420154	AI093155	Hs.95420	JM27 protein	44.0
432441	AW292425	Hs.163484	ESTs	41.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	39.9
431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypothe	37.9
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	36.0
446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	32.9
425075	AA506324	Hs.1852	acid phosphatase, prostate	31.1
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	30.0
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	29.8

	400302	N48056		folate hydrolase (prostate-specific memb	28.9
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	27.9
	432101	AI918950	Hs.123642	EphA3	26.3
5	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	26.2
	453096	AW294631	Hs.11325	ESTs	25.7
	400287	S39329	Hs.181350	kallikrein 2, prostatic	25.5
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	24.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	24.5
10	401424			NM_001172:Homo sapiens arginase, type II	24.5
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	22.4
	400292	AA250737	Hs.72472	BMP-R1B	22.3
	407202	N58172	Hs.109370	ESTs	22.3
	415989	AI267700		ESTs	20.2
15	407709	AA456135	Hs.23023	ESTs	20.0
	407168	R45175	Hs.117183	ESTs	19.6
	433444	AW975324	Hs.129816	ESTs	19.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	19.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	18.7
20	410929	H47233	Hs.30643	ESTs	18.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	17.9
	418961	AW967646	Hs.23023	ESTs	17.7
	452792	AB037765	Hs.30652	KIAA1344 protein	17.5
	403047			NM_005556*:Homo sapiens transmembrane pr	17.3
25	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3
	418396	AI765805	Hs.26691	ESTs	17.1
	433647	AA603367	Hs.222294	ESTs	16.9
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	16.7
	430487	D87742	Hs.241552	KIAA0268 protein	16.5
30	440260	AI972867	Hs.7130	copine IV	16.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	15.7
	429220	AW207206		ESTs	15.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	15.3
	418819	AA228776	Hs.191721	ESTs	14.8
35	421513	X00949	Hs.105314	relaxin 1 (H1)	14.8
	429918	AW873986	Hs.119383	ESTs	14.5
	420092	AA814043	Hs.88045	ESTs	14.5
	432473	AI202703	Hs.152414	ESTs	14.4
	450693	AW450461	Hs.203965	ESTs	14.4
40	431548	AI834273	Hs.9711	novel protein	14.4
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	14.3
	430187	AI799909	Hs.158989	ESTs	14.3
	441690	R81733	Hs.33106	ESTs	14.3
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	14.2
45	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	13.7
	450642	R39773	Hs.7130	copine IV	13.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	13.4
	432966	AA650114	Hs.325198	ESTs	13.4
	410330	AW023630	Hs.159425	ESTs	13.4
50	434666	AF151103	Hs.112259	T cell receptor gamma locus	13.1
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	13.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	12.8
	431474	AL133990	Hs.190642	ESTs	12.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	12.5
55	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	12.5
	434217	AW014795	Hs.23349	ESTs	12.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	12.3
	428398	AI249368	Hs.98558	ESTs	12.2
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	12.2
60	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	12.2
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	12.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	12.1
	436032	AA150797	Hs.109276	latexin protein	12.0
	432527	AW975028	Hs.102754	ESTs	12.0
65	434792	AA649253	Hs.132458	ESTs	12.0
	420424	AB033036	Hs.97594	KIAA1210 protein	11.9
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.9
	424846	AU077324	Hs.1832	neuropeptide Y	11.9
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	11.9
70	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	11.8
	432600	AI821085		gb:ns95a12.y5 NCL_CGAP_Pr3 Homo sapiens	11.8
	413597	AW302885	Hs.117183	ESTs	11.8
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	11.7
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	11.6
75	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	11.6
	432435	BE218886	Hs.282070	ESTs	11.5
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	11.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	11.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.5
80	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	11.0
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	10.8

	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.6
	400301	X03635	Hs.1657	estrogen receptor 1	10.5
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	10.5
5	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	10.5
	415539	AI733881	Hs.72472	BMP-R1B	10.4
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!!	10.4
	424432	AB037821	Hs.146858	protocadherin 10	10.3
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	10.3
10	434036	AI659131	Hs.197733	hypothetical protein MGC2849	10.3
	415263	AA948033	Hs.130853	ESTs	10.2
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	10.2
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	10.1
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
15	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	10.0
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	10.0
	432244	AI669973	Hs.200574	ESTs	10.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.9
	450164	AI239923	Hs.63931	ESTs	9.8
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	9.8
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	9.7
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	9.6
	433234	AB040928	Hs.65366	KIAA1495 protein	9.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	9.5
25	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.5
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	9.4
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	9.4
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	9.4
30	450325	AI935962	Hs.26289	ESTs	9.4
	427761	AA412205	Hs.140996	ESTs	9.4
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	9.4
	416795	AI497778	Hs.20509	HBV pX associated protein-8	9.3
	422805	AA436989	Hs.121017	H2A histone family, member A	9.3
35	418848	AI820961	Hs.193465	ESTs	9.2
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	9.2
	415788	AW628686	Hs.78851	KIAA0217 protein	9.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	9.1
	432437	W07088	Hs.293685	ESTs	9.1
40	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	9.1
	436962	AW377314	Hs.5364	DKFZP564I052 protein	9.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	9.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	9.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	9.0
45	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	8.8
	442082	R41823	Hs.7413	ESTs	8.8
	436671	AW137159	Hs.146151	ESTs	8.7
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	8.7
	440774	AI420611	Hs.153934	ESTs	8.7
50	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	8.7
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.6
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	8.6
	443646	AI085198	Hs.164226	ESTs	8.6
55	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	8.5
	428728	NM_016625	Hs.191381	hypothetical protein	8.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.5
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	8.5
	437866	AA156781		metallothionein 1E (functional)	8.5
60	453006	AI362575	Hs.303171	ESTs	8.4
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	8.3
	421040	AA715026	Hs.135280	ESTs	8.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	8.3
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	8.2
65	440749	W22335	Hs.7392	hypothetical protein MGC3199	8.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	8.2
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	8.2
	447156	AW274731	Hs.157920	ESTs	8.1
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.1
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	8.0
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.0
	435981	H74319	Hs.188620	ESTs	7.9
	442081	AA401863	Hs.22380	ESTs	7.9
	434988	AI418055	Hs.161160	ESTs	7.9
75	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	7.8
	420345	AW295230	Hs.25231	ESTs	7.8
	412324	AW978439	Hs.69504	ESTs	7.8
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	7.8
	408374	AW025430	Hs.155591	forkhead box F1	7.8
80	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	7.8
	453160	AI263307	Hs.239884	H2B histone family, member L	7.8
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp566J1922 (f	7.7
	416182	NM_004354	Hs.79069	cyclin G2	7.7
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	7.6

	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	7.6
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	7.5
	443180	R15875	Hs.258576	claudin 12	7.5
5	454119	BE549773	Hs.40510	uncoupling protein 4	7.5
	418693	AI750878	Hs.87409	thrombospondin 1	7.5
	426581	AB040956	Hs.135890	KIAA1523 protein	7.5
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	7.5
	439569	AW602166	Hs.222399	CEGP1 protein	7.4
10	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	7.4
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	7.4
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.3
15	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	7.3
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	7.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	7.3
	428218	AA424266	Hs.123642	EphA3	7.3
	434158	T86534	Hs.14372	ESTs	7.3
20	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	7.3
	430261	AA305127	Hs.237225	hypothetical protein HT023	7.3
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.3
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	7.2
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	7.2
25	420871	AA702972	Hs.65300	ESTs	7.2
	418278	AI088489	Hs.83937	hypothetical protein	7.1
	456516	BE172704	Hs.222746	KIAA1610 protein	7.1
	417511	AL049176	Hs.82223	chordin-like	7.1
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	7.1
30	414422	AA147224	Hs.249195	Homeo box A13	7.1
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	7.1
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.0
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.0
	437872	AK002015	Hs.5887	RNA binding motif protein 7	7.0
35	448148	NM_016578	Hs.20509	HBV pX associated protein-8	7.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.9
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	6.9
	457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo	6.9
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	6.9
40	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.9
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	6.9
	432887	AI926047	Hs.162859	ESTs	6.8
	444931	AV652066	Hs.75113	general transcription factor IIIA	6.8
	421823	N40850	Hs.28625	ESTs	6.8
45	426981	AL044675	Hs.173081	KIAA0530 protein	6.8
	425170	AU077315	Hs.154970	transcription factor CP2	6.8
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	6.8
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	6.8
	439492	AF086310	Hs.103159	ESTs	6.8
50	449919	AI674685	Hs.200141	ESTs	6.8
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	6.8
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	6.7
	441111	AI806867	Hs.126594	ESTs	6.7
	457498	AI732230	Hs.191737	ESTs	6.7
	415293	R49462	Hs.106541	ESTs	6.7
55	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.7
	433908	AW298141	Hs.157975	ESTs	6.7
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.7
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.7
60	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6
	443745	AB039670	Hs.9728	ALEX1 protein	6.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	6.6
	447805	AW627932	Hs.302421	gemin4	6.6
	440995	T57773	Hs.10263	ESTs	6.6
65	422173	BE385828	Hs.250619	phorbol-in-like protein MDS019	6.6
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.6
	437052	AA861697	Hs.120591	ESTs	6.6
	444030	AW021254	Hs.135055	ESTs	6.6
	416836	D54745	Hs.80247	cholecystokinin	6.6
70	447033	AI357412	Hs.157601	ESTs	6.5
	428927	AA441837	Hs.90250	ESTs	6.5
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	6.5
	448779	BE042877	Hs.177135	ESTs	6.4
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	6.4
75	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.4
	432682	AI376400	Hs.159588	ESTs	6.4
	441499	AW298235	Hs.101689	ESTs	6.4
	441676	BE564206	Hs.49889	ESTs	6.4
	421077	AK000061	Hs.101590	hypothetical protein	6.4
80	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	6.4
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	6.4
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	6.3
	452277	AL049013	Hs.28783	KIAA1223 protein	6.3

	412953	Z45794	Hs.238809	ESTs	6.3
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	6.3
	453390	AA862496	Hs.28482	ESTs	6.3
5	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	6.3
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	6.3
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.3
	433610	AA806822	Hs.112547	ESTs	6.3
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	6.3
10	412977	AA125910	Hs.191461	ESTs	6.3
	441217	AI922183	Hs.213246	ESTs	6.3
	443912	R37257	Hs.184780	ESTs	6.3
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	6.2
	435021	AA922192	Hs.54709	ESTs	6.2
15	425465	L18964	Hs.1904	protein kinase C, iota	6.2
	418821	AA436002	Hs.183161	ESTs	6.2
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	6.2
	448106	AI800470	Hs.171941	ESTs	6.2
	408418	AW963897	Hs.44743	KIAA1435 protein	6.2
20	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.2
	427078	AI676062	Hs.111902	ESTs	6.2
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	6.2
	449907	AA004825	Hs.103281	ESTs	6.1
	458509	AA654650	Hs.282906	ESTs	6.1
25	437323	AA371145	Hs.194397	leptin receptor	6.1
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	6.1
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	6.1
	412673	AL042957	Hs.31845	ESTs	6.0
	410150	AW382942	Hs.260024	ESTs	6.0
30	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	6.0
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	6.0
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	6.0
	409047	AW961434	Hs.31539	ESTs	6.0
	418601	AA279490	Hs.86368	calmegin	6.0
35	425710	AF030880	Hs.159275	solute carrier family, member 4	6.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	6.0
	414905	H40873	Hs.175971	ESTs	6.0
	450295	AI766732	Hs.210628	ESTs	6.0
	412505	AA974491	Hs.21734	ESTs	6.0
40	428730	AA625947	Hs.25750	ESTs	6.0
	445413	AA151342	Hs.12677	CGI-147 protein	6.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	5.9
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	5.9
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	5.9
45	431359	AW993522	Hs.292934	ESTs	5.9
	404632			NM_022490:Homo sapiens hypothetical prot	5.9
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	5.9
	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	405523			C8001409:gil7441226[pilr]S31212 collage	5.9
50	448807	AI571940	Hs.7549	ESTs	5.8
	404642			NM_021965:Homo sapiens phosphoglucomuta	5.8
	452598	AI831594		ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.8
55	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.8
	419038	AW134924	Hs.190325	ESTs	5.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.7
	432432	AA541323	Hs.115831	ESTs	5.7
	435937	AA830893	Hs.119769	ESTs	5.7
60	414528	AA148950	Hs.188836	ESTs	5.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	5.7
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	5.7
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	5.7
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	5.7
65	420184	AA188408	Hs.95665	hypothetical protein	5.7
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	5.7
	443250	AI041530	Hs.132107	ESTs	5.7
	443324	R44013	Hs.164225	ESTs	5.7
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	5.7
70	448172	N75276	Hs.135904	ESTs	5.7
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.6
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	5.6
	452242	R50956	Hs.159993	glycosyltransferase	5.6
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	5.6
75	418019	R68911	Hs.176275	ESTs	5.6
	450813	AI739625	Hs.203376	ESTs	5.6
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	5.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.6
	451684	AF216751	Hs.26813	CDA14	5.6
80	427674	NM_003528	Hs.2178	H2B histone family, member Q	5.6
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens	5.6
	417958	AA767382	Hs.193417	ESTs	5.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	5.6
	435176	AA744875	Hs.189413	ESTs	5.5

	428465	AW970976	Hs.293653	ESTs	5.5
	431316	AA502663	Hs.145037	ESTs	5.5
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	5.5
5	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	5.5
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.5
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.5
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	5.5
	416239	AL038450	Hs.48948	ESTs	5.4
10	421470	R27496	Hs.1378	annexin A3	5.4
	408177	AI241733	Hs.43871	ESTs	5.4
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	5.4
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	5.4
	448072	AI459306	Hs.24908	ESTs	5.4
15	420397	NM_007018	Hs.97437	centrosomal protein 1	5.4
	429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	5.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.4
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.4
20	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.4
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	5.4
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	5.4
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.3
25	412677	AW029608	Hs.17384	ESTs	5.3
	430412	AW341754	Hs.189305	ESTs	5.3
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	5.3
	421433	AI829192	Hs.22380	ESTs	5.3
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	5.3
30	458571	AV653731	Hs.282829	ESTs, Moderately similar to PC4259 ferri	5.3
	441054	AA913591	Hs.126480	ESTs	5.3
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	5.3
	433409	AI278802	Hs.25661	ESTs	5.3
	441102	AA973905		intermediate filament protein syncoilin	5.3
35	453387	AI990741	Hs.252809	ESTs	5.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.3
	433923	AI823453	Hs.146625	ESTs	5.3
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.2
	447574	AF162666	Hs.18895	tousled-like kinase 1	5.2
40	421896	N62293	Hs.45107	ESTs	5.2
	410870	U81599	Hs.66731	homeo box B13	5.2
	420729	AW964897	Hs.290825	ESTs	5.2
	425066	M82882	Hs.154365	E74-like factor 1 (els domain transcript	5.2
	429467	NM_004477	Hs.203772	F5HD region gene 1	5.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	5.2
	446553	AB021179	Hs.15299	HMBA-inducible	5.2
	453308	AW959731	Hs.323099	ESTs	5.2
	452576	AB023177	Hs.29900	KIAA0960 protein	5.2
	421437	AW821252	Hs.104336	hypothetical protein	5.2
50	422295	AF051151	Hs.114408	toll-like receptor 5	5.2
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.2
	400424	AJ276316	Hs.287374	zinc finger protein 304	5.2
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.2
	452588	AA889120	Hs.110637	homeo box A10	5.2
55	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.1
	413991	H44725	Hs.176090	ESTs	5.1
	444454	BE018316	Hs.11183	sorting nexin 2	5.1
	446795	AI797713	Hs.156471	ESTs	5.1
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.1
60	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	5.1
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogeni	5.1
	453293	AA382267	Hs.10653	ESTs	5.1
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	5.1
	409643	AW450866	Hs.257359	ESTs	5.1
65	427723	AI355260	Hs.279789	histone deacetylase 3	5.1
	438157	AW137011	Hs.49576	ESTs	5.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	5.1
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	5.1
	418051	AW192535	Hs.19479	ESTs	5.1
70	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.1
	425843	BE313280	Hs.159627	death associated protein 3	5.1
	440594	AW445167	Hs.126036	ESTs	5.1
	452449	AW068658	Hs.20943	ESTs	5.1
	429769	NM_004917	Hs.218366	kallikrein 4 (prostase, enamel matrix, p	5.1
75	428898	AB033070	Hs.194408	KIAA1244 protein	5.1
	415339	NM_015156	Hs.78398	KIAA0071 protein	5.1
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	5.1
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.0
	433023	AW864793	Hs.87409	thrombospondin 1	5.0
80	433862	D86960	Hs.3610	KIAA0205 gene product	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	418624	AI734080	Hs.104211	ESTs	5.0
	430291	AV660345	Hs.238126	CGI-49 protein	5.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.0

	429922	Z97630	Hs.226117	H1 histone family, member 0	5.0
	420218	AW958037	Hs.286	ribosomal protein L4	5.0
	425242	D13635	Hs.155287	KIAA0010 gene product	5.0
5	427176	AW381569	Hs.40334	ESTs	5.0
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.0
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.0
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	5.0
	450244	AA007534	Hs.125062	ESTs	5.0
10	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	5.0
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	5.0
	445866	H20899	Hs.13399	Homo sapiens clone 25032 mRNA sequence	4.9
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	4.9
15	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	4.9
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	4.9
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	4.9
	401451			NM_004496*:Homo sapiens hepatocyte nucle	4.9
20	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.9
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.9
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.9
	420608	BE548277	Hs.103104	ESTs	4.9
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.9
	424332	AA338919	Hs.101615	ESTs	4.9
25	430523	AW451385	Hs.161954	ESTs	4.9
	449300	AI656959	Hs.346514	ESTs	4.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	4.9
	438321	AA576635	Hs.6153	CGI-48 protein	4.9
30	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.9
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.8
	425174	D87450	Hs.154978	KIAA0261 protein	4.8
	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	4.8
	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	4.8
35	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	4.8
	449539	W80363	Hs.58446	ESTs	4.8
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.8
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	4.8
40	420210	AI557257	Hs.44811	ESTs	4.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.8
	428647	AA830050	Hs.124344	ESTs	4.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	4.8
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	4.8
45	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	4.8
	416030	H15261	Hs.21948	ESTs	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	4.8
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.7
50	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.7
	443684	AI681307	Hs.55098	ESTs	4.7
	415621	AI648602	Hs.55468	ESTs	4.7
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.7
	424433	H04607	Hs.9218	ESTs	4.7
55	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	4.7
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	4.7
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	4.7
	434973	AW449285	Hs.313636	EST	4.7
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.7
60	431587	NM_016179	Hs.262960	transient receptor potential channel 4	4.7
	452260	AA453208		RAB9, member RAS oncogene family	4.7
	412846	AW961245	Hs.55896	Homo sapiens PAC clone RP5-978E18 from 7	4.7
	418836	AI655499	Hs.161712	ESTs	4.7
	401558			ENSP00000220478*:SECRETOTRANIN III.	4.7
65	441647	AA534210	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H	4.7
	443881	R64512	Hs.237146	hypothetical protein FLJ12752	4.7
	417169	R13550	Hs.246773	ESTs	4.7
	423349	AF010258	Hs.127428	homeo box A9	4.7
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	4.7
70	444951	AI783767	Hs.148635	ESTs, Moderately similar to ALUB_HUMAN I	4.6
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.6
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.6
	423242	AL039402	Hs.125783	DEME-6 protein	4.6
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	4.6
75	419005	T86358	Hs.193931	ESTs, Weakly similar to I54374 gene NF2	4.6
	403046			NM_005656*:Homo sapiens transmembrane pr	4.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.6
	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	4.6
	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	4.6
80	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	4.6
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	4.6
	452994	AW962597	Hs.31305	KIAA1547 protein	4.6
	446091	AW022192	Hs.200197	ESTs	4.6
	432908	AI861896	Hs.304505	ESTs	4.6

	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	4.6
	431673	AW971302	Hs.293233	ESTs	4.6
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	4.6
5	452355	N54926	Hs.29202	G protein-coupled receptor 34	4.6
	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	4.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	4.6
	409019	AW385412	Hs.9615	myosin regulatory light chain 2, smooth	4.6
	413812	AW188687	Hs.44748	ESTs	4.6
10	414343	AL036166	Hs.323378	coated vesicle membrane protein	4.6
	434423	NM_006769	Hs.3844	LIM domain only 4	4.5
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	421724	AB037832	Hs.107287	KIAA1411 protein	4.5
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.5
15	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	4.5
	446720	AI439136	Hs.140546	ESTs	4.5
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.5
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	4.5
	423412	AF109300		prostate cancer associated protein 5	4.5
20	433507	AI817336	Hs.191791	ESTs	4.5
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.5
	423782	AI472209	Hs.323117	ESTs	4.5
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.5
25	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	4.5
	428715	AW293716	Hs.53126	ESTs	4.5
	429857	AF089897	Hs.294030	topoisomerase-related function protein 4	4.5
	459561	AI547306		ESTs	4.5
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.5
30	414272	AI651603	Hs.46988	ESTs	4.5
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	4.5
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	4.5
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.5
	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	4.5
35	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	4.5
	401519			C15000476*:gij12737279[refXP_012163.1]	4.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.5
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.4
40	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	4.4
	433517	AW022133	Hs.189838	ESTs	4.4
	429559	AI985345	Hs.26425	ESTs	4.4
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.4
	409190	AU076536	Hs.50984	sarcoma amplified sequence	4.4
45	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.4
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.4
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	4.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	4.4
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	4.4
50	434384	AA631910	Hs.162849	ESTs	4.4
	444564	AI167877	Hs.143716	ESTs	4.4
	447500	AI381900	Hs.159212	ESTs	4.4
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.4
	408380	AF123050	Hs.44532	diubiquitin	4.4
55	448766	AI473827	Hs.31793	ESTs	4.4
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.4
	432810	AA863400		ESTs	4.4
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	4.4
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.4
60	434022	R18374	Hs.117956	ESTs	4.4
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	4.4
	417728	AW138437	Hs.24790	KIAA1573 protein	4.4
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
65	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	4.3
	448550	AL161983	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (f	4.3
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.3
	452335	AW188944	Hs.61272	ESTs	4.3
70	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	4.3
	450316	W84446	Hs.226434	hypothetical protein MGC4643	4.3
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	4.3
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	4.3
	424534	D87682	Hs.150275	KIAA0241 protein	4.3
75	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	4.3
	435023	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	4.3
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	4.3
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.3
	421163	AA375974	Hs.32450	ESTs, Weakly similar to T23762 hypotheti	4.3
80	420405	AA743396	Hs.189023	ESTs	4.3
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.3
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	4.3
	439764	T26535	Hs.22744	hypothetical protein MGC13105	4.3
	446351	AW444551	Hs.35380	x 001 protein	4.3

5	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.3
	414312	AA155694	Hs.191060	ESTs	4.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	4.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	4.3
	414680	AA743331		hemoglobin, alpha 2	4.3
10	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	4.3
	440840	AW629666		ESTs, Weakly similar to S64054 hypothei	4.3
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	4.3
	434874	N62448	Hs.293970	methyilmalonate-semialdehyde dehydrogenas	4.2
	431429	AF072813		reticulon 3	4.2
15	413492	D87470	Hs.75400	KIAA0280 protein	4.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	4.2
	435846	AA700870	Hs.14304	ESTs	4.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	4.2
	450546	AA010200	Hs.175551	ESTs	4.2
20	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.2
	416445	AL043004	Hs.79337	KIAA0135 protein	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.2
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	4.2
25	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	4.2
	449685	AW296669	Hs.66095	ESTs	4.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
	450377	AB033091	Hs.74313	KIAA1265 protein	4.2
	419647	AA348947	Hs.91816	hypothetical protein	4.2
30	442049	AA310393	Hs.190044	ESTs	4.2
	430669	AW969657	Hs.291029	ESTs	4.2
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	4.1
	443634	H73972	Hs.134460	ESTs	4.1
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	4.1
35	422634	NM_016010	Hs.118821	CGI-62 protein	4.1
	445895	D29954	Hs.13421	KIAA0056 protein	4.1
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	4.1
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.1
	447752	M73700	Hs.105938	lactotransferrin	4.1
40	402855			NM_001839*:Homo sapiens calponin 3, acid	4.1
	443161	AI038316		gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_	4.1
	415827	H17462	Hs.23079	ESTs	4.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	4.1
	418365	AW014345	Hs.161690	ESTs	4.1
45	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	4.1
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	4.1
	446657	AI335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.1
	421141	AW117261	Hs.125914	ESTs	4.1
	430335	D80007	Hs.239499	KIAA0185 protein	4.1
50	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	4.1
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	4.1
	410592	R94088	Hs.43569	ESTs	4.1
55	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.1
	428634	AA811845	Hs.106290	Kelch motif containing protein	4.1
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	4.1
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.0
	443273	AI042063	Hs.132156	ESTs	4.0
60	428055	AA420564	Hs.101760	ESTs	4.0
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	4.0
	451294	AI457338	Hs.29894	ESTs	4.0
	430519	AF129534	Hs.49210	F-box only protein 4	4.0
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	4.0
65	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.0
	409706	BE158773	Hs.213207	ESTs	4.0
	447082	T85314		thioredoxin-like	4.0
70	418594	AI732083	Hs.187619	ESTs	4.0
	426501	AW043782	Hs.293616	ESTs	4.0
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	4.0
	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHst Homo	4.0
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	4.0
75	425920	AL049977	Hs.162209	claudin 8	4.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	4.0
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.0
	433209	AB040907	Hs.278436	KIAA1474 protein	4.0
	428801	AW277121	Hs.254881	ESTs	4.0
80	419629	AB020695	Hs.91662	KIAA0888 protein	4.0
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.9
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	3.9
	400695			C11002514*:gil11280151 pir E82756 beta-	3.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	3.9
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.sa	3.9
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	3.9
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.9

5	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	3.9
	427615	BE410107	Hs.179817	CGI-82 protein	3.9
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.9
	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	3.9
10	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.9
	431147	AI767751	Hs.20300	ESTs	3.9
	439192	AW970536	Hs.105413	ESTs	3.9
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.9
	451900	AB023199	Hs.27207	KIAA0982 protein	3.9
15	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	3.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.9
	442320	AI287817	Hs.129636	ESTs	3.9
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	3.9
	444636	T96667	Hs.17877	ESTs	3.9
20	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	3.9
	412576	AA447718	Hs.107057	ESTs	3.9
	423952	AW877787	Hs.136102	KIAA0853 protein	3.9
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	3.9
25	447280	BE617907	Hs.97635	ESTs	3.9
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.8
	450580	N40087		ESTs	3.8
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.8
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.8
30	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.8
	412652	AI801777	Hs.260024	ESTs	3.8
	426226	AA769045		gb:oa80h07.s1 NCI_CGAP_GCB1 Homo sapiens	3.8
	437816	AI823445	Hs.280699	ESTs	3.8
35	444534	AW271626	Hs.42294	ESTs	3.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	3.8
	408242	AA251594	Hs.43913	PIBF1 gene product	3.8
	443484	AI091458	Hs.134559	ESTs	3.8
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.8
40	428043	T92248	Hs.2240	uteroglobin	3.8
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.8
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.8
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	3.8
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.8
45	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.8
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	3.8
	408547	AA574291	Hs.57837	ESTs	3.8
	427635	BE397988	Hs.179982	tumor protein p53-binding protein	3.8
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.8
50	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.8
	453698	AA037615	Hs.42746	ESTs	3.8
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	3.8
	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	3.8
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.8
55	438138	R98299	Hs.177502	ESTs	3.8
	447906	AL050062	Hs.19999	DKFZP566K023 protein	3.8
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.7
	435655	AW105663	Hs.6947	HSPC069 protein	3.7
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	3.7
60	439398	AA284267	Hs.221504	ESTs	3.7
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	3.7
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	418576	AW968159	Hs.289104	Epithelial calcium channel 2, CaT-like A	3.7
	436024	AI800041	Hs.190555	ESTs	3.7
65	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.7
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.7
	442861	AA243837	Hs.57787	ESTs	3.7
	448207	AI475490	Hs.170577	ESTs	3.7
	450628	AW382884	Hs.204715	ESTs	3.7
70	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.7
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	3.7
	443031	AW134696	Hs.49418	ESTs	3.7
	447608	AW205042	Hs.18955	Homo sapiens cDNA FLJ20667 fis, clone KA	3.7
	408312	AF263613	Hs.44198	intracellular membrane-associated calciu	3.7
75	412777	AI335773	Hs.270123	ESTs	3.7
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.7
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	3.7
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	3.7
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.7
80	452129	AW291379	Hs.212827	ESTs	3.7
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	3.7
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.7
	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	3.7
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
	423855	AA331761	Hs.254859	ESTs	3.7
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.7

	434470	AA634818	Hs.298138	ESTs	3.7
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	3.7
	420026	AI831190	Hs.166676	ESTs	3.7
5	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	3.7
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	3.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.7
	445941	AI267371	Hs.172636	ESTs	3.6
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.6
10	412533	AA679863	Hs.69606	ESTs	3.6
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	3.6
	442710	AI015631	Hs.23210	ESTs	3.6
	448212	AI475858		gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sapiens	3.6
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.6
15	453038	AW292415	Hs.20509	HBV pX associated protein-8	3.6
	427661	AA410292	Hs.104761	ESTs	3.6
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	3.6
	414844	AA296874	Hs.77494	deoxyguanosine kinase	3.6
	441866	BE464341	Hs.21201	necln 3; DKFZP566B0846 protein	3.6
20	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	3.6
	423482	BE280172	Hs.129228	galactokinase 2	3.6
	424677	U09414	Hs.151689	zinc finger protein 137 (clone pHZ-30)	3.6
	430160	AW968210	Hs.293957	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.6
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	3.6
	433887	AW204232	Hs.279522	ESTs	3.6
25	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	3.6
	411890	H92738	Hs.75811	N-acylsphingosine amidohydrolase (acid c	3.6
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6
	431724	AA514535	Hs.283704	ESTs	3.6
30	435703	AW630133	Hs.83313	GK003 protein	3.6
	445674	BE410347	Hs.13063	transcription factor CA150	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.6
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	3.6
35	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	3.6
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	3.6
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	3.6
	439379	AA835002	Hs.125611	ESTs	3.6
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.6
40	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	3.6
	451367	AA923729	Hs.26322	cell cycle related kinase	3.6
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	3.6
	431263	AW129203	Hs.322915	ESTs	3.6
	431952	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.6
45	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	3.6
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	3.5
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.5
	419440	AB020689	Hs.90419	KIAA0882 protein	3.5
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.5
50	419241	AA523939	Hs.165258	ESTs	3.5
	410762	AF226053	Hs.66170	HSKM-B protein	3.5
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.5
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.5
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.5
55	420390	AA330047	Hs.191187	ESTs	3.5
	416662	T25853	Hs.7538	ESTs	3.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	421991	NM_014918	Hs.110488	KIAA0990 protein	3.5
60	413950	AA249096	Hs.32793	ESTs	3.5
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	3.5
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.5
	411149	N68715	Hs.269128	ESTs	3.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.5
65	418334	AA319233	Hs.5521	ESTs	3.5
	422583	AA410506	Hs.27973	KIAA0874 protein	3.5
	425717	X07282	Hs.171495	retinoic acid receptor, beta	3.5
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.5
	434569	AI311295	Hs.344478	KIAA0196 gene product	3.5
70	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	3.5
	437296	AA350994	Hs.20281	KIAA1700	3.5
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	439605	AF086431	Hs.22380	ESTs	3.5
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3.5
75	432589	AL135725	Hs.131708	ESTs	3.5
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.5
	421129	BE439899	Hs.89271	ESTs	3.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.5
80	434839	AI743069	Hs.134736	ESTs	3.5
	435166	AI391470	Hs.158618	ESTs	3.5
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.5
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.5
	453311	AW104911	Hs.126707	hypothetical protein FLJ11457	3.5

5	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
	449909	AA004681	Hs.59432	ESTs	3.5
10	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	3.5
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
15	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BE613337	Hs.234896	geminin	3.4
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
	423645	AI215632	Hs.147487	ESTs	3.4
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.4
20	434966	AA657494		gb:nt66f04.s1 NCL_CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902*:Homo sapiens progesteron induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
	436374	AA400709	Hs.96716	ESTs, Weakly similar to T17210 hypotheti	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
25	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056*:Plasma membrane calcium	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	449603	AI655662	Hs.197698	ESTs	3.4
30	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	437367	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.4
	430144	AI732722	Hs.187694	ERGL protein; ERGIC-53-like protein	3.4
35	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (3.4
	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	3.4
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
40	408267	AW380525	Hs.343564	tubulin-specific chaperone e	3.4
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AI148006	Hs.222120	ESTs	3.4
	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	3.4
45	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AI056769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.4
	443242	BE243910	Hs.9082	nucleoporin p54	3.4
50	445469	AW298370	Hs.153714	complement-c1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.4
	433037	NM_014158	Hs.279938	HSPC067 protein	3.4
	423044	AA320829	Hs.97266	protocadherin 18	3.4
55	434128	W93170	Hs.284164	protein x 0004	3.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.4
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.4
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
	438825	BE327427	Hs.79953	ESTs	3.4
60	446874	AW968304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.4
	419131	AA406293	Hs.41167	ESTs	3.4
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	433764	AW753676	Hs.39982	ESTs	3.4
65	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapi	3.3
	421234	AA907153	Hs.190060	ESTs	3.3
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.3
70	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
75	436664	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
	421476	AW953805	Hs.21887	ESTs	3.3
	422165	AL041199	Hs.1481	histidine decarboxylase	3.3
80	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263*:HSPC213.	3.3
	433404	T32982	Hs.102720	ESTs	3.3
	422546	AB007969	Hs.301478	KIAA0500 protein	3.3
	443884	N20617	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

5	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
	444170	AW613879	Hs.102408	ESTs	3.3
	445474	AI240014	Hs.259558	ESTs	3.3
10	450582	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
	444324	AI301330	Hs.143838	ESTs	3.3
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
15	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	3.3
	400880			NM_000611*:Homo sapiens CD59 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
	451968	H56196	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (fr	3.3
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
20	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
	428523	AW974540	Hs.98626	ESTs	3.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.3
25	432363	AA534489		gb:mf76g11.s1 NCL_CGAP_Co3 Homo sapiens	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	3.3
	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
30	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hfrb1)	3.3
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.3
	411373	BE326276	Hs.8861	ESTs	3.3
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
35	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
	420969	AI636310	Hs.28310	ESTs	3.3
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
40	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	3.3
	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.3
45	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.3
	426775	AA384564		ESTs	3.3
	432378	AI493046	Hs.146133	ESTs	3.3
50	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.3
	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	3.2
	433002	AF048730	Hs.279906	cyclin T1	3.2
55	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
	429377	AA813192	Hs.200596	KIAA0547 gene product	3.2
60	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.2
	420583	H77859	Hs.65450	reticulon 4	3.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.2
	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	3.2
	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chai	3.2
65	421029	AW057782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44656	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
	408412	AW193033	Hs.124436	ESTs	3.2
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
70	421887	AW161450	Hs.109201	CGI-86 protein	3.2
	432409	AA806538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
75	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	3.2
	414342	AA742181	Hs.75912	KIAA0257 protein	3.2
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
80	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.2
	452295	BE379936	Hs.28866	programmed cell death 10	3.2
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.2

	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	415691	AW963979	Hs.24723	ESTs	3.2
5	433852	AI378329	Hs.126629	ESTs	3.2
	439735	AI635386	Hs.142846	hypothetical protein	3.2
	428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
10	415715	F30364	Hs.302204	ESTs	3.2
	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450963	Hs.119991	ESTs	3.2
	436401	AI087958	Hs.29088	ESTs	3.2
15	408784	AW971350	Hs.63386	ESTs	3.2
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.2
	405558			Target Exon	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
20	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AI128606	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	3.2
25	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	3.2
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
30	420131	F08286	Hs.95262	nuclear factor related to kappa B bindin	3.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE393767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220950	ESTs	3.1
	406627	T64904	Hs.163780	ESTs	3.1
35	438666	AW014493	Hs.126727	ESTs	3.1
	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.1
40	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
45	437083	AW082597	Hs.244862	ESTs	3.1
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	419965	H16382	Hs.70258	ESTs	3.1
50	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.1
	446146	AI287539	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.1
55	423947	AW451954	Hs.135941	KIAA1048 protein	3.1
	451893	AW192083	Hs.290855	ESTs	3.1
	447726	AL137638	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.1
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.1
60	443331	AI052026	Hs.149995	ESTs	3.1
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
65	430092	AI821399	Hs.16514	ESTs	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	H80696	Hs.233313	ESTs	3.1
	437756	AA767537	Hs.197096	ESTs	3.1
70	438979	AW976218	Hs.32565	ESTs	3.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
75	438308	AI343469	Hs.127685	KIAA1627 protein	3.1
	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
80	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AI249502	Hs.29669	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	412088	AI689496	Hs.108932	ESTs	3.1
	434361	AF129755	Hs.88474	ESTs	3.1
5	400664			NM_002425:Homo sapiens matrix metallopro	3.1
	436354	AI879252	Hs.5151	RAN binding protein 7	3.1
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
	410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	415245	N59650	Hs.27252	ESTs	3.1
10	418647	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	3.1
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
	453716	AA037675	Hs.152675	ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
	408705	AA312135	Hs.46967	HSPCO34 protein	3.0
15	430280	AA361258	Hs.237868	interleukin 7 receptor	3.0
	445919	T53519	Hs.334692	hypothetical protein MGC14141	3.0
	441790	AW294909	Hs.132208	ESTs	3.0
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
20	422788	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.0
	439703	AF086538	Hs.196245	ESTs	3.0
	444489	AI151010	Hs.157774	ESTs	3.0
	453878	AW964440	Hs.19025	DC32	3.0
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
25	433680	AI805366	Hs.199945	ESTs	3.0
	426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
	426044	AA502490	Hs.170290	ESTs	3.0
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
30	445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
	452737	AK001680	Hs.30488	DKFZP434F091 protein	3.0
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	3.0
	435712	AA694607	Hs.176956	ESTs	3.0
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
35	414993	AW819403	Hs.77724	KIAA0586 gene product	3.0
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
	421988	AW450481	Hs.161333	ESTs	3.0
	432833	N51075	Hs.110028	ESTs	3.0
	445210	H09323	Hs.27133	ESTs	3.0
40	447620	AW290951	Hs.224965	ESTs	3.0
	449375	R07114	Hs.271224	ESTs	3.0
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.0
	443967	AW294013	Hs.200942	ESTs	3.0
	441224	AU076964	Hs.7753	calumenin	3.0
45	448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
	435688	H72286	Hs.128387	ESTs	3.0
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.0
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
	415954	AA171850	Hs.42251	ESTs	3.0
50	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	3.0
	420077	AW512260	Hs.87767	ESTs	3.0
	443475	AI066470	Hs.132809	ESTs	3.0
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	3.0
	438436	AA807168	Hs.271552	ESTs	3.0
55	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
	443280	AA299688	Hs.24183	ESTs	3.0
	448264	AI478933	Hs.188260	ESTs	3.0
	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
	453843	D25215	Hs.35804	hect domain and RLD 3	3.0
60	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	3.0
	445943	AW898533	Hs.181574	ESTs	3.0
	432286	AW327432	Hs.256843	ESTs	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	3.0
	432675	AI791855	Hs.105884	ESTs	3.0
65	443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.0
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
	423583	AL122055	Hs.129836	KIAA1028 protein	3.0
70	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	3.0
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
	410011	AB020641	Hs.57856	PFTAIRES protein kinase 1	3.0
	411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
	438986	AF085888	Hs.269307	ESTs	3.0
75	445921	AW015211	Hs.146181	ESTs	3.0
	447124	AW976438	Hs.17428	RBP1-like protein	3.0
	452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

TABLE 60B

Pkey: Unique Eos probeset Identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT Number	Accessions
5	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
10	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	415989	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
	416288	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
15	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162496 BE161005 AA190449 AW513465 BE161006 BE162499
	417379	167238_1	AA196390 AA507837 AA196468
	418304	173658_2	AA215702 AA368006 AA215703 BE066555 BE006876
20	418647	177521_1	AA226198 AA226513 AA383773
	418866	179788_1	T65754 AA229857 AA229658
	419536	185688_1	AA603305 AA244095 AA244183
	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	423412	228001_1	AF109300 AI299378 AI202654
25	423800	232161_1	AA331156 AA331157 AA331155
	426226	262918_1	AA769045 AA372590 AW963633
	426413	266650_1	AA377823 AW954494 AI022688
	426503	268283_1	AA380153 AA380233 AW963529
	426775	271683_1	AA384564 AW966475 H02121 N41297 D63213 AA886888 AI922414 AW044240 AW196808 AI076736 AA599294 AI954433 AW117617 AI640323 H98134
30	426991	27415_1	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
	428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340
	429163	300543_1	AA884766 AW974271 AA592975 AA447312
35	429220	301384_1	AW207206 AW341473 AA448195 AI951341
	429258	301917_1	AA448765 C04967 C03045 AA658293
	430935	325772_1	AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
	430968	326269_1	AW972830 AA527647 AA489820 AA570362
40	431429	33313_1	AF072813 AF119297 AA362885 AF059524 NM_006054 AA157365 AW163623 AA056148 AA227062 AA418057 AA227076 AA078753 AA233594 D58629 AA232373 AA233577 T35956 BE618035 AA354497 AA359082 T32010 AA134519 BE299901 BE268096 BE396826 AA324268 AL120308 AA187561 AA311680
	432093	341283_1	H28383 AW972670 H28359 AA525808
	432125	341776_1	AW972667 AA526539 AI057032 AW167842
	432189	342819_1	AA527941 AI810608 AI620190 AA635266
45	432340	345248_1	AA534222 AA632632 T81234
	432363	345469_1	AA534489 AW970240 AW970323
	432600	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
	432810	354375_1	AA863400 AI991439 AW016017 AW014704 AI367512 H17550 AA744752 R46187 AW471324 AI126670 AA626033 AI276287 AI094253 AI286003 AI147163 AI911443 AW512612 AA972102 AA999975 AI684428 AI335035 D63102 AI524234 AI539156 AA565542
50	434579	38916_1	T55958 T57205 AF147346
	434966	396504_1	AA657494 AI582663 AI581639
	435023	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
	437866	44433_2	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188
55	438147	45074_1	AW250553 L07876 Z36843 R30693 AI190097 AW965317
	439092	468554_1	AA830149 AW978407 M85983 AW503637
	439518	47334_1	W76326 AF086341 W72300
	439904	479942_1	AW892676 AA853877 D44747
60	440840	50357_2	AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877
	441102	509604_1	AA973905 AI299888 AA917019 H63235 T90771
	442562	54500_2	BE379584 R34211 BE544768 AW973709 AI653056 AI653173 AI266043 AI656750 H74180 AI492830 AI376090 AI472184 D59940 AW170056 AI082443 AW021142 AI167921 AI348677 AI278577 AW130886 AA761517 AI698203 AA115535 AI264790 R34328 D59939 AW205074 AA554902 D62102 AI0007
65	443161	561305_1	AI038316 AI344631 AI261653
	445808	65133_1	AV655234 AW966332 AA340239
	447082	707248_1	T85314 AI360684 T85528 T91254
	448212	755099_1	AI475858 AW969013
70	449625	8113_1	NM_014253 AF100772 BE088769 AI022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303
75	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936687
	452260	9074_1	AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228 BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI38752 AI659875 AW272338 AI423136 AI089270 AI160904 AA664354 BE1
	452598	92338_2	AI831594 AW970667 AW027959 AI129800 AI927949 AI650270 AI625105 AW514661 AI708393 AI138076 BE180510 AI926721 AI399955 AA749139 AI862160 AW874011 AI242763 AA262795 AA039864 H73499 AI093249 BE245661 AI816834 N25206 AA828301 AI084565 AI302816 AA026905 AA77255
80	452815	93255_1	AA418841 AI452657 AI768876 AA028973 BE179873 C00215 AA418930
	453802	981589_1	AL134757 AW079131
	455100	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034

457728 393853_1 AW974811 AA651634 AA650072

TABLE 60C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402031	7656761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59968
403790	8084957	Minus	87826-87947,89835-90002
404571	7249169	Minus	112450-112648
404632	9796668	Plus	45096-45229
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6083

Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of prostate tumor to normal adult body tissue
 R2: Ratio of prostate tumor to normal prostate tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2	42.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	3.2	26.5
420729	AW964897	Hs.290825	ESTs	3.7	15.8
401197			ENSP00000229263*:HSPC213.	3.0	12.6
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	12.4	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3	12.3
443271	BE568568	Hs.195704	ESTs	11.6	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.1	11.2
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4	9.4
417315	AI080042	Hs.180450	ribosomal protein S24	2.3	9.0
416182	NM_004354	Hs.79069	cyclin G2	8.4	8.4
421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	2.2	8.4
434217	AW014795	Hs.23349	ESTs	8.3	8.3
425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3	8.3
442501	AA315267	Hs.23128	ESTs	2.0	8.3
429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1	8.1
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.1	8.0
417407	AA923278	Hs.290905	ESTs, Weakly similar to proleaze [H.sapi	34.0	7.9
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5	7.5
419078	M93119	Hs.89584	insulinoma-associated 1	7.4	7.4
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	9.4	7.3
425018	BE245277	Hs.154196	E4F transcription factor 1	7.2	7.2
452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0	7.0
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.0	6.6
409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3	6.3
411373	BE326276	Hs.8861	ESTs	3.2	6.3
423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7	6.2
422683	AA410506	Hs.27973	KIAA0874 protein	2.3	6.2
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1	6.1
437147	AL049964	Hs.8358	hypothetical protein FLJ20366	2.6	6.0

5	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.3	5.9
	431548	AI834273	Hs.9711	novel protein	15.7	5.8
10	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7	5.7
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.5	5.6
15	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.5	5.5
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
	451684	AF216751	Hs.26813	CDA14	3.9	5.4
20	421470	R27496	Hs.1378	annexin A3	5.3	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
	437571	AA760894	Hs.153023	ESTs	5.2	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
25	444917	R68651	Hs.144997	ESTs	5.1	5.1
	417318	AW953937	Hs.240845	ESTs	4.6	5.1
	434170	AA626509	Hs.122329	ESTs	5.1	5.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	3.3	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
30	421823	N40850	Hs.28625	ESTs	5.0	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
	425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
	439024	R96696	Hs.35598	ESTs	5.4	4.8
35	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
	451952	AL120173	Hs.301663	ESTs	4.7	4.7
	431676	AI685464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	9.1	4.7
40	452242	R50956	Hs.159993	glycosyltransferase	4.7	4.7
	401519			C15000476*:gil12737279 ref XP_012163.1	4.6	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	2.1	4.6
45	408380	AF123050	Hs.44532	diubiquitin	4.2	4.6
	425907	AA365752	Hs.155965	ESTs	2.2	4.6
	427078	AI676062	Hs.111902	ESTs	4.8	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
50	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
	443250	AI041530	Hs.132107	ESTs	8.1	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
55	428826	AL048842	Hs.194019	atractin	2.0	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2	4.2
	429900	AA460421	Hs.30875	ESTs	4.2	4.2
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.2	4.2
60	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
	443622	AI911527	Hs.11805	ESTs	2.2	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1	4.1
65	421129	BE439899	Hs.89271	ESTs	4.1	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
	433887	AW204232	Hs.279522	ESTs	4.1	4.1
70	436556	AI364997	Hs.7572	ESTs	4.1	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
	443646	AI085198	Hs.164226	ESTs	4.1	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0	4.0
75	433409	AI278802	Hs.25661	ESTs	4.0	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9	3.9
	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
80	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.9	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.4	3.8
	452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
	410330	AW023630	Hs.159425	ESTs	6.2	3.8

5	422975	AA347720	Hs.122669	KIAA0264 protein	2.2	3.8
	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.7	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	4.1	3.8
10	418821	AA436002	Hs.183161	ESTs	2.8	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.1	3.8
	453160	AI263307	Hs.239884	H2B histone family, member L	9.2	3.8
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7	3.7
15	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7	3.7
	448807	AI571940	Hs.7549	ESTs	3.6	3.7
	439209	AF087993	Hs.91954	ESTs	2.1	3.6
	420077	AW512260	Hs.87767	ESTs	4.4	3.6
	451009	AA013140	Hs.115707	ESTs	4.1	3.6
20	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.2	3.6
	447033	AI357412	Hs.157601	ESTs	7.7	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6	3.6
25	414680	AA743331		hemoglobin, alpha 2	3.5	3.5
	417380	T06809	Hs.332086	ESTs	3.5	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoeiti	3.5	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.2	3.5
30	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5	3.5
	432101	AI918950	Hs.123642	EphA3	16.5	3.5
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.3	3.5
	435513	AW404075	Hs.42785	DC11 protein	2.2	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	2.1	3.5
35	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	6.7	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	2.1	3.4
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.1	3.4
	440749	W22335	Hs.7392	hypothetical protein MGC3199	2.5	3.3
	408374	AW025430	Hs.155591	forkhead box F1	4.3	3.3
40	400277			Eos Control	2.4	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3	3.3
	443912	R37257	Hs.184780	ESTs	3.3	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	9.9	3.3
45	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.4	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.6	3.3
	451367	AA923729	Hs.26322	cell cycle related kinase	3.3	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	11.5	3.2
50	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	2.0	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2	3.2
	402802			NM_001397:Homo sapiens endothelin conver	4.3	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	2.7	3.2
55	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2	3.2
	448944	AB014605	Hs.22599	alrophin-1 interacting protein 1; activi	3.8	3.2
	444489	AI151010	Hs.157774	ESTs	3.2	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2	3.2
60	453078	AF053551	Hs.31584	melaxin 2	2.1	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	10.6	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	2.8	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	2.1	3.1
	445840	AI277811	Hs.146291	ESTs	3.1	3.1
65	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	2.2	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1	3.1
	430519	AF129534	Hs.49210	F-box only protein 4	3.1	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	16.2	3.1
70	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	9.0	3.1
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	20.9	3.1
	420154	AI093155	Hs.95420	JM27 protein	27.4	3.1
	453293	AA382267	Hs.10653	ESTs	3.7	3.1
75	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypothe	2.4	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	2.9	3.0
	433285	AW975944	Hs.237396	ESTs	7.7	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0	3.0
80	445921	AW015211	Hs.146181	ESTs	4.3	3.0
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.5	3.0
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	2.5	3.0
	450580	N40087		ESTs	3.0	3.0
	447726	AL137638	Hs.19368	matrilin 2	3.9	2.9
	447816	NM_007233	Hs.274329	TP53 target gene 1	7.2	2.9
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	5.1	2.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	2.6	2.9

	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.9	2.9
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisoqu	2.9	2.9
	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	2.9	2.9
5	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
	442320	AI287817	Hs.129636	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
10	451796	AL133019	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (f	2.9	2.9
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.0	2.9
	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
	453628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
15	412324	AW978439	Hs.69504	ESTs	2.0	2.8
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.8	2.8
	433865	N29862	Hs.44104	ESTs	2.8	2.8
20	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
25	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
	444668	AA654650	Hs.282906	ESTs	2.2	2.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abl-interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
30	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
	450546	AA010200	Hs.175551	ESTs	2.2	2.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6	2.7
	458332	AI000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
35	412576	AA447718	Hs.107057	ESTs	2.7	2.7
	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
40	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
	447401	BE618582	Hs.97661	ESTs	2.7	2.7
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
45	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
	422805	AA436989	Hs.121017	H2A histone family, member A	13.6	2.7
	446238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	8.1	2.7
50	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
	410592	R94088	Hs.43569	ESTs	2.6	2.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.6	2.6
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.6	2.6
	433419	AI830342	Hs.211272	ESTs	2.9	2.6
55	447509	AF107454	Hs.107537	chromosome 7 open reading frame 2	2.0	2.6
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	2.4	2.6
	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
60	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
	414312	AA155694	Hs.191060	ESTs	2.6	2.6
	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
65	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.2	2.6
	406627	T64904	Hs.163780	ESTs	8.7	2.6
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.4	2.6
	425815	R94023	Hs.94560	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
	431474	AL133990	Hs.190642	ESTs	9.3	2.5
70	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
75	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.4	2.5
	403047			NM_005656*:Homo sapiens transmembrane pr	21.1	2.5
	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.5	2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
80	436401	AI087958	Hs.29088	ESTs	2.5	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

	446791	AI632278	Hs.195922	ESTs	2.5	2.5
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
	419791	AI579909	Hs.105104	ESTs	2.7	2.5
5	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.0	2.5
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	2.5	2.5
	447702	AI420256	Hs.161271	ESTs	2.1	2.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	2.4	2.4
10	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.4	2.4
	429128	AA446869	Hs.119316	ESTs	2.0	2.4
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	2.4	2.4
	435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
15	407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	4.3	2.4
	447713	AI420733	Hs.207083	ESTs	2.4	2.4
	456848	AL121087	Hs.296406	KIAA0685 gene product	2.2	2.4
20	437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
	432378	AI493046	Hs.146133	ESTs	5.2	2.4
	443180	R15875	Hs.258576	claudin 12	10.1	2.4
	445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
25	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.5	2.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
	421709	AA159394	Hs.107056	CED-6 protein	2.3	2.4
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
30	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
	433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
35	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.1	2.3
	450693	AW450461	Hs.203965	ESTs	2.3	2.3
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	2.3	2.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	4.1	2.3
40	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
	419438	AA406400	Hs.12482	glyceronephosphate O-acyltransferase	2.7	2.3
	443194	AI954968	Hs.279009	matrix Gla protein	2.1	2.3
	414869	AA157291	Hs.21479	ubiquitin 1	2.5	2.3
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.3	2.3
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
45	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	2.3	2.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hfb1)	4.1	2.3
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.2	2.3
	431147	AI767751	Hs.20300	ESTs	5.8	2.3
50	442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
	446091	AW022192	Hs.200197	ESTs	4.0	2.3
	431563	AI027643	Hs.120912	ESTs	2.2	2.3
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	3.5	2.3
55	405685			C2002829:gil4507689[ref NP_003298.1 tra	2.3	2.3
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	2.3	2.3
	450378	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	2.3	2.3
	429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
	417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
60	429277	AW452016	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.6	2.2
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	4.5	2.2
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.9	2.2
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
	431542	H63010	Hs.5740	ESTs	7.0	2.2
65	401558			ENSP00000220478*:SECRETOTRANIN III.	2.2	2.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
	422295	AF051151	Hs.114408	toll-like receptor 5	2.2	2.2
	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.2	2.2
	447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
70	452994	AW962597	Hs.31305	KIAA1547 protein	4.0	2.2
	450325	AI935962	Hs.26289	ESTs	11.9	2.2
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6	2.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
75	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	4.2	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
	422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
80	433293	AF007835	Hs.32417	hypothetical protein MGC4309	11.0	2.2
	410733	D84284	Hs.66052	CD38 antigen (p45)	3.1	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
	408833	AW612232	Hs.254835	ESTs	3.0	2.2

	422424	AI186431	Hs.296638	prostate differentiation factor	4.4	2.2
	433444	AW975324	Hs.129816	ESTs	11.7	2.2
	446354	AW449650	Hs.346335	ESTs	2.6	2.2
5	438869	AF075009		gb:Homo sapiens full length insert cDNA	5.9	2.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
	424036	AA770688		H2A histone family, member L	3.8	2.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.8	2.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	2.2	2.2
10	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
	406068			C2002008:gi 7303957 gb AAAF59000.1 (AE00	3.1	2.1
	415162	AF035718	Hs.78061	transcription factor 21	2.1	2.1
	423349	AF010258	Hs.127428	homeo box A9	5.9	2.1
	424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
15	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	2.1	2.1
20	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	2.1	2.1
	452959	AI933416	Hs.189674	ESTs	2.1	2.1
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
	408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
25	418727	AA227609	Hs.94834	ESTs	2.1	2.1
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
	432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
30	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	2.5	2.1
	434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
	438520	AA706319	Hs.98416	ESTs	2.7	2.1
	414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
35	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
	450861	AI523898	Hs.17617	ESTs	2.4	2.1
	419193	D29643	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.2	2.1
40	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
	407182	AA312561	Hs.230157	ESTs	2.1	2.1
	421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
	432833	N51075	Hs.110028	ESTs	2.1	2.1
	425170	AU077315	Hs.154970	transcription factor CP2	2.6	2.0
45	436278	BE396290	Hs.5097	synaptogyrin 2	2.8	2.0
	438719	AA357129	Hs.239625	integral membrane protein 2B	2.3	2.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.6	2.0
50	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.0	2.0
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
	413627	BE182082	Hs.246973	ESTs	3.3	2.0
	414133	AW022188	Hs.41167	ESTs	2.3	2.0
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	14.7	2.0
55	450244	AA007534	Hs.125062	ESTs	3.1	2.0
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
	409219	AA393383	Hs.133331	ESTs	2.1	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
	421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
60	434128	W93170	Hs.284164	protein x 0004	2.7	2.0
	434503	T96231	Hs.17762	ESTs	2.0	2.0
	443292	AK000213	Hs.9196	hypothetical protein	2.0	2.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
	448172	N75276	Hs.135904	ESTs	6.0	2.0
65	452039	AI922988	Hs.172510	ESTs	2.0	2.0
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	10.1	2.0
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
	451369	AA017321	Hs.269691	ESTs	2.1	2.0
70	434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	5.4	2.0
	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.7	2.0
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	5.5	2.0
	446783	AW138343	Hs.141867	ESTs	4.4	2.0
75	437323	AA371145	Hs.194397	leptin receptor	2.5	2.0
	410076	T05387	Hs.7991	ESTs	2.9	2.0
	421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	2.5	2.0
80						

TABLE 61B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
10	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	419733	187589_1	AW362955 H59488 AI040666 W60959 W94209 H27231 T84625 H75715 W04957 W63676 AA659693 AA514302 W63789 BE046412 T91396 AI951970 AW044233 N20018 AW663548 T90114 AI139947 AA809643 AA846232 AA581966 AA789002
15	424036	23460_1	AA770688 H15373 AW161070 BE304523 BE378517 AA989300 AA904029 BE254211 AA449148 AI268420 AI300495 AI215637 AI300494 AI268551 AA928971 AA179427 AA947684 BE393792 H98018 AI885781 AI188567 AI290658 C15404
	426413	266650_1	AA377823 AW954494 AI022688
	429258	301917_1	AA448765 C04967 C03045 AA658293
	431676	336411_1	AI685464 AW971336 AA513587 AA525142
20	432689	35275_1	AB018320 H56457 AA247916 N83488 N87920 AA095653 T19858 AL134279 AA094167 AI673378 AI000340 R47500 W16595 AW152297 AI625937 AA002027 AI814851 AA902666 AI039729 AW975053 BE302243 AI240793 AA193203 N5581
	438869	46651_1	AF075009 R63109 R63068
	439518	47334_1	W76326 AF086341 W72300
	442677	548626_1	AI557914 W81031 AW473764 AI814081 W81068 AW182826 AW173296 AI376594 AI220500 BE257195 BE246486 R55637 C20788 AI014407 AI248353 AW028015
25	445808	65133_1	AV655234 AW966332 AA340239
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T613
	450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86650 AA010295 BE160823 Z25353 AA150883 AW8
30	453802	981589_1	AL134757 AW079131

TABLE 61C

35

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

40

Pkey	Ref	Strand	Nt_position
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402802	3287156	Minus	53242-53432
403047	3540153	Minus	59793-59968
404641	9796810	Minus	32247-32362
405685	4508129	Minus	37956-38097
406068	9114084	Plus	382-543

45

50

Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

60

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of prostate tumor to normal prostate tissue

65

Pkey	ExAccn	UnigenelD	Unigene Title	R1	
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.5
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
	420729	AW964897	Hs.290825	ESTs	15.8
75	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	13.6
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	13.1
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	12.6
80	401197			ENSP00000229263*.HSPC213.	12.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	12.6
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4
	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3
	443271	BE568568	Hs.195704	ESTs	11.6
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	11.2

	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419553	N34145	Hs.101177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
5	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
10	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AI080042	Hs.180450	ribosomal protein S24	9.0
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.0
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
	425174	D87450	Hs.154978	KIAA0261 protein	8.6
20	445701	AF055581	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	8.4
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	8.4
25	434217	AW014795	Hs.23349	ESTs	8.3
	417363	AW129357	Hs.329700	ESTs	8.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
30	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
	443837	AI984625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
35	436962	AW377314	Hs.5364	DKFZP564I052 protein	7.9
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	7.3
	451900	AB023199	Hs.27207	KIAA0982 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
45	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153684	frizzled-related protein	7.1
	433867	AK000596	Hs.3618	hippocalcin-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
50	423359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20196	adenylate cyclase 9	6.9
55	426759	AI590401	Hs.21213	ESTs	6.8
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.7
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
60	452859	AI300555	Hs.288158	hypothetical protein FLJ23591	6.7
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA622037	Hs.166468	programmed cell death 5	6.6
65	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	6.5
	443020	AI350058	Hs.106129	ESTs	6.5
	415752	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	6.4
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	6.3
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.3
75	411373	BE326276	Hs.8861	ESTs	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	6.2
	418196	AI745649	Hs.26549	KIAA1708 protein	6.1
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1
80	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	6.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447965	AW292577	Hs.94445	ESTs	5.9

	449118	R67477	Hs.23103	Bel1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	5.9
	431548	AI834273	Hs.9711	novel protein	5.8
5	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
10	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	5.8
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7
	431055	AL157645	Hs.48793	sialyltransferase 6 (N-acetylglucosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
15	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
	407938	AA905097	Hs.85050	phospholamban	5.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
20	406672	M26041	Hs.198253	major histocompatibility complex, class	5.5
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.5
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AF013168	Hs.79393	tuberous sclerosis 1	5.5
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
25	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.4
30	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
	451684	AF216751	Hs.26813	CDA14	5.4
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	5.4
	445757	AW449065	Hs.13264	KIAA0856 protein	5.4
	449907	AA004825	Hs.103281	ESTs	5.4
35	419159	AW974945	Hs.268049	hypothetical protein	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.3
	403851			C5002154*.gil7299015[gb]AAF54217.1 (AE0	5.3
40	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	5.3
	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
45	422746	NM_004484	Hs.119651	glypican 3	5.2
	437571	AA760894	Hs.153023	ESTs	5.2
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
50	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	5.2
	453204	R10799	Hs.191990	ESTs	5.2
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	5.1
	444917	R68651	Hs.144997	ESTs	5.1
55	414212	AA136569	Hs.10848	KIAA0187 gene product	5.1
	451693	AF151879	Hs.26706	CGI-121 protein	5.1
	417318	AW953937	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
	433600	R42833	Hs.22232	ESTs	5.0
60	434170	AA626509	Hs.122329	ESTs	5.0
	424090	X99699	Hs.139262	XIAP associated factor-1	5.0
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435706	W31254	Hs.7045	GL004 protein	5.0
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
65	432897	AF155099	Hs.279780	NY-REN-18 antigen	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	5.0
	410762	AF226053	Hs.66170	HSKM-B protein	5.0
	421823	N40850	Hs.28625	ESTs	5.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
70	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.9
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	4.9
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	4.9
75	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.9
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KIAA0010 gene product	4.8
80	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	4.8
	439024	R96696	Hs.35598	ESTs	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8
	430935	AW072916		zinc finger protein 131 (clone pHz-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.7
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	4.7
5	451952	AL120173	Hs.301663	ESTs	4.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
	451831	NM_001674	Hs.460	activating transcription factor 3	4.7
	414522	AW518944	Hs.76325	step II splicing factor SLU7	4.7
	427176	AW381569	Hs.40334	ESTs	4.7
10	441390	AI692560	Hs.131175	ESTs	4.7
	447382	AW027790	Hs.182261	ESTs	4.7
	431676	AI685464		gb:tt88f04.x1 NCL_CGAP_Pr28 Homo sapiens	4.7
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7
15	401519			C15000476*:gij12737279[ref]XP_012163.1]	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.6
	414341	D80004	Hs.75909	KIAA0182 protein	4.6
20	408380	AF123050	Hs.44532	diubiquitin	4.6
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
	425907	AA365752	Hs.155965	ESTs	4.6
	419111	AA234172	Hs.137418	ESTs	4.6
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
	427078	AI676062	Hs.111902	ESTs	4.5
	419326	W94915	Hs.42419	ESTs	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.5
	408705	AA312135	Hs.46967	HSPCO34 protein	4.5
30	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
	449673	AA002064	Hs.18920	ESTs	4.5
	438440	AA807228	Hs.225161	ESTs	4.5
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	4.5
35	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	4.5
	456974	M12529	Hs.169401	apolipoprotein E	4.4
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.4
	436420	AA443956	Hs.31595	ESTs	4.4
40	443250	AI041530	Hs.132107	ESTs	4.4
	411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	4.4
45	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	4.4
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.4
	428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4
	436446	AW016809	Hs.119021	ESTs	4.3
50	450704	H85157	Hs.40696	ESTs	4.3
	438666	AW014493	Hs.126727	ESTs	4.3
	417308	H60720	Hs.81892	KIAA0101 gene product	4.3
	428826	AL048842	Hs.194019	atractin	4.3
	444212	AW503976	Hs.10649	basement membrane-induced gene	4.3
55	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
	447858	AW080339	Hs.80426	ESTs	4.3
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.3
	426827	AW067805	Hs.172665	methyleneetetrahydrofolate dehydrogenase	4.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	4.3
60	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.3
	417986	AA481003	Hs.97128	ESTs	4.3
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
	408088	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
	410853	H04588	Hs.30469	ESTs	4.3
65	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	4.2
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	4.2
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	4.2
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2
70	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.2
	429900	AA460421	Hs.30875	ESTs	4.2
	437672	AW748265	Hs.5741	flavohemoprotein b5?	4.2
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	4.2
	450661	AW952160	Hs.146550	ESTs	4.2
75	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	456804	AI421645	Hs.139851	caveolin 2	4.2
	414291	AI289619	Hs.13040	G protein-coupled receptor 86	4.2
80	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	4.2
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	4.2
	429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
	443622	AI911527	Hs.11805	ESTs	4.1

	436576	AI458213	Hs.77542	ESTs	4.1
	443958	BE241880	Hs.10029	cathepsin C	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1
5	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.1
	421129	BE439899	Hs.89271	ESTs	4.1
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.1
	430383	AI861854	Hs.210778	hypothetical protein FLJ10989	4.1
10	431475	AI567669	Hs.40342	putative nuclear protein	4.1
	446468	AI765890	Hs.16341	MAWD binding protein	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
	404390			Target Exon	4.1
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	4.1
15	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
	433887	AW204232	Hs.279522	ESTs	4.1
20	436556	AI364997	Hs.7572	ESTs	4.1
	430157	BE348706	Hs.278543	ESTs	4.1
	451259	NM_006052	Hs.26146	Down syndrome critical region gene 3	4.1
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1
25	443646	AI085198	Hs.164226	ESTs	4.1
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
	413275	W94748	Hs.48821	ESTs	4.0
30	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	4.0
	433409	AI278802	Hs.25661	ESTs	4.0
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	4.0
	417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
35	421921	H83363	Hs.6820	translocase of inner mitochondrial membr	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
	415710	J04543	Hs.78637	annexin A7	4.0
	457794	AA689292	Hs.246850	ESTs	4.0
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
40	424401	H67220	Hs.169681	death effector domain-containing	4.0
	435905	AW997484	Hs.5003	KIAA0456 protein	4.0
	442731	AI868167	Hs.131044	ESTs	4.0
	418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9
45	439394	AA149250	Hs.56105	ESTs	3.9
	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
	436758	AW977167	Hs.155272	ESTs	3.9
	451030	H40697	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
	405934			Target Exon	3.9
50	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
55	412978	AI431708	Hs.820	homeo box C6	3.9
	414962	AF273304	Hs.235376	XPMC2 protein	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	3.9
	449590	AA694070	Hs.268835	ESTs	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.9
60	450899	T77447	Hs.177864	ESTs	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.8
	452588	AA889120	Hs.110637	homeo box A10	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
65	450506	NM_004460		fibroblast activation protein, alpha	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
	415156	X84908	Hs.78060	phosphorylase kinase, beta	3.8
70	422975	AA347720	Hs.122669	KIAA0264 protein	3.8
	403100			C2001027*.gij7296271[gb]AAF51562.1[AE0	3.8
	422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
	424806	AA382523	Hs.105689	MSTP031 protein	3.8
75	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
	443441	AW291196	Hs.92195	ESTs	3.8
	432529	AI989507	Hs.162245	ESTs	3.8
	432908	AI861896	Hs.304505	ESTs	3.8
80	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
	424855	AW204725	Hs.25560	ESTs	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	3.8

	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
5	453160	AI263307	Hs.239884	H2B histone family, member L	3.8
	416072	AL110370	Hs.79000	growth associated protein 43	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
10	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7
	417348	AI940507	Hs.318526	hypothetical protein FLJ12661	3.7
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
	448807	AI571940	Hs.7549	ESTs	3.7
15	413403	AA129105	Hs.198425	ESTs, Moderately similar to S65657 alpha	3.7
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
	408089	H59799	Hs.42644	thioredoxin-like	3.7
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.7
20	439209	AF087993	Hs.91954	ESTs	3.6
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	3.6
	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	3.6
	456619	AV647917	Hs.107153	inhibitor of growth family, member 1-lik	3.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
25	411213	AA676939	Hs.69285	neuropilin 1	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
30	452260	AA453208		RAB9, member RAS oncogene family	3.6
	439506	AI361238	Hs.41136	ESTs	3.6
	420077	AW512260	Hs.87767	ESTs	3.6
	451009	AA013140	Hs.115707	ESTs	3.6
	436473	AI193122	Hs.132275	ESTs	3.6
35	413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
	443067	AI077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.6
	433269	AI343543	Hs.126890	ESTs	3.6
40	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
	447033	AI357412	Hs.157601	ESTs	3.6
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6
45	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
	443399	AI452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
	401807			C7001350:gil6578126[gb]AAF17706.1[AF0496	3.5
	413979	BE218090	Hs.279453	ESTs	3.5
	414680	AA743331		hemoglobin, alpha 2	3.5
50	417380	T06809	Hs.332086	ESTs	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	3.5
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.5
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	446416	AV658299	Hs.163959	ESTs	3.5
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
	456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
60	432101	AI918950	Hs.123642	EphA3	3.5
	453565	BE298808	Hs.33363	DKFZP434N093 protein	3.5
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.5
	450066	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
65	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
	415528	R17236		gb:yg12c04.r1 Soares infant brain 1NIB H	3.5
	435513	AW404075	Hs.42785	DC11 protein	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	3.5
70	409068	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
	439132	H72803	Hs.38363	ESTs	3.5
	451173	AI765082	Hs.48317	ESTs	3.5
	422673	N59027		gb:yv59d11.r1 Soares fetal liver spleen	3.4
	401597	AA172106		Rag C protein	3.4
75	401744			Target Exon	3.4
	432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	3.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.4
80	435411	AW444619	Hs.138211	ESTs	3.4
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
	437158	AW090198		KIAA1150 protein	3.4
	416375	H95567	Hs.124700	ESTs	3.4
	419441	AW023731	Hs.274368	MSTP032 protein	3.4

	432741	AI732358	Hs.185118	ESTs, Moderately similar to A37413 calbi	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
5	428466	AF151063	Hs.184456	hypothetical protein	3.4
	447397	BE247676	Hs.18442	E-1 enzyme	3.4
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AL046851	Hs.153053	CD37 antigen	3.4
10	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	3.4
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
15	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.4
	444480	AI150730	Hs.265640	ESTs, Moderately similar to A47582 B-cel	3.4
	403389			C3001393*:gij3327090[dbj]BAA31613.1[AB	3.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	3.3
	408374	AW025430	Hs.155591	forkhead box F1	3.3
20	410494	M36564	Hs.64016	protein S (alpha)	3.3
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.3
	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
25	417295	AW993524	Hs.43148	ESTs	3.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
30	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
	425836	AW955696	Hs.90960	ESTs	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
35	436499	AJ276678	Hs.283102	HEF like Protein	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
	426848	H72531	Hs.36190	ESTs	3.3
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	3.3
40	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.3
	430280	AA361258	Hs.237868	interleukin 7 receptor	3.3
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	3.3
	453548	AL079983	Hs.116774	integrin, alpha 1	3.3
45	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
50	410366	AI267589	Hs.302689	hypothetical protein	3.2
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
55	439047	AW979177		gb:EST391287 MAGE resequences, MAGP Homo	3.2
	444451	AV650179	Hs.282431	ESTs	3.2
	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	406973	M34996	Hs.198253	major histocompatibility complex, class	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
60	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
	406247			Target Exon	3.2
	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
65	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984788		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
	441683	BE564214	Hs.102946	ESTs	3.2
70	417386	AL037228	Hs.82043	D123 gene product	3.2
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	422473	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
75	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.2
	435129	AI381659	Hs.267086	ESTs	3.2
	424894	H83520	Hs.153678	reproduction 8	3.2
80	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
	410185	BE294068	Hs.737	immediate early protein	3.2
	451149	AL047506	Hs.10283	RNA binding motif protein 8B	3.2
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypotheli	3.2

	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
5	452413	AW082633	Hs.212715	ESTs	3.1
	409390	AI927212	Hs.3734	ESTs	3.1
	453078	AF053551	Hs.31584	metaxin 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	3.1
10	441124	T97717	Hs.119563	ESTs	3.1
	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	3.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	3.1
15	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
	427399	NM_014883	Hs.177664	KIAA0914 gene product	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
20	445840	AI277811	Hs.146291	ESTs	3.1
	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp434I1216 (f	3.1
	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
25	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
	400194			NM_003763:Homo sapiens syntaxin 16 (STX1	3.1
	400479			Target Exon	3.1
	402895			ENSP00000252117:Myelin transcription fac	3.1
30	403423			Target Exon	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
35	430519	AF129534	Hs.49210	F-box only protein 4	3.1
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	3.1
	422481	AL050163	Hs.117339	DNA-activation protein 10	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	3.1
40	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	3.1
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.1
45	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
50	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
	453293	AA382267	Hs.10653	ESTs	3.1
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	441527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
55	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.0
	411315	AW836547		gb:PM3-LT0032-030100-006-e08 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
60	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	3.0
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
65	421786	AI188653	Hs.21351	ESTs	3.0
	433285	AW975944	Hs.237396	ESTs	3.0
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
70	445345	AW003850	Hs.12532	chromosome 1 open reading frame 21	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
75	428130	AW444985	Hs.77603	ESTs	3.0
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
	426448	R06054		gb:ye89g07.r1 Soares fetal liver spleen	3.0
80	445921	AW015211	Hs.146181	ESTs	3.0
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

451102	AA015683	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	3.0
416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochondr	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

TABLE 62B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411962	126744_1	AA099050 AA099526 T47733
414279	143227_1	AW021691 AI537404 R45431 AI333439 AI741845 AI674468 R44190 R52535 R52617 AI220925 AI979148 AI744688 AW242437 AA618148
414680	147525_1	AI983837 AA399623 AI676204 AI420077 N24944 D51042 AA282786 AA137264 AW236107 AW769
415528	1539409_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288
416128	157163_1	AA708749 AA644620 AA652769 AA242975 AA151074 T19890
416882	162718_1	R17236 R52580 F11642
422673	219674_1	AA173632 AI174858 AA581361 AI700024 AA173988 BE165417 AI366964
426448	267323_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
430935	325772_1	AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
430968	326269_1	N59027 AA314694 N53937 R08100
431304	331286_1	R06054 AA378789 AW956453
431676	336411_1	AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
432125	341776_1	AW972830 AA527647 AA489820 AA570362
432363	345469_1	BE157283 BE157287 AA502438
437158	43392_5	AI685464 AW971336 AA513587 AA525142
437866	44433_2	AW972667 AA526539 AI057032 AW167842
439047	468139_1	AA534489 AW970240 AW970323
439518	47334_1	AW090198 AW173544 AW439860 AW007307 AI762577 W86516 AA160485 AA974203 AI589521 AW451857 AW450602 AI702529 AA630766
450506	836_1	AI801808 AW611634 AI393606 AW235356 AW000736 AW468599 AI582546 AA962057 AA523012 AW51
450580	83929_1	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
452260	9074_1	AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI666686 AI572124 AA04
453024	944876_28	AW979177 AA846994 AA829672
455473	1292917_1	W76326 AF086341 W72300
456719	222707_1	NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
		AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296
		N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
		AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228
		BE326331 AI934576 AI922378 AW276431 AI718486 N36566 AA904753 BE464245 AI338752 AI
		AW846787 AW903370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352
		AW839043 AW839049 AW903372 AW846755 AW846767 AW903368 AW846766 BE146826 AW839056 AW846802 AW
		AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984795 AW984793
		AW984789 AW984823 AW984802 AW984800 AW984799 AW984825 AW984792 AW984821 AW984820 AW
		Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863
		AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW2

TABLE 62C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400479	8439786	Minus	115386-116348
400658	8118459	Minus	73525-73644
400750	8119067	Plus	198991-199168,199316-199548
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-66031
401744	2576349	Plus	14595-14751
401807	7331536	Plus	152325-152912
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402802	3287156	Minus	53242-53432
402895	9967547	Plus	85537-85671,86379-86469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	69340-69615
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39624-40072
405141	8980911	Plus	99861-100054
405934	6758795	Plus	159913-160605
406038	8389537	Plus	37764-37877
406247	7417725	Minus	46234-46461

Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75th percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75th percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of normal prostate tissue to prostate tumor tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M81650	Hs.1968	semenogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X83957	Hs.83870	nebulin	20.7
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.99949	prolactin-induced protein	11.8
415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	AI738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	AI791314		gb:ae46g12.y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	AI459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
405001	U58196		interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.266720	ESTs	6.2
435805	AW470260	Hs.48496	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	5.6
404606			Target Exon	5.6
432326	AI280308	Hs.274361	amiloride-sensitive cation channel 2, ne	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C11000936:gil3746443[gb]AAC63969.1[AF0	4.8
416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	4.8
442082	R41823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440965	AI523646	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel,su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1NIB H	4.6
441040	AW449782	Hs.178803	ESTs	4.6
442764	AI762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
458895	AI535663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	AI801500	Hs.128457	ESTs	4.4
436781	AI914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004348*:Homo sapiens runt-related tra	4.3
442931	AI024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457136	AA428240	Hs.126083	ESTs	4.3
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
458840	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435866	AA704538	Hs.119740	ESTs	4.2
423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	4.2

	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
	400164			Eos Control	4.1
	435519	AI218950	Hs.125461	hypothetical protein FLJ11539	4.1
5	425094	AI955956	Hs.21417	ESTs	4.1
	415928	R46799	Hs.23966	ESTs	4.1
	415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
	426663	AI028767	Hs.262603	ESTs	4.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2)	4.1
10	404260			Target Exon	4.0
	453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
	401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	4.0
	415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
	402817	H24185		hypothetical protein	4.0
15	449233	BE048401	Hs.196511	ESTs	3.9
	435457	AA682421	Hs.59125	ESTs	3.9
	444105	AW189097	Hs.166597	ESTs	3.9
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
	411320	AW836646		gb:PM3-LT0032-090100-008-e05 LT0032 Homo	3.8
20	409679	BE250521		ras homolog gene family, member A	3.8
	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
	446175	AL036568	Hs.291	glutaryl aminopeptidase (aminopeptidase	3.8
	459707	AA631362	Hs.120866	gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens	3.8
	406917	X65964		gb:H.sapiens nestin gene.	3.8
25	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo	3.8
	443313	AI796730	Hs.55513	ESTs	3.8
	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W	3.8
	400499			C10001858:gil6679124[ref]NP_032759.1] ne	3.7
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
30	408229	AW176091		gb:QV0-BT0107-250899-007-b08 BT0107 Homo	3.7
	427318	AF186081	Hs.175783	zinc transporter	3.7
	417620	R02530	Hs.191198	ESTs	3.7
	404660			C9000841*:gil12654691[gb]AAH01185.1 AAH0	3.7
	409144	AW341187	Hs.279714	ESTs	3.7
35	436524	AA922236	Hs.221037	ESTs	3.7
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
	418833	AW974899	Hs.292776	ESTs	3.7
	424887	AA348112	Hs.259461	ESTs	3.7
	404984			Target Exon	3.7
40	454549	AW806910		gb:QV4-ST0023-160400-172-f04 ST0023 Homo	3.7
	426736	AA431615	Hs.130722	ESTs	3.7
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
	438040	AI222422	Hs.121846	ESTs	3.6
	443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
45	442097	AW015799	Hs.128474	ESTs	3.6
	435186	AL119470	Hs.145631	ESTs	3.6
	429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
	456521	AW373450	Hs.286212	hypothetical protein FLJ11729	3.6
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
50	400749			NM_003105*:Homo sapiens sortilin-related	3.6
	450295	AI766732	Hs.210628	ESTs	3.5
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
	434378	AA631739	Hs.335440	EST	3.5
	421342	AA504749		gb:aa63f08.r1 NCI_CGAP_GCB1 Homo sapiens	3.5
55	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
	429043	AI824977	Hs.145319	ESTs	3.5
	438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
	405258			Target Exon	3.4
	440207	AI371978	Hs.128326	ESTs	3.4
60	445045	AI652676	Hs.147256	ESTs	3.4
	406177			Target Exon	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	405735			ENSP00000252164*:KIAA1578 protein (Fragm	3.4
	445797	AI253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.4
65	444286	AI625304	Hs.190312	ESTs	3.4
	442027	AI652926	Hs.128395	ESTs	3.4
	447889	AW469180	Hs.346398	ESTs	3.4
	405152			Target Exon	3.4
	402460			C1001261*:gil2695979[emb]CAA70854.1] (Y0	3.4
70	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
	450588	AA010319	Hs.60389	ESTs	3.4
	447600	AI420990		ESTs	3.4
	406085			Target Exon	3.3
	417959	AW977642	Hs.291742	ESTs	3.3
75	418672	L44284	Hs.12915	ESTs	3.3
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.3
	446516	AW996692	Hs.257557	ESTs, Weakly similar to I38022 hypotheti	3.3
	415896	H08311	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.3
	410140	AL134435	Hs.247837	neurexin 3	3.3
80	458539	AI733837	Hs.145661	ESTs	3.3
	422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
	413381	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
	428561	AW973652	Hs.283105	ESTs	3.2

5	445608	AI830851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
	457733	AW974812	Hs.291971	ESTs	3.2
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	3.2
10	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AI423317	Hs.164680	ESTs	3.2
	418092	R45154	Hs.338439	ESTs	3.2
	411356	H45377		gb:yn99h03.r1 Soares adult brain N2b5HB5	3.1
15	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AJ010063	Hs.343603	titin-cap (telethonin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
	451686	AA059246	Hs.110293	ESTs	3.1
20	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
	401278			Target Exon	3.1
25	418087	AA961613	Hs.127838	ESTs	3.1
	421813	BE048255		gb:tz49b05.y1 NCI_CGAP_Brn52 Homo sapien	3.1
	402490			Target Exon	3.1
	448001	AW293237	Hs.202037	ESTs	3.1
	445316	AI219833	Hs.166767	ESTs	3.1
30	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
	433224	AB040919	Hs.210958	KIAA1486 protein	3.1
	421894	AI418464	Hs.190836	ESTs	3.1
35	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
	405422			ENSP00000216658*:HYPOTHETICAL 133.5 kDa	3.0
	420543	AA278221	Hs.173344	ESTs	3.0
40	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
	408025	AI692784	Hs.41767	PTD002 protein	3.0
	426349	AI308855	Hs.301497	arginyltransferase 1	3.0
45	444576	AI400974	Hs.182045	ESTs	3.0
	430661	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
	459647	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
	435713	AA699313	Hs.114071	ESTs	3.0
50	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	3.0
	456103	Z39430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
	449245	AI636539	Hs.224296	ESTs	3.0
	428132	AA421765		gb:zu24g02.s1 Soares_NhHMPu_S1 Homo sapi	3.0
55	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.9
	432718	AA563943	Hs.244371	ESTs	2.9
	435534	AA830927	Hs.117306	ESTs	2.9
60	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypotheti	2.9
	410289	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr	2.9
	453126	AA032155	Hs.61622	ESTs	2.9
	459421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
	441543	AI733014	Hs.269715	ESTs	2.9
65	442252	AI733395	Hs.129124	ESTs	2.9
	419254	AI469453	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	2.9
	453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	2.9
70	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
	433942	AW272166	Hs.123465	ESTs	2.9
	400461			Target Exon	2.9
75	442640	AI205646	Hs.147220	ESTs	2.9
	438814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.9
	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCI_CGAP_Lym12 Homo sapien	2.8
	407142	AA412535		gb:zi99b10.s1 Soares_testis_NHT Homo sap	2.8
80	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypotheti	2.8
	442907	AI023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
	438690	AA815031	Hs.123598	ESTs	2.8
	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fis, clone A	2.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALU6_HUMAN A	2.8
	451632	BE005934	Hs.310625	EST	2.8

	426481	AW963941		gb:EST376014 MAGE resequences, MAGH Homo	2.8
	401656			Target Exon	2.8
	407269	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.8
5	435754	AA700752	Hs.117341	ESTs	2.8
	433565	AA599763	Hs.112520	ESTs	2.8
	451004	AA044967		gb:zf53d09.r1 Soares retina N2b4HR Homo	2.8
	425223	AA352825	Hs.146065	gb:EST60880 Activated T-cells XX Homo sa	2.8
	405770			NM_002362:Homo sapiens melanoma antigen,	2.8
10	456227	T84239	Hs.189788	ESTs	2.8
	454445	AW749432		gb:RC3-BT0386-301299-011-a09 BT0386 Homo	2.8
	419494	W01060	Hs.34382	ESTs	2.8
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	2.8
	428079	AA421020	Hs.208919	ESTs	2.7
15	406337			C14000021:gil7242973[dbj]BAA92547.1 (AB	2.7
	401884			Target Exon	2.7
	406881	D16154		gb:Human gene for cytochrome P-450c11, e	2.7
	428986	AA442884	Hs.201201	ESTs	2.7
	450044	R66444	Hs.51891	ESTs	2.7
20	403630			C3001708*:gil4758028[ref]NP_004360.1 co	2.7
	445514	AI241280	Hs.148906	ESTs	2.7
	446362	AW612481	Hs.104105	ESTs	2.7
	432492	AW275110	Hs.271106	ESTs	2.7
	430889	U22491	Hs.248117	G protein-coupled receptor 7	2.7
25	434316	AW411330	Hs.118796	annexin A6	2.7
	413155	BE067952		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	2.7
	433329	AF015041	Hs.199291	numb (Drosophila) homolog-like	2.7
	446523	NM_003063	Hs.334629	sarcophilin	2.7
	449923	BE258051		gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
30	453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hibr1)	2.7
	405678			CX001454:gil8393794[ref]NP_056681.1 myo	2.7
	432789	D26361	Hs.3104	KIAA0042 gene product	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	449109	AW270992	Hs.120949	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
35	436255	F01143	Hs.284284	zinc finger 1111	2.7
	415984	R19046	Hs.5010	gb:yq21f11.r1 Soares infant brain 1N1B H	2.7
	402844			C1000118*:gil9951913[ref]NP_062832.1 pr	2.7
	456666	AA452512	Hs.76719	U6 snRNA-associated Sm-like protein	2.7
	414620	AA150120	Hs.244621	ribosomal protein S14	2.7
40	404979			Target Exon	2.7
	412318	AW936911	Hs.326729	hypothetical protein MGC11082	2.7
	424361	AK001551	Hs.145944	Homo sapiens cDNA FLJ10689 fis, clone NT	2.7
	412542	AW961516	Hs.95097	ESTs	2.7
	441975	AW173248	Hs.344285	EST	2.7
45	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	457861	AW450205	Hs.305890	BCL2-like 1	2.7
	439204	AF087987	Hs.42696	EST	2.7
	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	2.7
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
50	443359	AI792583	Hs.135354	ESTs	2.7
	447336	AW139383	Hs.245437	ESTs	2.7
	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
	422185	AL117530	Hs.112822	DKFZP434B172 protein	2.7
	436030	R02287	Hs.121052	ESTs	2.7
55	449589	AW752437	Hs.135258	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
	436092	AI345995	Hs.127383	ESTs	2.6
	415054	AI733907		gb:zo86h09.y5 Stratagene ovarian cancer	2.6
	412908	AA121913	Hs.293896	pregnancy-associated plasma protein-E	2.6
	409583	AW440117	Hs.256879	ESTs	2.6
60	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
	435383	R61083		wee1 (S. pombe) homolog	2.6
	426629	AI203933	Hs.97142	ESTs	2.6
	415831	H15145	Hs.30509	ESTs	2.6
	412281	AI810054	Hs.14119	ESTs	2.6
65	434898	AW500458	Hs.29956	KIAA0460 protein	2.6
	422229	AF134414	Hs.113271	ABO blood group (transferase A, alpha 1-	2.6
	447518	T80061		gb:yd22f08.s1 Soares fetal liver spleen	2.6
	458546	AI215667	Hs.175044	ESTs	2.6
	438648	AA813125	Hs.146335	ESTs	2.6
70	450399	AW511049	Hs.202007	ESTs	2.6
	420833	R47948	Hs.188732	ESTs	2.6
	453903	AW299606	Hs.232777	ESTs	2.6
	443650	AI698330	Hs.151444	ESTs	2.6
	427419	NM_000200	Hs.177888	histatin 3	2.6
75	423741	AA330362		gb:EST34074 Embryo, 12 week II Homo sapi	2.6
	451577	N69101	Hs.40730	ESTs	2.6
	441358	AW173212	Hs.129041	ESTs	2.6
	402706			Target Exon	2.6
	436054	AI076262	Hs.119813	ESTs	2.6
80	402749			Target Exon	2.6
	442472	AW806859		gb:MR0-ST0020-081199-004-c03 ST0020 Homo	2.6
	445762	AI734002	Hs.264590	ESTs, Moderately similar to ALU5_HUMAN A	2.6
	441420	AA932872		gb:oo57d07.s1 NCL_CGAP_Lu5 Homo sapiens	2.6
	405564			Target Exon	2.6

	406003		Target Exon	2.6	
	459584	AI910884	Hs.346429	ESTs	2.6
	441597	AW135032	Hs.203625	ESTs	2.6
5	411280	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	2.6
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfami	2.6
	445060	AA830811	Hs.282908	ESTs	2.6
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
	428717	T78001	Hs.133546	hypothetical protein FLJ21120	2.6
10	401716			C16000902:gi 403440 gb AAA73168.1 (M817	2.6
	416628	W03955		gb:za62d04.r1 Soares fetal liver spleen	2.6
	443864	N37059	Hs.36250	ESTs, Weakly similar to I38022 hypotheti	2.6
	440702	AA904178	Hs.148233	ESTs	2.6
	456310	AA225522		gb:nc25c06.r1 NCL_CGAP_Pr1 Homo sapiens	2.6
15	451255	AA020857	Hs.90744	ESTs	2.6
	455737	BE072246		gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
	445326	AI220072	Hs.344672	ESTs	2.6
	408432	AW195262		gb:xn67b05.x1 NCL_CGAP_CML1 Homo sapiens	2.6
	445874	BE326671	Hs.170058	ESTs	2.6
20	441063	AA913819	Hs.188025	ESTs	2.6
	455505	AW970640	Hs.309071	ESTs	2.6
	453491	AL040177		gb:DKFZp434F0213_r1 434 (synonym: htes3)	2.6
	455048	AW852749		gb:PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	2.6
25	444130	AI125263	Hs.170410	ESTs	2.6
	422210	BE269319	Hs.171937	steroid dehydrogenase-like	2.5
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.5
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.5
	400427	AB044934	Hs.287388	histamine H4 receptor	2.5
30	410443	BE062906	Hs.28338	KIAA1546 protein	2.5
	455210	AW866599		gb:QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
	429909	AW977090	Hs.184860	CGI-203 protein	2.5
	441191	AI693930	Hs.148816	ESTs	2.5
	413489	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	2.5
35	448215	N34740	Hs.6658	ESTs	2.5
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	2.5
	447610	AW296286	Hs.255534	ESTs	2.5
	450724	R55428		gb:yj79b05.r1 Soares breast 2NbHBst Homo	2.5
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	2.5
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	2.5
	447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755 protein,	2.5
	434152	AI792665	Hs.291190	ESTs	2.5
	412671	AW977734	Hs.37931	gb:EST389963 MAGE resequences, MAGO Homo	2.5
	456401	W28146		gb:43f11 Human retina cDNA randomly prim	2.5
45	404678			Target Exon	2.5
	408520	AA225063	Hs.161614	ESTs	2.5
	411332	AW837212		gb:QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.5
	429906	AL080137	Hs.193743	ESTs	2.5
50	433712	AF090887	Hs.306562	Homo sapiens clone HQ0085	2.5
	438353	BE539951	Hs.306996	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
	446224	AW450551	Hs.13308	ESTs	2.5

TABLE 63B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

60	Pkey	.CAT Number	Accession
	408229	1048462_1	AW176091 H24234
	408432	1058667_1	AW195262 R27868 AW811262
	409679	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
65	410483	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
	411320	1238624_1	AW836646 AW836580 AW836610 AW836636 AW836603 AW836632
	411332	1239102_1	AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
	411356	1240273_1	H45377 H21137 AW838640
	411426	1245515_1	BE141714 AW845993 AW845989
70	411829	1260309_1	AW865749 BE179419 BE179492
	411944	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	413155	1351148_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946
	413381	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
	413489	1373392_1	BE144228 BE144291
75	415054	151827_1	AI733907 AA159708 AI732614
	415098	1522174_1	D59687 D59694 D59656 D59589
	415131	1523680_1	D61119 D81508 D81734
	415386	1535560_1	Z43087 F07410 H15506 H54108 R95033 H98000
	415981	1564242_1	R35694 H12035 R53312
80	416628	1604848_1	W03955 H82332 H69247 H72486
	416935	163179_1	AA190712 AA190665 AA252564
	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	419896	1888662_1	Z99362 Z99363
	420778	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481

5	421342	201427_1	AA504749 AA287498
	421813	207654_1	BE048255 AA313083 AA298419
	422731	220507_1	AL138411 AL138412 AA315860
	423741	231582_1	AA330362 AW962525 H87796
	423772	23188_1	AA306637 NM_007241 AF156102 BE388339 BE614027 AW935016 AA315261 AW376418 AW304951 AI859820 AA367436 AW516957 BE614519 AI453152 AI453149 AI453139 AW168378 AI139491 AI538368 AW468227 AI680027 AW090513 AA662830 F30995 AI351985 AI424349 AW009599 C02215 AI6525
10	423871	232749_1	AA331906 AA332484
	426481	267878_1	AW963941 AW963944 AA379825 AA379564
	428132	287430_1	AA421765 AA456076 AI290275 AA455579
	431847	338402_1	AI791314 AI791434 AA516511
	434407	385744_1	AW815333 AW815409 AA632563
15	435383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
	436190	41555_1	AK001059 AA633055
	438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
	441420	516748_1	AA932872 W28068 W28643 T96110
	442472	543371_1	AW806859 AW806852 AF049582
20	445797	650943_1	AI253414 AI366014 R34822
	447518	724787_1	T80061 AI382804
	447600	728288_1	AI420990 AI399725 AI401757
	448516	766241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI525093
	449923	81926_1	BE258051 R45758 AA004732 BE255126
25	450724	844585_1	R55428 AI820704 AI732283 R54983
	451004	85453_1	AA044967 H86327 AA013079 AA058776 BE242713 AA019987
	452351	91233_1	AA025647 R45716 AW753786
	453412	966264_1	AJ003290 AJ003288 AW276947
	453491	969172_1	AL040177
30	453752	979899_1	AL120800 BE378580
	453826	982669_1	AL138129 AL138179 BE064231
	454445	1204468_1	AW749432 AW749434 R47332
	454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866611 AW866616
	455048	1250599_1	AW852749 AW852755 AW852620
35	455210	1260650_1	AW866599 AW866294 AW866468 AW866467
	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
	455737	1353892_1	BE072246 BE072229 BE072225 BE072210 BE072221 BE072256 BE072211 BE072242
	455791	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090686
	455887	1380836_1	BE154173 BE154098 BE154096
40	456075	1476756_1	N73442 R98100 BE410380
	456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
	456401	1844649_2	W28146 W28187

TABLE 63C

45	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham l. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham l. et al., Nature (1999) 402:489-495.		
50	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
55	Pkey	Ref	Strand	Nt_position
	400461	9929654	Plus	32727-32846,32929-33051
	400499	9796071	Minus	148495-148806
	400749	7331445	Minus	9162-9293
	400831	8576271	Minus	56502-57407
60	401278	9799936	Plus	98428-98573
	401411	7799787	Minus	144144-144329
	401656	9100664	Minus	1-382
	401716	6715703	Plus	174722-174911
	401884	8140731	Minus	89182-90053
65	401896	8569194	Plus	115129-115294
	401917	9502466	Plus	25054-25229
	402422	9796344	Minus	32843-33008
	402460	9796884	Minus	108901-109254,110246-110581,113613-113960
	402490	9797648	Plus	149982-150929
70	402706	8894426	Minus	148640-148805
	402749	9212740	Minus	68787-68882,76602-76768
	402797	3421043	Minus	15758-15930
	402817	6822166	Minus	48611-49012
	402844	9369286	Plus	54958-55313
75	403451	9838240	Plus	77382-78300
	403612	8469060	Minus	94723-94859
	403630	8559999	Minus	13909-14466,15251-15760,16898-17431,41742-42440
	403649	8705159	Minus	27141-27247
	404260	9366879	Plus	51396-51513
80	404267	9581792	Minus	12209-12313,18241-18397
	404606	9212936	Minus	22310-23269
	404660	9797068	Plus	168215-168916
	404678	9797204	Plus	115196-115448
	404979	4160139	Minus	87762-88217
	404984	6939882	Plus	87221-87505
	405001	6015406	Minus	104646-104819
	405150	9929758	Plus	126475-126773

405152	9965561	Minus	137662-137969
405258	7329310	Plus	129930-130076
405422	7243869	Minus	101938-102079, 102261-102443, 102896-103202
405564	2114222	Minus	16766-17344
405678	4079670	Plus	151821-152027
405735	9931101	Minus	29854-29976
405770	2735037	Plus	61057-62075
406003	8247800	Plus	42079-42516
406085	9123888	Plus	18665-18843
406177	7279760	Minus	18930-19148
406337	9213455	Plus	90117-90337
406398	9256276	Minus	118691-118959
406600	8248616	Minus	36296-36610

Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Cenbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of BPH tissue to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
420154	AI093155	Hs.95420	JM27 protein	49.6
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	47.2
419526	AI821895	Hs.193481	ESTs	43.6
432441	AW292425	Hs.163484	ESTs	42.7
431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypothe	30.2
407202	N58172	Hs.109370	ESTs	26.1
432101	AI918950	Hs.123642	EphA3	25.8
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	25.5
425075	AA506324	Hs.1852	acid phosphatase, prostate	24.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	24.4
410929	H47233	Hs.30643	ESTs	21.1
400287	S39329	Hs.181350	kallikrein 2, prostatic	20.3
446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	19.8
423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	18.6
415989	AI267700		ESTs	17.8
428336	AA503115	Hs.183752	microseminoprotein, beta-	17.3
450693	AW450461	Hs.203965	ESTs	16.7
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	16.7
407168	R45175	Hs.117183	ESTs	15.5
408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	15.5
454119	BE549773	Hs.40510	uncoupling protein 4	14.5
428819	AL135623	Hs.193914	KIAA0575 gene product	14.5
400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	14.4
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	14.3
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatmedi	14.2
432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	14.2
433444	AW975324	Hs.129816	ESTs	13.8
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	13.5
428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	12.9
401424			NM_001172:Homo sapiens arginase, type II	12.7
432435	BE218886	Hs.282070	ESTs	12.5
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	12.3
446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	12.0
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.9
407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U4 Homo sapiens	11.8
452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.7
432473	AI202703	Hs.152414	ESTs	11.3
410330	AW023630	Hs.159425	ESTs	11.2
431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	11.2
452792	AB037765	Hs.30652	KIAA1344 protein	11.2
418848	AI820961	Hs.193465	ESTs	10.9
400292	AA250737	Hs.72472	BMP-R1B	10.9
433647	AA603367	Hs.222294	ESTs	10.8
453160	AI263307	Hs.239884	H2B histone family, member L	10.8
409262	AK000631	Hs.52256	hypothetical protein FLJ20624	10.6
431474	AL133990	Hs.190642	CEGP1 protein	10.3
429220	AW207206		ESTs	10.3
428134	AA421773	Hs.161008	ESTs	10.2
408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	10.1
456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	9.8
434792	AA649253	Hs.132458	ESTs	9.7
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	9.5
428398	AI249368	Hs.98558	ESTs	9.4

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
5	429918	AW873986	Hs.119383	ESTs	9.1
	440260	AI972867	Hs.7130	copine IV	9.1
	453096	AW294631	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
10	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
15	450642	R39773	Hs.7130	copine IV	8.7
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
20	446336	AW815036	Hs.151251	ESTs	8.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417169	R13550	Hs.246773	ESTs	8.2
	453387	AI990741	Hs.252809	ESTs	8.2
25	434666	AF151103	Hs.112259	T cell receptor gamma locus	8.1
	417958	AA767382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
30	433923	AI823453	Hs.146625	ESTs	7.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441690	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	7.5
35	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	7.5
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
	409557	BE182896	Hs.211193	ESTs	7.3
40	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.3
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	7.1
	449300	AI656959	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	7.1
45	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AI799909	Hs.158989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	7.0
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	6.9
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	6.9
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	6.9
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
55	449821	AI671141	Hs.211122	ESTs	6.8
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.8
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	6.7
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
60	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	6.6
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
65	450164	AI239923	Hs.63931	ESTs	6.5
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
70	440911	AA909536	Hs.143562	ESTs	6.4
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	6.3
	435375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	6.3
75	431359	AW993522	Hs.292934	ESTs	6.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403667			Target Exon	6.1
	424846	AU077324	Hs.1832	neuropeptide Y	6.1
	439569	AW602166	Hs.222399	CEGP1 protein	6.1
80	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
	448004	AW451477	Hs.257456	ESTs	6.1
	431770	BE221800	Hs.268555	5'-3' exoribonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	6.0
	415621	AI648602	Hs.55468	ESTs	6.0

	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.0
	432527	AW975028	Hs.102754	ESTs	5.9
	447156	AW274731	Hs.157920	ESTs	5.9
5	404003			Target Exon	5.9
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
	438138	R98299	Hs.177502	ESTs	5.9
10	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.8
	434973	AW449285	Hs.313636	EST	5.8
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	5.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
	434485	AI623511	Hs.118567	ESTs	5.8
15	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	5.7
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
20	432966	AA650114	Hs.325198	ESTs	5.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	5.7
	425810	AI923627	Hs.31903	ESTs	5.6
	414312	AA155694	Hs.191060	ESTs	5.6
25	404571			NM_015902*:Homo sapiens progesteron induce	5.6
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
	439092	AA830149		gb:cc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
	427078	AI676062	Hs.111902	ESTs	5.6
	422805	AA436989	Hs.121017	H2A histone family, member A	5.6
30	417511	AL049176	Hs.82223	chordin-like	5.6
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	5.6
	433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
	441676	BE564206	Hs.49889	ESTs	5.5
	421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
35	432682	AI376400	Hs.159588	ESTs	5.5
	435021	AA922192	Hs.54709	ESTs	5.5
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	5.5
	426581	AB040956	Hs.135890	KIAA1523 protein	5.5
	439079	AF085937	Hs.38348	ESTs	5.5
40	443635	AI080230	Hs.134214	ESTs	5.5
	400080			Eos Control	5.5
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
	436578	AI091435	Hs.134859	ESTs	5.5
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
45	450325	AI935962	Hs.26289	ESTs	5.4
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	5.4
	435072	AW592176	Hs.116932	ESTs	5.4
	428647	AA830050	Hs.124344	ESTs	5.4
50	441111	AI806867	Hs.126594	ESTs	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	450244	AA007534	Hs.125062	ESTs	5.3
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.3
	415539	AI733881	Hs.72472	BMP-R1B	5.3
55	437267	AW511443	Hs.258110	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
	446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
60	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.3
	423101	M83941	Hs.123642	EphA3	5.3
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
	450813	AI739625	Hs.203376	ESTs	5.3
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	5.2
65	415890	H08225	Hs.268712	ESTs	5.2
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	441054	AA913591	Hs.126480	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
70	448072	AI459306	Hs.24908	ESTs	5.2
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.2
	421040	AA715026	Hs.135280	ESTs	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
75	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	445238	AA883971	Hs.187506	ESTs	5.1
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
80	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	440995	T57773	Hs.10263	ESTs	5.0
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0

5	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	5.0
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	5.0
10	403696			C4001100*:gil5852342[gb]AAD54015.1] (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
15	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
	414422	AA147224	Hs.249195	Homeo box A13	4.9
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.9
20	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	435937	AA830893	Hs.119769	ESTs	4.8
	435136	R27299	Hs.10172	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
25	447058	AI939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29882		ESTs	4.8
	420871	AA702972	Hs.65300	ESTs	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
30	453843	D25215	Hs.35804	hect domain and RLD 3	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypothi	4.7
	452843	AI796769	Hs.208320	ESTs	4.7
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	4.7
35	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
	443361	AI792628	Hs.133273	ESTs	4.6
40	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AI831190	Hs.166676	ESTs	4.6
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.6
	415788	AW628686	Hs.78851	KIAA0217 protein	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
45	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	434408	AI031771	Hs.132586	ESTs	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
	447805	AW627932	Hs.302421	gemin4	4.6
	438875	AA827640	Hs.189059	ESTs	4.6
50	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
	418836	AI655499	Hs.161712	ESTs	4.5
55	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AI760833	Hs.293971	ESTs	4.5
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
60	420133	AA426117	Hs.155543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
	431060	AF039307	Hs.249171	homeo box A11	4.5
65	445372	N36417	Hs.144928	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
	418019	R68911	Hs.176275	ESTs	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
70	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412643	AW971239	Hs.136433	ESTs	4.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.4
	445210	H09323	Hs.27133	ESTs	4.4
75	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	4.4
	420608	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	444030	AW021254	Hs.135055	ESTs	4.4
80	435655	AW105663	Hs.6947	HSPC069 protein	4.4
	400533			ENSP00000209376*:PRED65 protein (Fragmen	4.4
	435285	AW272603	Hs.266134	ESTs	4.4
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
	432960	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	4.3
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	4.3

5	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW968065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.3
10	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	405348			C7001664:gi12698061 dbj BAB21849.1 (AB	4.3
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
15	449603	AI655662	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
	432887	AI926047	Hs.162859	ESTs	4.3
	420905	AA521307	Hs.186651	ESTs	4.2
20	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
	450597	AI701635	Hs.207077	ESTs	4.2
25	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	AB040907	Hs.278436	KIAA1474 protein	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
30	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	440594	AW445167	Hs.126036	ESTs	4.2
	458912	AI911066		ESTs	4.2
35	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
	436714	AA728964	Hs.293399	ESTs	4.1
40	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	430523	AW451385	Hs.161954	ESTs	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
45	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	449907	AA004825	Hs.103281	ESTs	4.1
	430487	D87742	Hs.241552	KIAA0268 protein	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
50	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL039402	Hs.125783	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
55	446416	AV658299	Hs.163959	ESTs	4.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.0
	442338	AI761976	Hs.156080	ESTs	4.0
60	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415861	Z43123	Hs.144513	ESTs	4.0
	418259	AA215404		ESTs	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
65	432229	AW290976	Hs.143587	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
70	448131	AI675054	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partia	4.0
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	4.0
75	452221	C21322	Hs.288057	hypothetical protein FLJ22242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
80	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	457498	AI732230	Hs.191737	ESTs	3.9
	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.9
	424940	AA985308	Hs.283902	ESTs	3.9

5	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	446862	AV660697	Hs.282700	ESTs	3.9
10	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.9
	401403			Target Exon	3.9
	448779	BE042877	Hs.177135	ESTs	3.9
	420533	AI809510	Hs.118971	ESTs	3.9
15	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
	423453	AW450737	Hs.128791	CGI-09 protein	3.9
	434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
20	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	419038	AW134924	Hs.190325	ESTs	3.9
	421129	BE439899	Hs.89271	ESTs	3.9
	424332	AA338919	Hs.101615	ESTs	3.9
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	3.9
25	447033	AI357412	Hs.157601	ESTs	3.9
	439306	BE220199		WD40 protein C1a01	3.8
	410352	AW969725	Hs.150444	KIAA0373 gene product	3.8
	407961	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	3.8
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.8
30	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	3.8
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.8
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	3.8
35	447280	BE617907	Hs.97635	ESTs	3.8
	438379	N23018	Hs.171391	C-terminal binding protein 2	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	423044	AA320829	Hs.97266	protocadherin 18	3.8
40	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	3.8
	433507	AI817336	Hs.191791	ESTs	3.8
	437718	AI927288	Hs.196779	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
45	426981	AL044675	Hs.173081	KIAA0530 protein	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
50	433908	AW298141	Hs.157975	ESTs	3.8
	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypothe	3.7
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	3.7
55	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	423096	AA732684	Hs.278428	progesterone induced protein	3.7
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
	428055	AA420564	Hs.101760	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
60	451746	M86178	Hs.311258	ESTs	3.7
	453293	AA382267	Hs.10653	ESTs	3.7
	436671	AW137159	Hs.146151	ESTs	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	408418	AW963897	Hs.44743	KIAA1435 protein	3.7
65	420092	AA814043	Hs.88045	ESTs	3.7
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	3.7
	441865	AA384726	Hs.5722	hypothetical protein FLJ23316	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	431231	AA653552	Hs.116532	ESTs	3.7
70	418348	AI537167	Hs.96322	hypothetical protein FLJ23560	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
75	440947	AA910403		ESTs	3.7
	404561			trichorhinophalangeal syndrome I gene (T	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	3.6
	444794	AI419991	Hs.145225	ESTs	3.6
80	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.6
	431316	AA502663	Hs.145037	ESTs	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypothe	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	411067	AI681006	Hs.71721	ESTs	3.6
	436326	BE085236		aldo-keto reductase family 1, member B1	3.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

5	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	416239	AL038450	Hs.48948	ESTs	3.6
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
10	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	425465	L18964	Hs.1904	protein kinase C, iota	3.5
15	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C12000517*:gij4758712[ref]NP_004659.1 a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
20	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
	427304	AA761526	Hs.163853	ESTs	3.5
	434763	AA648618		gb:ns07a11.1 r1 NCL_CGAP_Ew1 Homo sapiens	3.5
25	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
	438680	AA906121	Hs.173421	ESTs	3.5
30	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheri	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5
35	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AI800041	Hs.190555	ESTs	3.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
40	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
	409047	AW961434	Hs.31539	ESTs	3.4
45	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfami	3.4
	436340	R42246	Hs.21606	ESTs	3.4
50	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
55	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
60	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.19928	hypothetical protein SP329	3.4
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.4
	408784	AW971350	Hs.63386	ESTs	3.4
65	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.4
70	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
75	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50128	Hs.173400	ESTs	3.3
	427615	BE410107	Hs.179817	CGI-82 protein	3.3
	429588	AI080271	Hs.134533	ESTs	3.3
80	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23606	ESTs	3.3

	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	436854	AA749167	Hs.173911	ESTs	3.3
	430865	AI073424	Hs.5232	HSPC125 protein	3.3
5	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	423645	AI215632	Hs.147487	ESTs	3.3
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	3.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
	418051	AW192535	Hs.19479	ESTs	3.3
10	418719	AW975590	Hs.161707	ESTs	3.3
	437714	AA766346	Hs.293242	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
15	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.3
	423412	AF109300		prostate cancer associated protein 5	3.3
	436962	AW377314	Hs.5364	DKFZP564I052 protein	3.3
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	3.3
20	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	433213	AW665130	Hs.137190	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.2
	428043	T92248	Hs.2240	uteroglobin	3.2
25	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	3.2
	423595	R82826	Hs.220702	ESTs	3.2
	407021	U52077		gb:Human mariner1 transposase gene, comp	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
30	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.2
	425657	T89839	Hs.119471	ESTs	3.2
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
35	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
	451025	AW028689	Hs.301985	ESTs	3.2
	401416			C14000338*:g j7459502 pir jS74665 outer	3.2
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
40	436995	AI160015	Hs.118112	ESTs	3.2
	428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	3.2
45	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	437866	AA156781		metallothionein 1E (functional)	3.2
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
50	410870	U81599	Hs.66731	homeo box B13	3.2
	438899	AF085833	Hs.135624	ESTs	3.2
	415862	R51034	Hs.144513	ESTs	3.2
	420969	AI636310	Hs.28310	ESTs	3.2
	415467	R60891	Hs.260274	ESTs	3.2
55	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	417380	T06809	Hs.332086	ESTs	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
60	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	452862	AW378065	Hs.8687	ESTs	3.2
	405548			Target Exon	3.1
	439584	AA838114	Hs.221612	ESTs	3.1
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
65	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
70	416836	D54745	Hs.80247	cholecystokinin	3.1
	432589	AL135725	Hs.131708	ESTs	3.1
	420512	AA262886	Hs.143817	ESTs	3.1
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
	423855	AA331761	Hs.254859	ESTs	3.1
75	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
80	421823	N40850	Hs.28625	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	445784	AI253155	Hs.146065	ESTs	3.1
	434384	AA631910	Hs.162849	ESTs	3.1
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1

5	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
	433610	AA806822	Hs.112547	ESTs	3.1
	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	444800	AW119071	Hs.153287	ESTs	3.1
10	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.1
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	3.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	3.1
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.1
	407349	AA825449	Hs.83332	Homo sapiens cDNA: FLJ22437 fis, clone H	3.1
15	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	425480	AB023198	Hs.158135	KIAA0981 protein	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
20	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	3.1
	433852	AI378329	Hs.126629	ESTs	3.0
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.0
	452242	R50956	Hs.159993	glycosyltransferase	3.0
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	3.0
25	405264			NM_030813*:Homo sapiens suppressor of po	3.0
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.0
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.0
	434497	AI821803	Hs.136580	ESTs	3.0
	420355	AW968263	Hs.123126	ESTs	3.0
30	403481			Target Exon	3.0
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.0
	416642	T96118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
35	426174	AA547959	Hs.115838	ESTs	3.0
	430459	BE178539	Hs.278634	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	446258	AI283476	Hs.263478	ESTs	3.0
	448686	AA158659	Hs.334712	hypothetical protein FLJ14744	3.0
40	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	3.0
	414441	AA234759	Hs.132950	ESTs	3.0
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	3.0
	437048	AA743240	Hs.91582	ESTs	3.0
	450963	AI864668	Hs.48832	ESTs	3.0
45	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.0
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.0
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
50	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	3.0
	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
55	437323	AA371145	Hs.194397	leptin receptor	3.0
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.0
	450580	N40087		ESTs	3.0
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.0
	418365	AW014345	Hs.161690	ESTs	3.0
60	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.0
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	418819	AA228776	Hs.191721	ESTs	3.0
	428634	AA811845	Hs.106290	Kelch motif containing protein	3.0
65	431869	AA521136	Hs.190176	ESTs	3.0
	435008	AF150262	Hs.162898	ESTs	3.0
	448880	AW205507	Hs.32360	ESTs, Highly similar to I38587 retroviri	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 64B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

80	Pkey	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1	AW846433 AW846159 AW846377 AW846528

5	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214 BE046680 BE046738 BE044958 BE064415 BE064430 BE064448 BE145899 BE145848 BE145849 BE145853 BE145927 BE145925 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086 Z43062 R13213 H14422 H51299 H44619 H46391 R86024 H51892 T72744 AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597 AA215404 AI990909 BE464132 AW271459 N74332 AI262061 T65754 AA229857 AA229658 AI217097 AW886090 W38035 W38792 AA232835 AW936043 AA603305 AA244095 AA244183 AA255652 AA280911 AW967920 AA262684 BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 AF109300 AI299378 AI202654 AA337221 AA336756 AW966196 AA377823 AW954494 AI022688 AA380153 AA380233 AW963529 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266 AA418703 AA418711 BE071915 BE071920 BE071912 AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340 AA884766 AW974271 AA592975 AA447312 AW207206 AW341473 AA448195 AI951341 AW968485 AW968670 AA480922 BE350425 AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339 AJ003429 AJ003367 AA564825 H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320 AA648618 AW974389 H51771 N73895 AJ001872 BE085236 BE085317 X04236 AA577934 AA578392 AA502836 AA595852 AA578258 AW270791 AA507151 AA559152 T57040 BE503281 AW593405 AI825755 AI350499 AI655710 AI972281 AI654949 BE073961 BE073962 BE041399 AW750214 AA228488 BE074016 AI908706 AW270601 AW873282 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188 AA830149 AW978407 M85983 AW503637 BE220199 W01813 AF086118 N07060 BE221405 AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877 AA910403 AI815593 W58361 AW162520 AI816550 N99828 BE079873 AI110738 AF074645 AV653771 BE089370 AI458682 H24240 R14537 R18426 AW867082 AI151418 W60401 AW631238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053 AW889353 AA521308 AA001203 W92828 AI207798 AA746655 R78710 W24617 AA024605 C01747 AW173095 W61229 W92685 AA742467 H00789 R76925 AW1828 AA001793 AA001871 NM_014253 AF100772 BE088769 AI022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 AI692689 R14223 R18395 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303 AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878 AA495800 AA495737 AA010736 AA654716 AA640726 BE173515 BE173560 AI902860 T79703 T96307 AL079725 AW998716 AW022148 N68020 AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892 AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 AW753456 AW753036 AW854868 AW854862 AW835767 AW835537 BE160187 AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033 BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362 BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 BE072049 BE069471 BE069489 BE069478 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464 AA493662 AW897396 BE154814 AI911066 AI933734 AI680888 AJ003599
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TABLE 64C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
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5	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401403	7710966	Plus	146180-146294
	401416	7452889	Minus	121456-121626
	401424	8176894	Plus	24223-24428
	403242	7637817	Minus	11297-12511
	403481	9965004	Plus	93496-93633
10	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403696	3135242	Minus	143467-143634
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
15	404571	7249169	Minus	112450-112648
	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	405264	7329374	Plus	28556-28684
	405348	2914717	Minus	43310-43462
20	405510	7630909	Minus	101028-101174
	405548	1532158	Plus	11552-11686

Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85th percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of BPH tissue to prostate tumor tissue

	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	428134	AA421773	Hs.161008	ESTs	9.4
	446336	AW815036	Hs.151251	ESTs	9.3
40	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	8.9
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	400533			ENSP00000209376*:PREDD65 protein (Fragmen	8.7
	418310	AA814100	Hs.86693	ESTs	8.7
45	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	8.1
	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
	400080			Eos Control	7.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	7.4
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
50	438231	AW594539	Hs.155689	ESTs	7.3
	418387	R18085		gb:yg16b12.r1 Soares infant brain 1NIB H	7.2
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	6.9
55	404967			Target Exon	6.9
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	6.9
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	6.9
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	6.8
	412988	BE046680		gb:hn42h03.x1 NCL_CGAP_RDF2 Homo sapiens	6.8
60	400440	X83957	Hs.83870	nebulin	6.6
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	6.6
	400086			Eos Control	6.4
	440911	AA909536	Hs.143562	ESTs	6.4
	425312	AA354940	Hs.145958	ESTs	6.4
65	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
	419015	T79262	Hs.14463	ESTs	6.3
	453789	AA628517	Hs.118502	ESTs	6.2
	424940	AA985308	Hs.283902	ESTs	6.1
	403667			Target Exon	6.1
70	429014	AI800518	Hs.118158	ESTs	6.0
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitte	6.0
	419999	AI760942	Hs.191754	ESTs	6.0
	405348			C7001664:gi12698061 dbj BAB21849.1 (AB	6.0
	404003			Target Exon	5.9
75	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
	432319	AW510770	Hs.128386	ESTs	5.7
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
	443361	AI792628	Hs.133273	ESTs	5.6
80	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	5.6
	439079	AF085937	Hs.38348	ESTs	5.5
	422081	AW136820	Hs.196011	ESTs	5.5
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	5.5
	423529	T87318	Hs.120411	ESTs	5.5

	436578	AI091435	Hs.134859	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
5	414403	AW969551	Hs.76064	ribosomal protein L27a	5.4
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
10	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypothe	5.3
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
15	446495	D60923	Hs.153460	ESTs	5.2
	435375	AI733610	Hs.187832	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	5.2
	405321			Target Exon	5.1
20	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	438206	AA780385	Hs.187885	ESTs	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
25	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	440354	AA889386	Hs.125468	ESTs	5.0
	440388	AI693520	Hs.223000	ESTs	4.9
	421188	AA284658	Hs.261493	ESTs	4.9
	403481			Target Exon	4.8
30	438132	AA907076	Hs.122060	ESTs	4.8
	403333			NM_002518*:Homo sapiens neuronal PAS dom	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
35	452843	AI796769	Hs.208320	ESTs	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.205679	ESTs	4.7
40	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	442160	AI337127	Hs.156325	ESTs	4.6
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.6
	434589	AF147363		gb:Homo sapiens full length insert cDNA	4.6
	404995			ENSP00000251890*:Monocytic leukemia zinc	4.6
45	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
	405549			C7001976*:gil4758712[ref]NP_004659.1] al	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sap	4.5
50	444800	AW119071	Hs.153287	ESTs	4.5
	403371			Target Exon	4.5
	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	4.5
	439752	T78968	Hs.14411	ESTs	4.5
55	414441	AA234759	Hs.132950	ESTs	4.5
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	4.5
	454585	BE069128		gb:QV3-BT0379-310100-071-g06 BT0379 Homo	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
60	418059	AA211586		gb:zn56d05.s1 Stralagene muscle 937209 H	4.4
	451469	NM_014809	Hs.26441	KIAA0319 gene product	4.4
	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	4.3
65	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	415467	R60891	Hs.260274	ESTs	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.3
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	4.3
70	441620	R59595	Hs.26675	ESTs	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	448108	AW300021	Hs.170685	ESTs	4.2
	436345	AA873008	Hs.121572	ESTs	4.2
75	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	4.2
	413525	BE145899		gb:MRO-HT0208-221299-204-b10 HT0208 Homo	4.2
	403305	NM_006825		transmembrane protein (63kD), endoplasm	4.2
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
80	430124	AW204994	Hs.253450	ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	H54253	Hs.205241	ESTs, Weakly similar to S65657 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

	445206	AI350199	Hs.269990	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
5	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AI761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo	4.0
10	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
15	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.9
	453387	AI990741	Hs.252809	ESTs	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
20	454806	AW872430	Hs.273743	ESTs	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
25	407834	AW084991	Hs.26100	ESTs	3.9
	400398	AF137396	Hs.283879	ubiquilin 3	3.9
	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C14000482*:gil9790241[ref NP_062628.1] S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
30	444911	U06117	Hs.250	xanthene dehydrogenase	3.9
	436350	AA713661	Hs.121091	ESTs	3.9
	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321 Homo	3.8
	452320	AA042873	Hs.160412	ESTs	3.8
35	402145			Target Exon	3.8
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
40	434381	AA631834		gb:np77h05.s1 NCL_CGAP_Pr2 Homo sapiens	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	433523	H29882		ESTs	3.8
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
45	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
50	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
	449264	AI637649	Hs.196105	ESTs	3.8
	443635	AI080230	Hs.134214	ESTs	3.7
	428200	AI039624	Hs.98388	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
55	418759	AA227879	Hs.187621	ESTs	3.7
	450497	H64159	Hs.15328	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
60	448135	AI470874	Hs.343799	ESTs	3.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	3.7
65	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.7
70	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
75	440947	AA910403		ESTs	3.7
	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
80	429073	AA446167	Hs.47385	ESTs	3.6
	419002	T78625	Hs.268594	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	3.6

	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	AI671141	Hs.211122	ESTs	3.6
5	451193	N29850	Hs.44098	ESTs	3.6
	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	427235	AI126288	Hs.192232	ESTs	3.6
10	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.5
	401132			C12000517:gij4758712[ref NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813*:Homo sapiens suppressor of po	3.5
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
15	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
20	403510			Target Exon	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	3.4
25	434497	AI821803	Hs.136580	ESTs	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769*:BG153O3.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
30	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.4
35	427033	AI457449	Hs.192817	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	410551	R36730	Hs.21816	ESTs	3.4
	423357	AI285124	Hs.157505	ESTs	3.4
	450582	AI339732		G-rich RNA sequence binding factor 1	3.4
40	437662	AA765387	Hs.145095	ESTs	3.4
	442388	AW663442	Hs.129485	ESTs	3.4
	445004	AI204616	Hs.148701	ESTs	3.4
	450597	AI701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
45	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
50	407344	AI038025	Hs.271418	gb:ox29f07.x1 Soares_total_fetus_Nb2HF8_	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
55	453328	AW292635	Hs.346145	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	449256	AA059050	Hs.59847	ESTs	3.3
	432550	AW297206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
60	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	3.3
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
65	452011	AW628911	Hs.211429	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	420355	AW968263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypothe	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
70	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501*:gij129092[sp P23270]OLF7_RAT O	3.2
	411552	AW851255		gb:IL3-CT0220-160200-066-H02 CT0220 Homo	3.2
75	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
	435786	H09175	Hs.26085	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
80	447183	AI554733	Hs.173182	ESTs	3.2
	426629	AI203933	Hs.97142	ESTs	3.2
	447892	AI435848	Hs.172978	ESTs	3.2
	457136	AA428240	Hs.126083	ESTs	3.2
	443585	AW466983	Hs.283949	enamelin	3.1

5	451399	AL042110	Hs.326728	ESTs	3.1
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	458251	AL040927	Hs.210422	ESTs	3.1
	439950	AW937417	Hs.293561	ESTs	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
10	403805			Target Exon	3.1
	422666	AA677981	Hs.119023	SMC2 (structural maintenance of chromoso	3.1
	408799	AA059412	Hs.47986	hypothetical protein MGC10940	3.1
	429350	AI754634	Hs.131987	ESTs	3.1
	430454	AW469011	Hs.105635	ESTs	3.1
15	441817	AW969706	Hs.293332	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	445758	R60715	Hs.25804	ESTs	3.1
	403291			Target Exon	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	455772	W28799		gb:52g11 Human retina cDNA randomly prim	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	438142	T90309	Hs.269651	ESTs	3.1
	416423	H54375	Hs.268921	ESTs	3.1
25	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	3.1
	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.1
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.1
	420721	AA927802	Hs.159471	ZAP3 protein	3.1
	436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L	3.1
30	441492	AI149998	Hs.146346	ESTs	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	435628	W88732	Hs.36107	ESTs	3.0
	444326	AI939357	Hs.270710	ESTs	3.0
35	413774	AA131782	Hs.182314	ESTs	3.0
	434352	AF129505	Hs.86492	small muscle protein, X-linked	3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	3.0
	416642	T96118	Hs.226313	ESTs	3.0
40	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	427813	D29833	Hs.2207	salivary proline-rich protein	3.0
	405733			NM_021140*:Homo sapiens ubiquitously tra	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	3.0
	410929	H47233	Hs.30643	ESTs	3.0
50	458187	D56919	Hs.265848	myomegalin	3.0
	429430	AI381837	Hs.155335	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0

55 TABLE 65B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408304	1050848_1	AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515 AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288 AW810263 AW810325 AW810443 AW8
65	409189	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
	410559	1208283_1	AW754192 W00554 AW857797 AW754203 AW754197 AW754193
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
70	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1	AW846433 AW846159 AW846377 AW846528
	411518	1248692_1	AW850246 AW850251 AW850302
	411552	1249255_1	AW851255 AW851432 AW850955
75	412701	1322288_1	AW984757 AW984797 AW984734 AW984745
	412988	1342150_1	BE046680 BE046738 BE044958
	413081	1348563_1	BE064415 BE064430 BE064448
	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	416009	1566379_1	Z43062 R13213 H14422
80	416422	1593811_1	H60457 H68709 H73528 H54335 R87154
	418059	171879_1	AA211586 F35799 AA211641 F29720 AW937387 AW937408
	418387	174731_1	R18085 AA219028 R17712 Z44345
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043

5	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	421926	209246_1	AA300591 AW963893 AA300493
	424200	236595_1	AA337221 AA336756 AW966196
	424686	242486_1	AA345504 AA345251 AW963243
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
10	432765	353907_1	AJ003429 AJ003367 AA564825
	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 AI792312 AI792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
15	436295	41733_1	N73895 AJ001872
	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE089370
	449570	81018_1	AA001793 AA001871
20	450317	831956_1	AI692689 R14223 R18395
	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
	453682	977454_1	T79703 T96307 AL079725
25	454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE069023 AW809375
	454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
30	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
35	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
	455490	1297826_1	AW953477 Z41970 F12435 T73989 T09387
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
40	455772	1363114_1	W28799 BE086078
	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
	457374	328758_1	AA493662 AW897396 BE154814

TABLE 65C

50	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

55	Pkey	Ref	Strand	Nt_position
	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401459	9212270	Minus	182001-183323
60	402145	8018280	Plus	113086-114800
	402454	7534025	Minus	14826-15803
	402703	8705069	Minus	15335-15500
	403242	7637817	Minus	11297-12511
	403291	7230870	Plus	95177-95435
	403305	8099945	Plus	114632-114805
65	403333	8568833	Minus	124794-124941
	403371	9087278	Plus	105655-106050
	403433	9719611	Minus	72225-72437
	403481	9965004	Plus	93496-93633
70	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403805	8140491	Minus	51483-51742,53429-53511
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
75	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	404967	7523744	Minus	89944-90729
	404995	6006247	Minus	154015-154123
	405264	7329374	Plus	28556-28684
80	405321	3419846	Minus	44654-45210
	405348	2914717	Minus	43310-43462
	405510	7630909	Minus	101028-101174
	405549	1552494	Plus	10878-11048
	405733	9884689	Plus	124832-125051

Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85th percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigenelD:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of BPH tissue to prostate tumor and normal body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
410929	H47233	Hs.30643	ESTs	21.1
450693	AW450461	Hs.203965	ESTs	16.7
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432473	AI202703	Hs.152414	ESTs	11.3
446336	AW815036	Hs.151251	ESTs	10.9
407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens	10.7
428134	AA421773	Hs.161008	ESTs	10.2
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
415293	R49462	Hs.106541	ESTs	9.1
458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
428927	AA441837	Hs.90250	ESTs	8.6
420345	AW295230	Hs.25231	ESTs	8.5
453387	AI990741	Hs.252809	ESTs	8.2
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	7.5
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4
400080			Eos Control	7.4
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
438231	AW594539	Hs.155689	ESTs	7.3
410330	AW023630	Hs.159425	ESTs	7.2
449300	AI656959	Hs.346514	ESTs	7.1
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	6.8
454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	6.6
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.6
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
424433	H04607	Hs.9218	ESTs	6.5
442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.4
425312	AA354940	Hs.145958	ESTs	6.4
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
440911	AA909536	Hs.143562	ESTs	6.4
400533			ENSP00000209376*:PRED65 protein (Fragmen	6.2
418310	AA814100	Hs.86693	ESTs	6.2
403667			Target Exon	6.1
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
404003			Target Exon	5.9
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.9
438138	R98299	Hs.177502	ESTs	5.9
424940	AA985308	Hs.283902	ESTs	5.8
434485	AI623511	Hs.118567	ESTs	5.8
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
443361	AI792628	Hs.133273	ESTs	5.6
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
439079	AF085937	Hs.38348	ESTs	5.5
430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5
436578	AI091435	Hs.134859	ESTs	5.5
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
435072	AW592176	Hs.116932	ESTs	5.4
435375	AI733610	Hs.187832	ESTs	5.4
444609	AW571659	Hs.278081	ESTs	5.4
416602	NM_006159	Hs.79389	nel (chicken)-like 2	5.4
433087	AI720686	Hs.152520	ESTs	5.3
439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.3
437267	AW511443	Hs.258110	ESTs	5.3
441916	AA993571	Hs.129075	ESTs	5.3
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypothe	5.3

	423101	M83941	Hs.123642	EphA3	5.3
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
	415890	H08225	Hs.268712	ESTs	5.2
5	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
10	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.1
15	445238	AA883971	Hs.187506	ESTs	5.1
	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	440354	AA889386	Hs.125468	ESTs	5.0
20	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	4.9
25	450497	H64159	Hs.15328	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	414818	BE541217	Hs.23606	ESTs	4.8
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	433523	H29882		ESTs	4.8
30	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	443635	AI080230	Hs.134214	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	AI796769	Hs.208320	ESTs	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
35	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.7
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
40	405348			C7001664:gi12698061 dbj BAB21849.1 (AB	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	447058	AI939456	Hs.160870	ESTs	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
	430697	AA484207	Hs.211867	ESTs	4.5
45	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
	449821	AI671141	Hs.211122	ESTs	4.5
	420905	AA521307	Hs.186651	ESTs	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	420154	AI093155	Hs.95420	JM27 protein	4.4
55	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	4.4
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	433597	AA708205	Hs.100343	ESTs	4.3
60	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	4.2
65	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	420355	AW968263	Hs.123126	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
70	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
75	450597	AI701635	Hs.207077	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
80	438875	AA827640	Hs.189059	ESTs	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	404967			Target Exon	4.0
	427203	AW629517	Hs.244855	ESTs	4.0

	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypothe	4.0
5	435136	R27299	Hs.10172	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
10	448882	AJ001531	Hs.22404	protease, serine, 12 (neurolypsin, moto	4.0
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
15	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.9
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
20	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	414441	AA234759	Hs.132950	ESTs	3.9
	425810	AI923627	Hs.31903	ESTs	3.9
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
25	440450	AI333129	Hs.156147	ESTs	3.8
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
30	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
35	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
	432101	AI918950	Hs.123642	EphA3	3.7
40	418759	AA227879	Hs.187621	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	448568	AA149121	Hs.71947	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
45	436345	AA873008	Hs.121572	ESTs	3.7
	446862	AV660697	Hs.282700	ESTs	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
50	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
55	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	403481			Target Exon	3.6
60	404561			trichorhinophalangeal syndrome I gene (T	3.6
	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021987	Hs.59970	ESTs	3.6
65	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	420026	AI831190	Hs.166676	ESTs	3.6
70	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
75	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.5
	401132			C12000517*:gil4758712[ref[NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
80	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5

	430865	AI073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153287	ESTs	3.5
	428647	AA830050	Hs.124344	ESTs	3.5
5	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AI760833	Hs.293971	ESTs	3.4
	436714	AA728964	Hs.293399	ESTs	3.4
10	404848			ENSP00000240769*:BG153O3.1 (similar to C	3.4
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
15	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
20	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
25	419964	AA811657	Hs.220913	ESTs	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
30	433628	AI821784	Hs.188578	ESTs	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AI126288	Hs.192232	ESTs	3.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
35	428923	BE047698	Hs.188785	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
40	448108	AW300021	Hs.170685	ESTs	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
45	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	432229	AW290976	Hs.143587	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
50	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
	416662	T25853	Hs.7538	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
	428715	AW293716	Hs.53126	ESTs	3.3
55	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AI821803	Hs.136580	ESTs	3.2
	439306	BE220199		WD40 protein C1a01	3.2
60	420608	BE548277	Hs.103104	ESTs	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
65	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	3.2
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	402145			Target Exon	3.2
	448131	AI675054	Hs.200481	ESTs	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
70	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	447183	AI554733	Hs.173182	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
75	434408	AI031771	Hs.132586	ESTs	3.2
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.2
	453789	AA628517	Hs.118502	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
80	419088	AI583823	Hs.52620	integrin, beta 8	3.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AI458682		gb:tk13e01.x1 NCL_CGAP_Lu24 Homo sapiens	3.2
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

	405321		Target Exon	3.1
	429569	AA454993	Hs.138343 ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941 ESTs	3.1
5	452102	U04343	Hs.27954 CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	433444	AW975324	Hs.129816 ESTs	3.1
	410821	AI114811	Hs.92526 ESTs, Weakly similar to T00365 hypotheti	3.1
	415861	Z43123	Hs.144513 ESTs	3.1
	422299	AK000181	Hs.114556 hypothetical protein FLJ20174	3.1
10	432527	AW975028	Hs.102754 ESTs	3.1
	427773	AA412290	Hs.98124 ESTs	3.1
	441817	AW969706	Hs.293332 ESTs	3.1
	416812	H91010	Hs.44940 ESTs	3.1
	417958	AA767382	Hs.193417 ESTs	3.1
15	407426	AF129533	gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921 ESTs	3.1
	418037	AI990212	Hs.86447 ESTs	3.1
	419197	N48921	Hs.27441 KIAA1615 protein	3.1
	420179	N74530	Hs.21168 ESTs	3.1
20	436295	N73895	gb:za62d06.s1 Soares fetal liver spleen	3.1
	405548		Target Exon	3.1
	423595	R82826	Hs.220702 ESTs	3.1
	412533	AA679863	Hs.69606 ESTs	3.1
	434072	H70854	Hs.283059 Homo sapiens PRO1082 mRNA, complete cds	3.1
25	405264		NM_030813*:Homo sapiens suppressor of po	3.1
	410869	AW808361	gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	425354	U62027	Hs.155935 complement component 3a receptor 1	3.1
	441492	AI149998	Hs.146346 ESTs	3.1
	447078	AW885727	Hs.9914 ESTs	3.1
30	435021	AA922192	Hs.54709 ESTs	3.0
	408832	AW085690	Hs.63428 ESTs, Weakly similar to Z195_HUMAN ZINC	3.0
	450580	N40087	ESTs	3.0
	432319	AW510770	Hs.128386 ESTs	3.0
	453713	R20640	Hs.79133 cadherin 8, type 2	3.0
35	445784	AI253155	Hs.146065 ESTs	3.0
	416642	T96118	Hs.226313 ESTs	3.0
	418948	AI217097	gb:gd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997 ESTs	3.0
	439182	AF086030	Hs.21621 hypothetical protein DKFZp762O076	3.0
40	404995		ENSP00000251890*:Monocytic leukemia zinc	3.0
	444794	AI419991	Hs.145225 ESTs	3.0
	443634	H73972	Hs.134460 ESTs	3.0
	420133	AA426117	Hs.155543 ESTs	3.0
	407829	AA045084	Hs.29725 hypothetical protein FLJ13197	3.0
45	426743	AA383833	Hs.245022 ESTs	3.0
	442326	H92962	Hs.124813 hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016 ESTs	3.0
	454096	AW062757	gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	419622	AA452054	Hs.119338 ESTs	3.0
50	449745	AI668593	gb:yl38a05.x5 Soares breast 3NbHBst Homo	3.0
	428412	AA428240	Hs.126083 ESTs	3.0
	428200	AI039624	Hs.98388 ESTs	3.0
	414951	AW794931	Hs.100861 hypothetical protein FLJ14600	3.0
	431869	AA521136	Hs.190176 ESTs	3.0
55	451391	AA017410	Hs.40568 ESTs	3.0
	452959	AI933416	Hs.189674 ESTs	3.0

TABLE 66B

60	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
65	Pkey _i	CAT Number	Accession	
	410790	1221131_1	AW803357 AW803423 AW812233 R06814	
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934	
			AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739	
			AW808704 AW808558 AW808714 AW808420 AW8	
70	411436	1245660_1	AW846433 AW846159 AW846377 AW846528	
	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069	
			AW848905 AW848214	
	412988	1342150_1	BE046680 BE046738 BE044958	
	413081	1348563_1	BE064415 BE064430 BE064448	
75	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925	
	416009	1566379_1	Z43062 R13213 H14422	
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043	
	420111	190755_1	AA255652 AA280911 AW967920 AA262684	
80	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280	
	424200	236595_1	AA337221 AA336756 AW966196	
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564	
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912	

428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438
		AI092404 AI085630 AA731340
430535	319643_1	AW968485 AW968670 AA480922 BE350425
432765	353907_1	AJ003429 AJ003367 AA564825
433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
434763	392847_1	AA648618 AW974389 H51771
436295	41733_1	N73895 AJ001872
439092	468554_1	AA830149 AW978407 M85983 AW503637
439306	47088_1	BE220199 W01813 AF086118 N70760 BE221405
440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
442481	543588_1	N99828 BE079873 AI110738 AF074645
445432	63943_1	AV653771 BE089370
448044	747196_1	AI458682 H24240 R14537 R18426 AW867082
449570	81018_1	AA001793 AA001871
449745	814534_1	AI668593 AI820774 R86205 H39971 H22177 H26241
450317	831956_1	AI692689 R14223 R18395
450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
		AA164518 AA730973 W00417 W65303
450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
452452	918580_1	BE173515 BE173560 AI902860
453682	977454_1	T79703 T96307 AL079725
454037	996287_1	AW998716 AW022148 N68020
454096	1007449_1	AW062757 AW176890 AW052758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
454457	1207274_1	AW753456 AW753036 AW854868 AW854862
454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
454860	1237732_1	AW835767 AW835537 BE160187
454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
455067	1252050_1	AW854538 AW854418 AW854412
455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
457374	328758_1	AA493662 AW897396 BE154814
458912	823104_1	AI911066 AI933734 AI680888 AJ003599

TABLE 66C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277595
400746	7329328	Minus	147703-147896
401132	8705350	Minus	85679-85795
402145	8018280	Plus	113086-114800
403242	7637817	Minus	11297-12511
403481	9965004	Plus	93496-93633
403510	7652047	Plus	61866-62027
403667	6850483	Minus	1344-1442,1545-1697
404003	8655948	Plus	198349-199096
404561	9795980	Minus	69039-70100
404592	9943965	Minus	39067-39225
404848	8248647	Minus	23955-24034,25143-25264
404967	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28556-28684
405321	3419846	Minus	44654-45210
405348	2914717	Minus	43310-43462
405510	7630909	Minus	101028-101174
405548	1532158	Plus	11552-11686

TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	65.0
	432441	AW292425	Hs.163484	ESTs	56.0
	446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
	400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	48.1
10	414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
	419526	AI821895	Hs.193481	ESTs	35.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
15	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
	400292	AA250737	Hs.72472	BMP-R1B	28.8
	400287	S39329	Hs.181350	kallikrein 2, prostatic	28.8
20	425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
	415539	AI733881	Hs.72472	BMP-R1B	27.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
	409262	AK000631	Hs.52255	hypothetical protein FLJ20624	25.5
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
	407168	R45175	Hs.117183	ESTs	24.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
	428336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
30	403047			NM_005656*:Homo sapiens transmembrane pr	23.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
	407709	AA456135	Hs.23023	ESTs	21.5
	401424			NM_001172:Homo sapiens arginase, type II	20.6
35	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
	434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
	415989	AI267700		ESTs	17.9
	437052	AA861697	Hs.120591	ESTs	17.8
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
40	431548	AI834273	Hs.9711	novel protein	16.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	16.5
	413597	AW302885	Hs.117183	ESTs	16.1
45	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	15.3
	407122	H20276	Hs.31742	ESTs	15.1
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
	426501	AW043782	Hs.293616	ESTs	13.9
	428898	AB033070	Hs.194408	KIAA1244 protein	13.7
	418961	AW967646	Hs.23023	ESTs	13.3
	448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	13.2
55	418848	AI820961	Hs.193465	ESTs	13.1
	428398	AI249368	Hs.98558	ESTs	13.0
	429220	AW207206		ESTs	12.7
	401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
60	419078	M93119	Hs.89584	insulinoma-associated 1	12.3
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.4
	429918	AW873986	Hs.119383	ESTs	11.3
65	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	412446	AI768015		ESTs	11.1
	433404	T32982		ESTs	10.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	10.4
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
	418278	AI088489	Hs.83937	hypothetical protein	10.3
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	10.2
75	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	10.1
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	10.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	10.0
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	9.8
	437718	AI927288	Hs.196779	ESTs	9.8
80	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
	453160	AI263307		H2B histone family, member L	9.7
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
	450325	AI935962	Hs.91973	ESTs	9.6
	434170	AA626509	Hs.122329	ESTs	9.6
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	9.6

	447033	AI357412	Hs.157601	ESTs	9.5
	401747			Homo sapiens keratin 17 (KRT17)	9.3
	434423	NM_006769	Hs.3844	LIM domain only 4	9.3
5	411887	AW182924	Hs.128790	ESTs	9.2
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	9.2
	415263	AA948033	Hs.130853	ESTs	9.2
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
	421896	N62293	Hs.45107	ESTs	9.1
10	432101	AI918950	Hs.123642	EphA3	9.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	8.9
	420218	AW958037		ribosomal protein L4	8.8
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
15	424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	8.5
	446100	AW957109	Hs.13804	hypothetical protein DJ462O23.2	8.5
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.5
20	416182	NM_004354	Hs.79069	cyclin G2	8.5
	431542	H63010	Hs.5740	ESTs	8.4
	447397	BE247676	Hs.18442	E-1 enzyme	8.3
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	8.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	8.1
25	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
	451684	AF216751	Hs.26813	CDA14	8.1
	437124	AA554458		KIAA0666 protein	8.0
	416239	AL038450	Hs.48948	ESTs	8.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
30	424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
	428728	NM_016625	Hs.191381	hypothetical protein	7.9
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.8
	442049	AA310393	Hs.190044	ESTs	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
35	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
	443180	R15875	Hs.258576	claudin 12	7.5
	433285	AW975944	Hs.237396	ESTs	7.5
	410870	U81599	Hs.66731	homeo box B13	7.4
	418836	AI655499	Hs.161712	ESTs	7.4
40	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
	431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	7.3
	432586	AA568548		ESTs	7.3
45	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
	435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.3
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
	426108	AA622037	Hs.166468	programmed cell death 5	7.1
	433323	AA805132	Hs.159142	ESTs	7.1
50	423349	AF010258	Hs.127428	homeo box A9	7.0
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
55	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
	418601	AA279490	Hs.86368	calmegin	6.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	6.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	6.8
	425465	L18964	Hs.1904	protein kinase C, iota	6.6
60	450377	AB033091		KIAA1265 protein	6.6
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	6.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	6.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
65	440774	AI420611	Hs.153934	ESTs	6.5
	413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
70	451027	AW519204	Hs.40808	ESTs	6.4
	436063	AK000028		ribosomal protein S24	6.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
75	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.2
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.1
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	6.1
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
80	448045	AJ297436	Hs.20166	prostate stem cell antigen	6.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.0
	433517	AW022133	Hs.189838	ESTs	6.0
	424036	AA770688		H2A histone family, member L	5.9

	420092	AA814043	Hs.88045	ESTs	5.9
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.8
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP56680846 protein	5.8
5	450244	AA007534	Hs.125062	ESTs	5.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
	451952	AL120173	Hs.301663	ESTs	5.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
10	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	5.7
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	5.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
	415621	AI648602	Hs.55468	ESTs	5.7
15	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	5.5
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.4
20	425211	M18667	Hs.1867	progastricin (pepsinogen C)	5.4
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.4
	410762	AF226053	Hs.66170	HSKM-B protein	5.4
	440594	AW445167	Hs.126036	ESTs	5.4
25	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
	447805	AW627932	Hs.302421	gemin4	5.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
	453308	AW959731	Hs.323099	ESTs	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
30	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.2
	404632			NM_022490:Homo sapiens hypothetical prot	5.1
	450861	AI523898	Hs.17617	ESTs	5.1
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.1
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.1
35	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
	410037	AB020725	Hs.58009	KIAA0918 protein	5.1
	410240	AL157424	Hs.61289	synaptojanin 2	5.0
	403046			NM_005656*:Homo sapiens transmembrane pr	5.0
	419647	AA348947	Hs.91816	hypothetical protein	5.0
40	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	5.0
	450164	AI239923	Hs.63931	ESTs	5.0
	417318	AW953937	Hs.240845	ESTs	4.9
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
45	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
	433852	AI378329	Hs.126629	ESTs	4.9
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.8
50	441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
	453171	R76472	Hs.65646	ESTs	4.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	4.8
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	4.8
	419440	AB020689	Hs.90419	KIAA0882 protein	4.8
55	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.8
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	4.7
60	431724	AA514535	Hs.283704	ESTs	4.7
	423242	AL039402	Hs.125783	DEME-6 protein	4.7
	434485	AI623511	Hs.118567	ESTs	4.7
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	4.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	4.6
65	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.6
	439735	AI635386	Hs.142846	hypothetical protein	4.6
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
70	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
	426006	R49031	Hs.22627	ESTs	4.5
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.5
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.5
75	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
	423583	AL122055	Hs.129836	KIAA1028 protein	4.4
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.4
80	429467	NM_004477	Hs.203772	FSHD region gene 1	4.4
	451752	AB032997		KIAA1171 protein	4.3
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.3
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.3
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
	427308	D26067	Hs.174905	KIAA0033 protein	4.3
	435706	W31254	Hs.7045	GL004 protein	4.3
5	416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	4.2
	410076	T05387	Hs.7991	ESTs	4.2
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.2
10	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
	442501	AA315267	Hs.23128	ESTs	4.2
	436761	AI817776	Hs.236557	ESTs	4.2
	420380	AA640891	Hs.102406	ESTs	4.2
	436556	AI364997	Hs.7572	ESTs	4.2
15	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
	446416	AV658299	Hs.163959	ESTs	4.2
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.2
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.1
20	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.1
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	4.1
	408418	AW963897	Hs.44743	KIAA1435 protein	4.1
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.1
25	432363	AA534489		gb:nf76g11.s1 NCL_CGAP_Co3 Homo sapiens	4.1
	447574	AF162666	Hs.18895	tousled-like kinase 1	4.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.0
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.0
	444108	R55784	Hs.140942	ESTs	4.0
30	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.0
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
35	438825	BE327427	Hs.79953	ESTs	4.0
	433233	AB040927	Hs.301804	KIAA1494 protein	4.0
	415276	U88666	Hs.78353	SFRS protein kinase 2	4.0
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
	407819	R42185		ESTs	4.0
40	450402	BE218027	Hs.89969	ESTs	4.0
	432527	AW975028	Hs.102754	ESTs	4.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.9
45	432435	BE218886	Hs.282070	ESTs	3.9
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	3.9
	411031	W37943	Hs.34892	KIAA1323 protein	3.9
50	429259	AA420450	Hs.292911	Plakophilin	3.9
	407813	AL120247	Hs.40109	KIAA0872 protein	3.9
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.9
	417958	AA767382	Hs.193417	ESTs	3.9
	427176	AW381569	Hs.40334	ESTs	3.9
55	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.8
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.8
	432675	AI791855		ESTs	3.8
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.8
	427479	BE410092	Hs.178471	KIAA0798 gene product	3.8
60	443162	T49951	Hs.9029	DKFZP434G032 protein	3.8
	413950	AA249096	Hs.32793	ESTs	3.8
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.8
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	3.8
65	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.8
	447620	AW290951		ESTs	3.8
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
70	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.8
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8
	459284	AF155660	Hs.300496	mitochondrial solute carrier	3.8
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	3.7
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	3.7
75	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.7
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.7
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.7
	453469	AB014533	Hs.33010	KIAA0633 protein	3.7
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	3.7
80	422072	AB018255	Hs.111138	KIAA0712 gene product	3.7
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420522	AW957137	Hs.98541	hypothetical protein	3.6
	408833	AW612232	Hs.254835	ESTs	3.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.6

	456177	NM_012391	Hs.79414	prostate epithelium-specific Els transcr	3.6
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.6
	422424	AI186431	Hs.296638	prostate differentiation factor	3.6
5	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.6
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.6
	421887	AW161450	Hs.109201	CGI-86 protein	3.6
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
10	412520	AA442324	Hs.795	H2A histone family, member O	3.6
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.6
	441224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.5
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
15	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.5
	418113	AI272141	Hs.83484	SRV (sex determining region Y)-box 4	3.5
20	428055	AA420564	Hs.101760	ESTs	3.5
	418827	BE327311	Hs.47166	HT021	3.5
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	3.5
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
25	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
	439671	AW162840	Hs.6641	kinesin family member 5C	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.4
30	443884	N20617	Hs.194397	leptin receptor	3.4
	403752			NM_002753*:Homo sapiens mitogen-activate	3.4
	427723	AI355260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
35	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.4
	433647	AA603367	Hs.222294	ESTs	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
40	437617	AI026701	Hs.5716	KIAA0310 gene product	3.3
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.3
	435655	AW105663	Hs.6947	HSPC069 protein	3.3
45	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
50	420568	F09247	Hs.247735	protocadherin alpha 10	3.3
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	3.3
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
55	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
	409960	BE261944		hexokinase 1	3.3
	433891	AA613792		gb:nc97h03.s1 NCI_CGAP_Pr2 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
60	419972	AL041465	Hs.182982	golgin-67	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
	419879	Z17805	Hs.93564	Horner, neuronal immediate early gene, 2	3.3
65	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.3
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
	414922	D00723		glycine cleavage system protein H (amino	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26691	ESTs	3.2
70	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.2
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
	401519			C15000476*:gil12737279[ref]XP_012163.1	3.2
75	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.2
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.2
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upt3, variant A	3.2
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
80	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
	439593	BE073597	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	AI249502	Hs.29669	ESTs	3.2
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2

5	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	425810	AI923627	Hs.31903	ESTs	3.2
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
10	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
	414222	AL135173		sorbitol dehydrogenase	3.1
	419749	X73608	Hs.93029	sparc/osteoneclin, cwcv and kazal-like d	3.1
15	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.1
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.1
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
20	436489	AJ272269	Hs.121429	zinc-binding protein Rbcc728	3.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.1
	445943	AW898533	Hs.181574	ESTs	3.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
25	432426	AW973152	Hs.31050	ESTs	3.1
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.1
	423453	AW450737	Hs.128791	CGI-09 protein	3.1
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.1
30	436278	BE396290	Hs.5097	synaptogyrin 2	3.1
	432908	AI861896		ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.1
35	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	409757	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
	434293	NM_004445	Hs.3796	EphB6	3.1
	410001	AB041036	Hs.57771	kallikrein 11	3.1
40	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278962	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
	448807	AI571940	Hs.7549	ESTs	3.1
45	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1
	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	3.0
50	429638	AI916662	Hs.211577	kineclin 1 (kinesin receptor)	3.0
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
55	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
	449459	BE546846	Hs.195048	ESTs	3.0
60	438523	H66220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.0
	429966	BE081342	Hs.283037	HSPC039 protein	3.0
65	412652	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	3.0
	436032	AA150797	Hs.109276	latexin protein	3.0
70	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
	415172	AF079529	Hs.78106	phosphodiesterase 8B	2.9
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
75	413142	M81740	Hs.75212	ornithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
	439609	AW971945	Hs.293236	ESTs	2.9
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
80	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420061	AW024937	Hs.29410	ESTs	2.9
	431663	NM_016569	Hs.267182	TBX3-iso protein	2.9
	417622	AW298163	Hs.82318	WAS protein family, member 3	2.9
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI632278	Hs.195922	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

5	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	2.9
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	2.9
10	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	2.9
	413125	BE244589	Hs.75207	glyoxalase I	2.9
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.9
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
15	437296	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.9
	445109	AF039916	Hs.12330	ecdonucleoside triphosphate diphosphohyd	2.9
	423551	AA327598	Hs.89633	ESTs	2.9
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	2.9
20	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bromodomain-containing 1	2.8
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	2.8
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	2.8
25	444367	H54892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	2.8
	418166	AI754416		Cdc42 effector protein 3	2.8
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
30	413550	W03011	Hs.306881	MSTP043 protein	2.8
	426170	BE161065	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
	425320	U29344	Hs.83190	fatty acid synthase	2.8
	431631	AA548906	Hs.122244	ESTs	2.8
35	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	2.8
40	439778	AL109729	Hs.99364	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
	450546	AA010200	Hs.175551	ESTs	2.7
	431674	AA098901	Hs.301642	G-protein coupled receptor	2.7
45	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	443181	AI039201	Hs.283316	ESTs	2.7
	448913	AA194422	Hs.22564	myosin VI	2.7
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	2.7
50	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	2.7
	434747	AA837085		ESTs	2.7
55	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	2.7
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypothesi	2.7
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.7
60	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	2.7
	438157	AW137011	Hs.49576	ESTs	2.7
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	2.7
65	409648	AW451449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
	400301	X03635	Hs.1657	estrogen receptor 1	2.7
	453390	AA862496	Hs.28482	ESTs	2.7
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
70	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	2.7
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	2.7
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	2.7
75	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypothesi	2.7
	409650	T08490	Hs.288969	HSCARG protein	2.7
	452707	AI093823	Hs.45070	ESTs	2.7
80	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	2.7
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.7
	406627	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6

	440695	AW088363	Hs.246240	ESTs	2.6
	416941	BE000150	Hs.48778	niban protein	2.6
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.6
5	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	2.6
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
	401197			ENSP00000229263*:HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 f1s, clone H	2.6
	410297	AA148710		lumican	2.6
10	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.6
	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
15	408157	AA047685	Hs.62946	ESTs	2.6
	420805	L10333	Hs.99947	reticulon 1	2.6
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	2.6
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	2.6
20	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
	425174	D87450	Hs.154978	KIAA0261 protein	2.6
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75360	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
25	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	2.6
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406670	W79632	Hs.256301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
30	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
	449518	BE395253	Hs.30861	ESTs	2.6
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.6
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.6
35	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.6
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.6
	434672	AW294020	Hs.117721	ESTs	2.6
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.6
	452576	AB023177	Hs.29900	KIAA0960 protein	2.6
40	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.6
	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
45	451040	AA324743	Hs.40808	ESTs	2.6
	445636	AW105401		ribosomal protein L29	2.6
	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.6
50	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.6
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	2.5
	406789	AI041403		ribosomal protein L29	2.5
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.5
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.5
55	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.5
	436165	AI373544	Hs.331328	intermediate filament protein syncollin	2.5
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.5
	452827	AI571835	Hs.55468	ESTs	2.5
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
60	431108	AA991508	Hs.105317	ESTs	2.5
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA826425	Hs.192375	ESTs	2.5
65	421091	W22821		ribosomal protein L26	2.5
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.5
	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.5
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.5
70	431615	AW295859	Hs.235860	ESTs	2.5
	433037	NM_014158	Hs.279938	HSPC067 protein	2.5
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
	450628	AW382884	Hs.204715	ESTs	2.5
75	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.5
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
80	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.5
	416737	AF154335	Hs.79691	LIM domain protein	2.5
	414869	AA157291	Hs.21479	ubiquitin 1	2.5
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.5
407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.5
414556	AW975063	Hs.343443	ribosomal protein L36	2.5
446911	N27605	Hs.16492	DKFZP564G2022 protein	2.5
435126	AI393666	Hs.42315	p10-binding protein	2.5
421866	M24470	Hs.1435	guanosine monophosphate reductase	2.5
426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.5
447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.5
443837	AI984625	Hs.9884	spindle pole body protein	2.5
421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
435021	AA922192	Hs.73962	ESTs	2.5
435750	AB029012	Hs.4990	KIAA1089 protein	2.5
435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.5
407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
425976	C75094	Hs.334514	NG22 protein	2.5
449458	AI805078	Hs.208261	ESTs	2.5
428013	AF151020	Hs.181444	hypothetical protein	2.5
424369	R87622	Hs.26714	KIAA1831 protein	2.5
431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
452779	AA418775	Hs.47234	ESTs	2.5
433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.5
438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.5
427515	T79526	Hs.179516	integral type I protein	2.5
418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.5

TABLE 67B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259
412446	63467_1	BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41443 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815 BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39435 T32982 R54110 BF115783 F09044 BF808433 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
433404	7392_1	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336
449625	249224_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AM93770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
453160	6028_5	AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422
432586	6633_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548
438869	52134_1	AF075009 R63109 R63068
450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164
436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW29495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
424036	6226_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465 AL531028 BG437151 BE868021 AA179427
450203	19009_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024796 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192
451752	10408_5	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295901 BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333 AW970240 AA534489 AW970323
432363	1234917_1	

5	422890	61426_1	AK057805 AW162343 AI190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 BI792383 BF056928 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI366013 AI867923 BG911906 D81142 C15616 AL538697 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40698 AW204071 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
	417379 407819	1610005_1 7392_2	AA196390 AA507837 AA196468 AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185 AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706664 BE706539 BE153177 BF084925 AL133779 AW961788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826 AW973834 AI791932 AI791855 AI732640 AA558833 AA559897 AI821610 AI973051 AI400921 AI796154 AW241817 AW290951 NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435520 AI356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677 BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296868 AI268977 R168133 BM352065 AI262769 BF941976 AI056920 AA481861 BF763697 AL565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111012 AA908246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257 AW182329 AA613792 T05304 AW858385 BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI695677 AL562079 AI700926 AI470561 BF063058 AW196387 AU132984 BI064046 AI970157 R02122 H55924 AI521721 AA808206 AA725223 AI766003 AW339821 AA805951 AI287969 AW664827 BC021085 AL527872 AL526296 AL557087 BI255090 AU143499 AL560356 BG823170 BE736988 AU141388 AL580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726986 AL564735 BE155962 BE155979 BF741679 H67776 H59234 H89665 AW117774 AW274435 L29008 NM_003104 U07361 BF002824 BI222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW069877 AW015214 AI948718 BE219706 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI420449 AW275385 BG36950 BE501521 BF740566 AA311404 AA384639 BI772535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AL564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AL581093 AU158964 AU158917 AL282516 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 AI284986 AA857926 BF327568 AA570172 AI753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N55172 AW013929 AI826274 AI871237 C75260 AA934846 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AU106667 AU159238 AU1282517 AA406317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW438877 AI800550 AW328268 AI244886 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 N70983 H44325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AA706106 AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635 AF119847 AA437261 AA436987 AI132965 AF150424 AI861896 AA570057 AV738855 AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981 AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AI134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422 AK055915 BE867252 AI523348 AA765350 BF446858 Z43675 R19529 AI133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA376592 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI096810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA249732 AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974 AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102 AA602964 AA609200 AW976537 AI033582 AA837085 AA745261 AA648395 BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AW185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355 AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA661791 BM474307 BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893 AI989299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299 R70463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI624611 BG271780 AI497723 H88862 D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 Z32966 BE883841 R61003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z39807 BF954386 NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099 AL538039 BG701311 BE255806 BF805256 F12128 AL566773 BI828686 BF761480 AI204971 BG818818 BI199245 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833
10	419733	7612_3	
	432675 447620 409151	1237917_1 687223_1 4123_1	
15			
20	409960	39576_1	
25	433891 414922	647290_1 1563_2	
30	414222	18695_1	
35			
40			
45	426991	29771_1	
50	434194 432908 412652	62680_1 452541_1 18858_2	
55	437179	12239_1	
60			
65	418166	18858_1	
70	431416 447881	120918_1 44623_1	
75			
80	407192 434747 410297	2200202_1 117643_1 2990_1	

445636 8561_5 BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310
AA090672

419175 35068_1 AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331
AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA365626
Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618
AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AI037576 AA534314 BE814964 BE973713 N49493 BE006634
BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572
AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AV044188 AI203159 N49403
F02090 AI187299 AI609644 Z40516 AW952314

10 441128 20932_1 BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071
BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706
N90525 AW973623 AI359627 BG674574 BE903322

15 406789 0_0 AI041403 Z49148
421091 24941_2 AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161
BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358396
AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AL568301 AL567278 BI522445 BI754384
BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116
BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842
H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896

20 400263 18977_1 Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935
BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095
BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241
BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685
BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671
BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206
BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964
BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 67C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401519	6649315	Plus	157315-157950
401785	7249190	Minus	165776-165996, 166189-166314, 166408-16656
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833, 5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 995 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 995 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	85.5
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	68.6
446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cali	65.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	AI821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fls, clone PL	44.9
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	40.9
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
5	400292	AA250737	Hs.72472	BMP-R1B	31.4
	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	31.4
	428819	AL135623	Hs.193914	KIAA0575 gene product	31.2
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	30.3
10	407168	R45175	Hs.117183	ESTs	29.6
	400287	S39329	Hs.181350	kallikrein 2, prostatic	29.6
	415539	AI733881	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.8
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	28.1
15	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.5
	403047			NM_005656*:Homo sapiens transmembrane pr	27.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	25.7
	428336	AA503115	Hs.183752	microseminoprotein, beta-	25.0
	401424			NM_001172:Homo sapiens arginase, type II	24.9
20	407709	AA456135	Hs.23023	ESTs	24.7
	407122	H20276	Hs.31742	ESTs	24.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	23.2
	415989	AI267700		ESTs	23.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.7
25	437052	AA861697	Hs.120591	ESTs	22.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	22.5
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	21.2
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	20.8
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	20.5
30	427958	AA418000	Hs.98280	potassium intermediate/small conductance	20.5
	431548	AI834273	Hs.9711	novel protein	19.8
	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.4
	426501	AW043782	Hs.293616	ESTs	19.3
	413597	AW302885	Hs.117183	ESTs	18.9
35	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	18.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	18.0
	429220	AW207206		ESTs	17.9
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.6
	418961	AW967646	Hs.23023	ESTs	17.3
40	428898	AB033070	Hs.194408	KIAA1244 protein	17.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.8
	428398	AI249368	Hs.98558	ESTs	16.3
	419078	M93119	Hs.89584	insulinoma-associated 1	15.8
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.4
45	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	15.2
	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
	447033	AI357412	Hs.157601	ESTs	14.9
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	14.7
50	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	14.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.4
	418848	AI820961	Hs.193465	ESTs	14.3
	429918	AW873986	Hs.119383	ESTs	14.2
55	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
	418278	AI088489	Hs.83937	hypothetical protein	14.1
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	13.9
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	13.3
	432101	AI918950	Hs.123642	EphA3	13.3
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	13.1
60	412446	AI768015		ESTs	12.7
	437718	AI927288	Hs.196779	ESTs	12.6
	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	12.6
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.5
65	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.5
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	12.4
	453160	AI263307		H2B histone family, member L	12.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	12.1
70	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	12.1
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	11.9
	424692	AA429834	Hs.151791	KIAA0092 gene product	11.7
	415263	AA948033	Hs.130853	ESTs	11.3
75	416182	NM_004354	Hs.79069	cyclin G2	11.3
	420218	AW958037		ribosomal protein L4	11.3
	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.2
80	450325	AI935962	Hs.91973	ESTs	11.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.1
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	11.0

	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_006769	Hs.3844	LIM domain only 4	10.6
5	434170	AA626509	Hs.122329	ESTs	10.6
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.5
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
10	401747			Homo sapiens keratin 17 (KRT17)	10.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247676	Hs.18442	E-1 enzyme	10.0
	433285	AW975944	Hs.237396	ESTs	10.0
15	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	9.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.190044	ESTs	9.6
20	443180	R15875	Hs.258576	claudin 12	9.5
	406964	M21305		FGENES predicted novel secreted protein	9.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
25	451684	AF216751	Hs.26813	CDA14	9.5
	440594	AW445167	Hs.126036	ESTs	9.4
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	calmegin	9.3
30	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
	437124	AA554458		KIAA0666 protein	9.2
	428728	NM_016625	Hs.191381	hypothetical protein	9.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.9
35	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
	418836	AI655499	Hs.161712	ESTs	8.8
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
40	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isof	8.7
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	8.7
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	8.7
	425465	L18964	Hs.1904	protein kinase C, iota	8.5
45	416239	AL038450	Hs.48948	ESTs	8.5
	436962	AW377314	Hs.5364	DKFZP564I052 protein	8.4
	450164	AI239923	Hs.63931	ESTs	8.4
	452744	AI267652	Hs.245107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AI420611	Hs.153934	ESTs	8.3
50	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
	410870	U81599	Hs.66731	homeo box B13	8.3
	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
55	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	8.2
	423349	AF010258	Hs.127428	homeo box A9	8.1
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.1
	432586	AA568548		ESTs	8.0
	426108	AA622037	Hs.166468	programmed cell death 5	8.0
60	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	8.0
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	7.9
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kallikrein 4 (prostase, enamel matrix, p	7.7
65	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
	433323	AA805132	Hs.159142	ESTs	7.7
	451952	AL120173	Hs.301663	ESTs	7.7
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
70	420092	AA814043	Hs.88045	ESTs	7.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (7.6
	440749	W22335	Hs.7392	hypothetical protein MGC3199	7.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
75	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.4
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	7.4
	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AI648602	Hs.55468	ESTs	7.4
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
80	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
	450244	AA007534	Hs.125062	ESTs	7.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AI623511	Hs.118567	ESTs	7.2

5	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	7.1
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
	436063	AK000028		ribosomal protein S24	7.0
10	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.9
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
	436476	AA326108	Hs.33829	bHLH protein DEC2	6.8
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
15	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	6.6
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
20	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0918 protein	6.5
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
	409648	AW451449	Hs.57749	ESTs	6.4
25	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.3
	404632			NM_022490:Homo sapiens hypothetical prot	6.3
30	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
	410762	AF226053	Hs.66170	HSKM-B protein	6.3
	436032	AA150797	Hs.109276	latexin protein	6.3
35	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	6.2
	424036	AA770688		H2A histone family, member L	6.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
40	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183161	ESTs	6.1
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	6.1
	432527	AW975028	Hs.102754	ESTs	6.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
45	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.0
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
	419647	AA348947	Hs.91816	hypothetical protein	6.0
50	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
	446416	AV658299	Hs.163959	ESTs	5.9
	407819	R42185		ESTs	5.9
55	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	5.9
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.9
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	5.8
	410240	AL157424	Hs.61289	synaptojanin 2	5.8
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	5.7
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.7
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	5.7
65	433852	AI378329	Hs.126629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	5.6
	419440	AB020689	Hs.90419	KIAA0882 protein	5.6
	435706	W31254	Hs.7045	GL004 protein	5.6
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
70	442409	BE208843	Hs.129544	hypothetical protein MGC15438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.6
	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	5.5
75	403046			NM_005656*:Homo sapiens transmembrane pr	5.5
	447805	AW627932	Hs.302421	gemin4	5.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	5.4
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
80	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	5.4
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	D26067	Hs.174905	KIAA0033 protein	5.4
	409151	AA306105		SEC22, vesicle trafficking protein (S. c	5.4
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.4
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88666	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
	417318	AW953937	Hs.240845	ESTs	5.3
5	429467	NM_004477	Hs.203772	FSHD region gene 1	5.3
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.2
10	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
	436420	AA443966	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
15	450832	AW970602	Hs.105421	ESTs	5.1
	448807	AI571940	Hs.7549	ESTs	5.1
	420568	F09247	Hs.247735	protocadherin alpha 10	5.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
20	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	452576	AB023177	Hs.29900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
25	407103	AA424881	Hs.256301	hypothetical protein MGC13170	5.0
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
30	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
	444108	R55784	Hs.140942	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.9
35	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.9
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.9
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.9
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.9
40	442501	AA315267	Hs.23128	ESTs	4.8
	439735	AI635386	Hs.142846	hypothetical protein	4.8
	451752	AB032997		KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
45	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	4.8
	433313	W20128	Hs.296039	ESTs	4.8
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.8
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	4.7
50	447574	AF162666	Hs.18895	tousled-like kinase 1	4.7
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.7
	411031	W37943	Hs.34892	KIAA1323 protein	4.7
55	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.7
	441224	AU076964	Hs.7753	calumenin	4.7
	407813	AL120247	Hs.40109	KIAA0872 protein	4.7
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.7
60	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.7
	414922	D00723		glycine cleavage system protein H (amino	4.7
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.79953	ESTs	4.7
	425174	D87450	Hs.154978	KIAA0261 protein	4.7
65	420380	AA640891	Hs.102406	ESTs	4.7
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.7
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.6
	436761	AI817776	Hs.236557	ESTs	4.6
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.6
70	404922			NM_003071:Homo sapiens SWI/SNF related,	4.6
	436556	AI364997	Hs.7572	ESTs	4.6
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	4.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.6
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.5
75	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.5
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.5
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.5
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.5
80	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.5
	453390	AA862496	Hs.28482	ESTs	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	4.5

	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.4
5	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.4
	417958	AA767382	Hs.193417	ESTs	4.4
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
15	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	4.3
	429259	AA420450	Hs.292911	Plakophilin	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	4.3
	459284	AF155660	Hs.300496	mitochondrial solute carrier	4.3
20	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.3
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
25	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	4.3
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
	450402	BE218027	Hs.89969	ESTs	4.3
	428055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.3
	432676	AI791855		ESTs	4.2
30	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
	445707	AI248720	Hs.114390	ESTs	4.2
	410297	AA148710		lumican	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
35	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
	447620	AW290951		ESTs	4.2
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.2
40	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	4.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	4.2
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	AI355260	Hs.279789	histone deacetylase 3	4.2
45	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	4.2
	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
50	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypothei	4.1
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	4.1
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.1
	427479	BE410092	Hs.178471	KIAA0798 gene product	4.1
55	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	4.1
	449459	BE546846	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
60	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	412520	AA442324	Hs.795	H2A histone family, member O	4.0
	448663	BE614599		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433647	AA603367	Hs.222294	ESTs	4.0
65	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	4.0
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014533	Hs.33010	KIAA0633 protein	4.0
70	418827	BE327311	Hs.47166	HT021	4.0
	446791	AI632278	Hs.195922	ESTs	4.0
	443884	N20617	Hs.194397	leptin receptor	4.0
	416857	AA188775	Hs.292453	ESTs	4.0
	401519			C15000476*:gil 12737279 ref XP_012163.1	4.0
75	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.0
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.9
	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AW105663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
80	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.9
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ubiquitin 1	3.9
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
5	435021	AA922192	Hs.73962	ESTs	3.9
	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
10	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421887	AW161450	Hs.109201	CGI-86 protein	3.8
	434614	AI249502	Hs.29669	ESTs	3.8
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.8
15	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.8
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.8
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
20	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	AI186431	Hs.296638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
25	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.8
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440695	AW088363	Hs.246240	ESTs	3.8
	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
30	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
	411190	AA306342	Hs.69171	protein Kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
35	432426	AW973152	Hs.31050	ESTs	3.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	3.7
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	AI861896		ESTs	3.7
40	432800	BE391046	Hs.278962	AIM-1 protein	3.7
	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	AL041465	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kallikrein 11	3.7
	432205	AI806583	Hs.125291	ESTs	3.7
45	401197			ENSP00000229263*:HSPC213.	3.7
	420061	AW024937	Hs.29410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284192	ESTs	3.7
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
50	420805	L10333	Hs.99947	reticulon 1	3.7
	401866			Target Exon	3.7
	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	3.7
55	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451945	BE504055	Hs.211420	ESTs	3.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.6
60	454229	AW957744	Hs.278469	lacrimal proline rich protein	3.6
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.6
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
65	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	3.6
	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.6
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
70	450649	NM_001429	Hs.25272	E1a binding protein p300	3.6
	436489	AJ272269	Hs.121429	zinc-binding protein Rbccc728	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	3.6
75	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
	427715	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.6
	403752			NM_002753*:Homo sapiens mitogen-activate	3.6
80	418559	AA225048	Hs.104207	ESTs	3.6
	438523	H66220	Hs.278177	ESTs	3.6
	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	3.5
5	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
	433891	AA613792		gb.no97h03.s1 NCL CGAP_Pr2 Homo sapiens	3.5
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434672	AW294020	Hs.117721	ESTs	3.5
10	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.5
	434970	AW272262	Hs.225767	ESTs	3.5
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.5
	445943	AW898533	Hs.181574	ESTs	3.5
15	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.5
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
20	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
	436087	BE300296	Hs.5054	CGI-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.5
25	439609	AW971945	Hs.293236	ESTs	3.5
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	3.5
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
30	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
	442323	AW016669	Hs.29190	ESTs	3.5
	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104336	hypothetical protein	3.5
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
35	450628	AW382884	Hs.204715	ESTs	3.4
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.4
40	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.4
	434293	NM_004445	Hs.3796	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
45	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	3.4
	411078	AI222020	Hs.182364	CocoaCrisp	3.4
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
50	431674	AA098901	Hs.301642	G-protein coupled receptor	3.4
	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.4
55	452295	BE379936	Hs.28866	programmed cell death 10	3.4
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
	439593	BE073597	Hs.124863	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.4
60	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412652	AI801777		ESTs	3.3
	415172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
65	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	3.3
	425010	T16837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
	442064	AI422867	Hs.88594	ESTs	3.3
70	431663	NM_016569	Hs.267182	TBX3-Iso protein	3.3
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	3.3
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	3.3
75	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.3
	436278	BE396290	Hs.5097	synaptogyrin 2	3.3
	424560	AA158727	Hs.150555	protein predicted by clone 23733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418166	AI754416		Cdc42 effector protein 3	3.3
80	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.2
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase I	3.2

	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.2
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	3.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	3.2
5	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	3.2
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	3.2
	422173	BE385828	Hs.250619	phorbol-in-like protein MDS019	3.2
10	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	3.2
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.2
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.2
	406214			NM_016371:Homo sapiens hydroxysteroid (1	3.2
15	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.2
	438714	AA814859	Hs.160074	ESTs	3.2
	433213	AW665130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	3.2
20	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	3.2
	437179	AA393508		serologically defined colon cancer antig	3.2
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.2
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.2
25	450546	AA010200	Hs.175551	ESTs	3.2
	409995	AW960597	Hs.129206	ESTs	3.2
	408739	W01556	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638:Homo sapiens hypothetical prot	3.2
30	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	3.1
	414341	D80004	Hs.75909	KIAA0182 protein	3.1
	423044	AA320829	Hs.97266	protocadherin 18	3.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
35	423551	AA327598	Hs.89633	ESTs	3.1
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
	413550	W03011	Hs.306881	MSTP043 protein	3.1
	431933	AI187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99364	putative transmembrane protein	3.1
40	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.1
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
	421254	AK001724	Hs.102950	coat protein gamma-cop	3.1
	424339	BE257148		endoglycan	3.1
45	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	3.1
	425320	U29344	Hs.83190	fatty acid synthase	3.1
	426170	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.1
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	3.1
	417622	AW298163	Hs.82318	WAS protein family, member 3	3.1
50	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	433036	AA574091	Hs.105964	ESTs	3.1
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.1
	408380	AF123050	Hs.44532	diubiquitin	3.1
55	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	3.1
	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.1
	437296	AA350994	Hs.20281	KIAA1700	3.1
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	3.1
60	448913	AA194422	Hs.22564	myosin VI	3.1
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.0
	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
65	437546	AW074836	Hs.173984	T-box 1	3.0
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
70	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	3.0
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406627	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
75	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	3.0
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	3.0
	431416	AA532718		ESTs	3.0
	431631	AA548906	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
80	434974	AA778711		eukaryotic translation initiation factor	3.0
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	3.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279938	HSPC067 protein	3.0

	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
5	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	3.0
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	3.0
	432810	AA863400	Hs.23054	ESTs	3.0
10	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.0
	445596	R89543	Hs.12942	vesicle trafficking protein	3.0
	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.0
15	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.0
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.9
	425920	AL049977	Hs.162209	claudin 8	2.9
	409927	T69981		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
20	447881	BE620886		GCN1 (general control of amino-acid synt	2.9
	439584	AA838114	Hs.221612	ESTs	2.9
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CGI-83 protein	2.9
25	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.9
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.9
30	429351	AK001490	Hs.200016	hypothetical protein FLJ10628	2.9
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
35	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.9
	428801	AW277121	Hs.254881	ESTs	2.9
	430462	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98806	hypothetical protein	2.9
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
40	418222	AI675881	Hs.86538	ESTs	2.9
	433009	AA761668		gb:nz24c08.s1 NCL_CGAP_GCB1 Homo sapiens	2.9
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.9
45	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371048	Hs.93758	H4 histone family, member H	2.9
	409650	T08490	Hs.288969	HSCARG protein	2.9
50	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas	2.9
	412719	AW016610		ESTs	2.9
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	439621	AI200281	Hs.123910	ESTs, Highly similar to B34087 hypothe	2.9
	437050	AA766420		ESTs	2.9
55	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
	416941	BE000150	Hs.48778	niban protein	2.9
	421694	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
60	436823	AW749865		ESTs, Weakly similar to I38022 hypothe	2.8
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.8
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
65	400860			Target Exon	2.8
	436165	AI373544	Hs.331328	intermediate filament protein syncoilin	2.8
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	2.8
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.8
70	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
	435703	AW630133	Hs.83313	GK003 protein	2.8
	431108	AA991508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40808	ESTs	2.8
	443837	AI984625	Hs.9884	spindle pole body protein	2.8
75	418196	AI745649	Hs.26549	KIAA1708 protein	2.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.8
80	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.8
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	2.8

	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467064	Hs.5740	ESTs	2.8
5	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
	452827	AI571835	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	2.8
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	2.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor , S. cerev	2.8
10	419286	AA236005	Hs.128764	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266619	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
15	440080	AW051597		ESTs	2.8
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	2.8
	431525	AA506656	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.8
20	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.8
	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41690	desmocollin 3	2.8
	442013	AA506476	Hs.10600	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
	453038	AW292415	Hs.20509	HBV pX associated protein-8	2.8
25	419175	AW270037		KIAA0779 protein	2.8
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75360	carboxypeptidase E	2.8
30	432651	AW973744	Hs.293100	ESTs	2.8
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
	414556	AW975063	Hs.343443	ribosomal protein L36	2.8
35	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.7
	440340	AW895503	Hs.125276	ESTs	2.7
40	410339	AI916499	Hs.298258	ESTs	2.7
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
45	410099	AA081630		KIAA0036 gene product	2.7
	422000	M30599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
	432745	AI821926		gb.n78f05.x5 NCL_CGAP_Pr3 Homo sapiens	2.7
50	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.7
	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rii-related antigen, integr	2.7
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	2.7
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.7
55	400263			Eos Control	2.7
	435750	AB029012	Hs.4990	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.7
	421709	AA159394	Hs.107056	CED-6 protein	2.7
	421077	AK000061	Hs.101590	hypothetical protein	2.7
60	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
65	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	2.7
	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW206942	Hs.253594	intron of: trichorhinophalangeal syndro	2.7
	420223	N27807		ribosomal protein L4	2.7
70	427515	T79526	Hs.179516	integral type I protein	2.7
	447673	AI823987	Hs.182285	ESTs	2.7
	411960	R77776	Hs.18103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613416	Hs.336425	Homo sapiens, clone MGC:17296, mRNA, com	2.7
75	441551	AA318224	Hs.296141	ESTs	2.7
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA806164	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.7
80	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
	432450	AI990739	Hs.158184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.7
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.7

	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.7
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.7
	431615	AW295859	Hs.235860	ESTs	2.7
5	418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.7
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.7
	438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
15	441094	U33819	Hs.7647	MYC-associated zinc finger protein (puri	2.7
	451356	AA748418	Hs.164577	ESTs	2.7
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2.7
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	2.7
20	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	2.7
	404913			NM_024408*:Homo sapiens Nclh (Drosophil	2.7
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.7
	441054	AA913591		ESTs	2.6
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.6
25	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein Lsm8	2.6
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443666	AI458179	Hs.41528	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	2.6
30	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.6
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	2.6
35	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.6
	430341	NM_006348	Hs.239631	golgi transport complex 1 (90 kDa subuni	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
40	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	420164	AW339037	Hs.24908	ESTs	2.6
	443444	AW952619	Hs.17235	Homo sapiens clone TCCCIA00176 mRNA sequ	2.6
45	412774	AA120865	Hs.23136	ESTs	2.6
	445922	AI337316	Hs.147998	ESTs	2.6
	429925	NM_000786		cytochrome P450, 51 (lanosterol 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
50	417327	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famil	2.6
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
	408743	AL110246	Hs.47367	KIAA1785 protein	2.6
	434011	AW953437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.6
55	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	2.6
60	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.6
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	446258	AI283476	Hs.263478	ESTs	2.6
65	440191	AI990417		tubulin, beta 5	2.6
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
70	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	2.6
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.6
	416751	T48130	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	2.6
75	458946	AA009716	Hs.42311	ESTs	2.6
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.6
	449458	AI805078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	2.6
80	442336	AW340958	Hs.7572	ESTs	2.6
	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

5	436972	AA284679	Hs.25640	claudin 3	2.6
	426809	BE313114	Hs.29706	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
	457638	AI792670	Hs.144405	ESTs	2.6
	442821	BE391929	Hs.8752	transmembrane protein 4	2.5
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L36	2.5
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
10	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	2.5
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	2.5
15	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.5
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	456050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
20	414528	AA148950	Hs.188836	ESTs	2.5
	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-like	2.5
25	448163	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	2.5
	408796	AA688292	Hs.170345	ESTs	2.5
	407627	AI419020	Hs.62620	chromosome 6 open reading frame 1	2.5
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthase	2.5
	415862	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.5
35	449500	AW956345	Hs.12926	ESTs	2.5
	457090	AL080243	Hs.180920	ribosomal protein S9	2.5
	445389	NM_016831	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
40	450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.5
	419430	AI878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA260722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	2.5
45	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40696	ESTs	2.5
	400262			Eos Control	2.5
50	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
	418039	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypotheti	2.5
	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.5
55	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
60	431188	W05656	Hs.169755	ESTs	2.5
	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437762	T78028	Hs.154679	synaptotagmin I	2.5
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.5
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.5
65	451585	AK001171	Hs.326422	hypothetical protein MGC4549	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.5
	446054	AB014537	Hs.13604	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
70	421026	AL047332	Hs.101067	GCN5 (general control of amino-acid synt	2.5
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 68B

75	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
80	Pkey	CAT Number	Accession	
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236	
	429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259	

449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
412446	63467_1	BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
433404	7392_1	BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433
453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336
420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
437124	59408_1	AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA42765 AI292318 AA829886 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA88970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 NA9381 R49886 D61278 BI756612 AA508234 R49885 BF850422
438869	52134_1	AF075009 R63109 R63068
428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967
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432586	6633_1	AK055952 BG182168 BG220105 BG191599 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024796 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192
450377	12109_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548
436063	5483_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AI050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866
424036	6226_1	AI699181 N73808 H08164
407819	7392_2	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
409151	4123_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465 AL531028 BG437151 BE868021 AA179427
422890	61426_1	AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185
451752	10408_5	NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA34006 BG435520 AI356111 H00525 AV749060 BG944497 BG292031
432363	1234917_1	AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136
417379	1610005_1	AA484677
414922	1563_2	AK057805 AW162343 AI190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 BI792383 BF056928 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735
419733	7612_3	AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW955110 AI366013 AI867923 BG911906 D81142 C15616 AL538697 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
432675	1237917_1	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295901
410297	2990_1	BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333 AW970240 AA534489 AW970323
429163	1238297_1	AA196390 AA507837 AA196468
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		AW339821 AA805951 AI287969 AW664827
		AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706664 BE706539 BE153177 BF084925 AL133779 AW961788 AA659693 AA347970
		AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826
		AW973834 AI791932 AI791855 AI732640 AA558833 AA559897 AI821610
		BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907
		AW340368 AA928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355
		AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA661791 BM474307
		BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893
		AI899299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303
		AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299
		R70463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI624611 BG271780 AI497723 H88862
		D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006
		N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441
		W19723 R32966 BE883841 R61003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z38007 BF954386
		AI973051 AI400921 AI796154 AW241817 AW290951
		AA602964 AA609200
		AF119847 AA437261 AA436987 AI132965
		BE966763 AA659765 AI961656 AI520918 AA761743 AA281477 N66431 BE463652 AA281329 AW272944 AA058687 BM145087 AA045516
		AW341820 AA112515 AA258766 AI886639 AA741133 AA768245 AA035533 AI630459 T20165 AW971268 BE966269 AA522722
		AW974271 AA592975 AA447312 AA884766

	426991	29771_1	AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635
5	432908	452541_1	AF150424 AI861896 AA570057 AV738855
	433891	647290_1	AW182329 AA613792 T05304 AW858385
	409960	39576_1	BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296868 AI268977 AI168133 BM352065 AI262769 BF941976 AI056920 AA481861 BF763697 AL565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111012 AA908246 AA319849 AA318136 AL514271 BF364291 AI515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW968088 BM360872 AA319160 AA130778 AL514257
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15			AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AL570058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981
20			AK055915 BE867252 AI523348 AA765350 BF446858 Z43675 R19529 AI133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA376592 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI096810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA249732
25	412652	18858_2	AW976537 AI033582 AA837085 AA745261 AA648395
	437179	12239_1	AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422
30	418166	18858_1	AW867082 AI458682 H24240 R18426 R14537
	434747	117643_1	NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099
35	424339	50559_1	AL538039 BG703131 BE255806 BF805256 F12128 AL566773 BI828686 BF761480 AI204971 BG818818 BI199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164
40			AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833
	418259	133853_1	BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA18444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240
45			BI009308 BI009893 BF922023 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291 AW905577 AW975593 AA713730 AW863781 AA666384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555 AA586369 AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389
50	431416	120918_1	AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680
	434974	77302_1	AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974
55			AL079283 BF792538 AA744861 AI871888 AI478580 AI207075 AI888937 AI808966 BE463436 BF725510 AW675767 BF589111 BE855951
			AW197232 AW272173 AI480335 BF589044 AA443540 AI420128 AI056029 AI650755 AW274589 AW183510 AI440198 AI271801 AW080345 AW189506 AW008293 AA884731 AA579802 AI968645 AI620822 AI222117 AA677146 AI346296 BI792788 AA4446615 AI183486 AA897113 AW271851 AW241299 W90134 AA482921 AI049496 AA492010 AA846639 AA983603 AA969293 AI809036 BI254992 AA63513 AA476659
60			AW673442 AL557763 AA868312 H28886 AA778711 AA081838 AI989340 AL557762 N99654 Z28545 N28874 AA442388 AW887818 AW663156 BG252539 BG501262 BG714174 BG499052 AA058524 BE881198 C75278 R59648 AI829311 AA037656 AW026747 N64518 AW103253 BF529731 AW241677 AW194855 AA917531 R96578 H94036 AA856665 T10342 AW439112 AI090044 AA661591 N71704 AI474928 AU152235 D53426 N21634 R59590 R51072 R96601 H06171 AA084440 H84172 AW118714 C04928 W90092 AA039267 AA136445 R52391 T66024 BG778916
	431155	1235742_1	AA428153 N41394 AA283639 R96600 H94122 BF743684 AA147009 T65867 Z19487 BF697478
	409927	2333801_1	AW971213 AA493925 AA493567 AA876839 AA934462
	447881	44623_1	T69981 T69924 AA078476
65			AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261
			AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119
			AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805
			AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723
			BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
70	433009	2142268_1	AA761668 AA573621 R09670 R92814
	412719	1634_2	BI918715 BF594193 AI073494 AI363077 AI656655 AA121979 BF983131 AA491795 BG152545 AI350401 BF939121 AI479401 BI493099 BF057693
			AI970550 BF111919 BF448282 BI493100 AW043768 AW006202 AI564010 BF433292 AI458202 AI954746 BE220962 AI375411 AI361048
			AA115853 AI364474 AI669815 AA133407 AI928647 AW016610 AA133334 AA504948 AI291629 AI161208 AA837042 AI867138 AA987255 AI830219
			AU150404 AI680674 AW969901
75	437050	1240141_1	AW976442 AA743319 AA766420
	436823	MH1660_153	AG180003 AW975741 AW749865 AA731828 AA731829
	457733	119160_1	AW974812 AI821822 AI821820 AI821075 AI821073 AA651643 AA651662
	453912	32562_3	BM472224 BI966849 BI966735 AW973032 BI962894 BI963048 AA548765 AI926504 AA041551 AW043754 AI086702 AW008105 AA974849
			AW614893 AA553737 AA916996 AW262982 AI580991 BF726843 AV693312 W35325 AA039927 BG460936 AW388482 AW388420 BF374777
			W01360 N94710 H87967
80	440080	517737_1	AW051597 AI733052 AI167287 AI732999 AI566918 AI476787 AI791542 AA887204 AW025394 AA863338 AI240285 AI791393
	419175	35068_1	AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331
			AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA365626
			Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618

			AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA255551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314
5	421091	24941_2	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI835916 AA912295 BG910887 AI568301 AL557278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AI536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896
10	441128	20932_1	BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322
15	406789 410099	0_0 16732_1	AI041403 Z49148 AK055674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 BI917678 BG819395 BG911971 BG820167 AI174254 AA348720 AA364503 BG714279 AW893230 AA081774 H24222 AV727176 BF875715 AA081630 BE000834 AA334880 AL563737 BG029709 W52882 AI439658 BE551237 AA283724 BF109530 AI457096 AI805992 BE467736 AA693467 AI697593 AI887863 AI167419 AW901980 AW901768 BE702179 AA484549 T23811 BE327043 AA716027 AA917004 AA167714 BF339675 AA084618 AI418634 T31586 AA436630 AI366472 AA706191 AI422304 AI204899 AI041169 AA211402 AW827081 AA788593 T32736 AI767935 AA747914 T03534 AW959843 AL119527 BE327037 AW901982 AW993370 AW901977 AW902071 W60090 N79906 D52685 T07735 BE702069 BE702172 T08671 BE767121 BE767117 BE767113 AA658826 AI821926 AI791191 AA635129 AA564492
20	432745 400263	112643_1 18977_1	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI99487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084
30	411605	10026_3	BG256892 H10532 N46614 R52610 AW977696 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09686 BI838226 BF034269 AA429173 BE741829 AW867495 AI123683 AW006831 BE831162 AW452753 AV742717 W86152 BF115102 AI633815 BF921562 AA094230 BE092587 W86151 AA526153 AI672156 BF914496 R12579 BF852352 AA689780 T57386 BF903022 R09933 AA678298 BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672
35	420223 423476	191648_1 32437_1	N27807 AA256634 BE276324 AF263306 BF951698 T66089 F11783 F11794 H29379 R19493 H18042 AL133995 AW134660 AI299437 AA057405 AA917450 AI002692 T09262 R43839 H29290 T65008 N78357
40	441054 429925	2641490_1 33135_1	AI221207 AI659856 AA913591 AI220302 NM_000786 U23942 BI601050 BG771947 BG773455 BI561558 BI460206 BG714348 BM126447 AU129411 AU129401 AL119303 AV724389 AU099323 AU127089 BG701614 BM150364 D55653 AV702235 BE090408 AU151526 AW149661 BG054754 W42624 W52098 AV709923 W79867 W74235 AV709052 AI217668 AA399409 BE182318 BM128040 AI693998 AW615411 AW070426 AI124550 AW778736 AA477781 AW263013 AA59619 AA860513 BF809548 AA643635 AA864975 H42020 AW901189 AA904786 BF432722 BI916393 BM407055 BI333211 AA095636 BI256415 U47727 BG773392 N58531 AA226450 BG679564 AA292178 W56883 BE813131 C03646 BG287974 AA386261 H47580 R48858 T91611 H42019 BI869421 BG502073 BG425943 W37290 W31363 BE004451 BF208311 BI048717 N78122 AA226597 AI525334
45	434976 440191	121716_1 MH790_2	AI963821 AA657925 AA935436 AW975068 BC000222 AL136871 NM_032261 BC009497 BM461705 BG470749 BG826905 BG285127 BI253235 BE397026 BG704967 AW961225 BM352817 BI227161 BG820180 AA454463 AA255685 N31549 AA326504 BC019924 BG257230 BI092368 BI869896 BG251883 BF034444 BG286577 BE260391 AA599912 BF686779 AI755222 AA452272 W241170 AU155655 F28259 T16319 AA326506 N64515 BM016416 BM458963 BG739972 AV729565 BE268285 BE867433 BM011110 BG285856 AI922439 BE270975 AL119339 BF956085 AI565178 AL554305 AL573240 AL572917 AI129627 AL546640 BE392285 AI092843 AI371057 BE302410 AI608753 AW674261 AI750057 AI052649 N47822 AL156249 AI589903 BG258439 AI123662 AI126014 AA778101 AA243218 AW498837 AA748311 AI754395 T15728 AA775369 AA858195 W73625 AA216784 AW513778 AW243958 AI061112 AI783806 AL569622 AA070466 BF229936 N58159 H80288 N32598 H80293 H80279 AL581253 AW571884 AI361698 AW073321 AA876464 H95640 T34421 AA331419 N99897 H80274 BI262120 AA205826 AA070716 AA653206 AA653483 BG389811 W20432 AA670295 AA653197 D51888 AA362527 BG056668 AW118162 AW073071 BE293868 BF792321 BF792258 BG107176 T56604 BM193566 H03238 AA618045 AA906004 BI085686 AA564566 AI221630 D52045 C14510 AA029390 W60153 H98743 AI682641 H28485 AA723093 AI081730 AA641309 AA687083 BI224818 AW204722 AI309186 AI215122 AI200785 BE467373 BM352502 AI304400 AI193071 AI742483 AW003408 AI400201 AI656740 AW665173 AI215120 AI147599 AI803429 AI076110 AI754349 AW205103 AI262491 AI808243 AI281007 AI051273 AI004801 AW768918 AW103289 AI474637 AI264446 AI699509 BE704420 AA989278 AA918256 AA830956 AA989425 AA911929 AA262598 BE740563 BE727592 BE781003 BG030940 BE256750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H94863 N69544 AA181762 D20132 T55734 T60692 R76858 AA022948 AW770291 R50934 AA205918 R97811 H40328 R86252 AA936029 AI813809 AA933607 AA129695 AA548261 AA714393 AA775006 AA653439 AA983808 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007 AA489663 D52138 D51696 D55942 D52740 AI000118 AL516304 AL534259 N54940 AL579194 AI669399 AI342925 BE939201 AA633000 BI222963 AI619676 AW190306 BF035010 AW087897 AI864969 T57243 R48211 AA113880 R26594 C14467 C14444 BI195459 BE896346 BE270780 AL568073 BG389833 BE891549 BI223147 AW381001 AA448464 AW799744 AA412194 AA948107 AA927157 AA983841 BF752571 BE731304 AI380443 AI240179 AA977516 AA884643 AW079380 AW294316 AI913755 AI864320 AI685770 H25135 AI972654 AI538592
50			AI174783 R12271 R83569 AI274757 AI559500 AW022192 AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60656
55			Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI99487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084
60			
65	440409 444610 446091 431843	588375_1 2145292_1 515091_1 445334_1	
70	400262	18977_1	
75			
80			

TABLE 68C

Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859,56369-56511
404922	7341893	Plus	13248-13428
401519	6649315	Plus	157315-157950
401197	9719705	Plus	176341-176452
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833,5708-5895
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
406214	7342036	Plus	86320-86523
403532	8076842	Minus	81750-81901
400860	9757499	Minus	151830-152104,152649-152744
404913	7341740	Plus	97717-97976

Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

TABLE 69A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

Pkey	ExAccn	UnigenelD	Unigene Title	R1
424806	AA382523	Hs.105689	MSTP031 protein	1.51
418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.94
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1.60
442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.73
417944	AU077196	Hs.82985	collagen, type V, alpha 2	1.48
410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	1.91
452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.59
425139	AW630488	Hs.25338	protease, serine, 23	1.63
402463			NM_014624:Homo sapiens S100 calcium-bind	1.50
423798	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon	1.31
412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (2.06
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
441457	AW996651	Hs.43838	ESTs	1.30
408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	1.87
413795	AL040178	Hs.142003	ESTs	1.64
441689	AI123705	Hs.289068	ESTs	1.44
412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
424432	AB037821	Hs.146858	protocadherin 10	1.65
432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	1.31
418683	U90908	Hs.87241	hypothetical protein from clones 23549 a	1.42
453085	AW954243		KIAA0251 protein	1.47
438887	R68857	Hs.265499	ESTs	1.49
436729	BE621807		transmembrane 4 superfamily member 1	1.91
400494			ENSP00000238970*:CIG30 (Fragment).	1.34
442506	BE566411		ESTs	1.54
425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	1.55
414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	2.65
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
422389	AF240635	Hs.115897	protocadherin 12	1.38
417124	BE122762	Hs.25338	ESTs	2.13
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	1.54
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
450534	AI570189	Hs.25132	KIAA0470 gene product	1.43
449618	AI076459	Hs.15978	KIAA1272 protein	1.42
446098	AW072215	Hs.208470	ESTs	1.53
413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
448674	W31178	Hs.154140	ovary-specific acidic protein	1.47
407061	X97748		gb:H.sapiens PTX3 gene promotor region.	1.33

	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
5	453789	AA628517	Hs.118502	ESTs	1.41
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.62
	401234			mitogen-activated protein kinase 8 inter	1.48
	420174	AI824144	Hs.199749	ESTs	1.75
10	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
	418693	AI750878	Hs.87409	thrombospondin 1	1.89
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	1.64
15	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.49
	422099	AA156022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	445119	AF035121	Hs.12337	kinase insert domain receptor (a type II	1.40
20	438142	T90309	Hs.269651	ESTs	1.45
	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.51
	442711	AF151073	Hs.8645	hypothetical protein	1.42
25	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	1.32
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA659037	Hs.163780	(AB075832) KIAA1952 protein [Homo sapien	1.76
	418825	AA228881	Hs.22394	hypothetical protein FLJ10893	1.40
30	417805	U38545	Hs.82587	phospholipase D1, phosphatidylcholine-spe	1.35
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
35	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	1.75
	452298	AI039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T59538		gb:yb65g12.s1 Stratagene ovary (937217)	1.52
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
	433374	AI821409	Hs.304471	EST	1.45
40	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.14
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.52
	453983	H94997	Hs.16450	ESTs	1.94
	406506			Target Exon	1.97
45	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW580939	Hs.97199	complement component C1q receptor	2.36
	426596	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.61
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	1.41
50	450152	AI138635	Hs.22968	intron of VEGFR	1.70
	437269	AA334384	Hs.149420	ESTs	1.60
	445279	R41900	Hs.22245	ESTs	1.59
	409509	AL036923	Hs.322710	ESTs	1.52
	410240	AL157424	Hs.61289	synaptojanin 2	1.61
55	424711	NM_005795	Hs.152175	calcitonin receptor-like	1.96
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	1.81
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	1.91
	410057	R66634	Hs.268107	multimerin	1.85
	446727	AB011095	Hs.16032	KIAA0523 protein	1.67
60	412564	X83703		cardiac ankyrin repeat protein	1.51
	414786	AI246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.71
	410276	AI554545	Hs.71832	angiopoietin-2	1.91
	406627	T64904	Hs.163780	ESTs	1.76
	405025			Bone morphogenetic protein 6	1.69
65	422648	D86983	Hs.118893	Melanoma associated gene	2.33
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.78
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	1.79
	432004	BE018302	Hs.2894	placental growth factor, vascular endothe	2.02
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.93
70	429276	AF056085	Hs.198612	G protein-coupled receptor 51	1.65
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.48
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	2.01
	434398	AA121098	Hs.3838	serum-inducible kinase	1.83
	416851	AW963951	Hs.85618	ESTs	1.65
75	412420	AL036668	Hs.73853	bone morphogenetic protein 2	1.69
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.71
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.86
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	1.65
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	1.83
80	428206	AB020643	Hs.183006	KIAA0836 protein	1.77
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	2.00
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	1.94

	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	1.74
	444409	AI792140	Hs.49265	ESTs	1.88
	421340	F07783	Hs.1369	decay accelerating factor for complement	1.74
5	445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
	444009	AI380792	Hs.135104	ESTs	1.90
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.16
	416940	N75620	Hs.43157	ESTs	2.03
	418922	AW956580	Hs.42699	ESTs	2.09
10	431548	AI834273	Hs.9711	novel protein	1.81
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
	434558	AW264102	Hs.39168	ESTs	1.93
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
	428438	NM_001955	Hs.2271	endothelin 1	2.46
15	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
	439410	AA632012	Hs.188746	ESTs	1.93
	453467	AI535997	Hs.30089	ESTs	2.39
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
20	417933	X02308	Hs.82962	thymidylate synthetase	1.70
	436420	AA443966	Hs.31595	ESTs	1.97
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	1.80
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
	413745	AW247252	Hs.75514	nucleoside phosphorylase	1.99
	405121			mitogen-activated protein kinase 8 inter	2.99
30	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
	421937	AI878857	Hs.109706	hematological and neurological expressed	1.65
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
35	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
	408243	Y00787	Hs.624	interleukin 8	2.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
	407891	AA486620	Hs.41135	endomucin-2	2.34
	407891	AA486620	Hs.41135	endomucin-2	2.34
40	436032	AA150797	Hs.109276	latexin protein	2.24
	439382	BE247684	Hs.103070	ESTs	2.07
	419172	AW338625	Hs.22120	ESTs;similar to TRANSMEMBRANE 4 SUPERF	2.00
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.33
	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
45	432128	AA127221	Hs.296502	ESTs	2.27
	417426	NM_002291	Hs.82124	laminin, beta 1	2.11
	434217	AW014795	Hs.23349	ESTs	2.03
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	2.08
	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
50	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.37
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	2.55
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.09
	449722	BE280074	Hs.23960	cyclin B1	1.76
55	413794	AF234532	Hs.61638	myosin X	2.01
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	2.15
	406964	M21305		gb:Human alpha satellite and satellite 3	3.08
	448231	AI701916	Hs.202509	ESTs	2.27
	408989	AW361666	Hs.49500	KIAA0746 protein	1.43
60	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	2.18
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
	417308	H60720	Hs.81892	KIAA0101 gene product	1.86
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	2.92
65	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
	400666			NM_002425:Homo sapiens matrix metallopro	2.59
	431728	NM_007351	Hs.268107	multimerin	2.72
	440086	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom	2.25
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.76
70	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	3.37
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	3.11
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
	444330	AI597655	Hs.49265	ESTs	3.08
	422424	AI186431	Hs.296638	prostate differentiation factor	2.96
75	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	11.91

TABLE 69B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey CAT Number Accession

453085	10017_1	BC017336 BG716430 BG501286 BI458528 AI582223 N98532 AI338138 AI273442 AW102617 AA831177 AA745642 AA412583 AA355375 BG547492 AW954243 BI766546 BG057641 AI192435 AI338935 AI312651 AI708679 AI191125 AI206832 AA676899 AI078010 AI888718 AA452830 BF445542 N69930 AA715017 BF446713 BE046852 AW771909 AA907729 AI143749 AI761290 AA890233 BF925759 AI783713 AI767267 AA814538 W56778 AA918481 BG743526 BE645242 AI025328 AI298436 AI290445 H27710 AI475034 BG740023 AI090348 AI340003 BI602481 W38495 AI183314 AI927418 BG397181 AA878310 W19369 W56507 C05751 AW380760 AW380770 AW380790 BF930729 H28425 AA037326 AA375805 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI700033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI599264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191397 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL555866 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 NM_002640 L40377 BG227962 AI925897 W60100 BG980023 AA853496 AA360401 AW956168 W61361 AI074846 AA373798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068728 AW976385 AL121194 AI767324 BM054718 AW366882 AA156151 Z25109 C05177 AW975688 AA731063 N67084 AF147374 T59538 T59589 T59598 T59542 X83703 NM_014391 BC018667 AU139209 BE924924 BE924899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA969184 BE924898 BF229066 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943776 AA488072 AA486364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 C04160 C04483 BF229048 AW975183 AA973583 AI365103 AI699495 AI301787
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TABLE 69C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402463	9796896	Minus	8818-8952
400494	9714719	Plus	169845-170272
401234	9929642	Plus	120173-120337
406506	7711374	Minus	6843-8077
405025	7107727	Plus	105267-105343, 106184-106294, 106387-10653
405121	8102330	Minus	35816-36004, 36587-36684
400666	8118496	Plus	17982-18115, 20297-20456

TABLE 70A:

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigenelD:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of the mean of the vessel A1's to the mean of the HUVEC A1's

Pkey	ExAccn	UnigenelD	Unigene Title	R1
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	0.99
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.06
412636	NM_004415		desmoplakin (DPI, DPII)	1.25
426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.36
414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.50
417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.55
414572	AU077174	Hs.288181	cathepsin H	1.64
415314	N88802	Hs.5422	glycoprotein M6B	1.70
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	1.75
406973	M34996	Hs.198253	major histocompatibility complex, class	1.88
456974	M12529	Hs.169401	apolipoprotein E	1.90
430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.91
406828	AA419202	Hs.84298	CD74 antigen (invariant polypeptide of m	1.97
422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	1.99

5	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	2.12
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	2.15
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.17
	437536	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.26
	446945	AI193115	Hs.16611	tumor protein D52-like 1	2.27
10	422639	AI929377	Hs.173724	creatine kinase, brain	2.29
	427451	AI690916	Hs.178137	transducer of ERBB2, 1	2.31
	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pseudosyndostosis)	2.38
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	2.39
15	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
	427393	AB029018	Hs.177635	KIAA1095 protein	2.47
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.49
	414063	H26904	Hs.75736	apolipoprotein D	2.50
20	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	2.51
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	2.51
	410532	T53088	Hs.155376	hemoglobin, beta	2.56
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (2.58
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.58
25	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427980	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8603	p8 protein (candidate of metastasis 1)	2.62
30	425751	T19239	Hs.1940	crystallin, alpha B	2.63
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	2.63
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.66
	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	2.67
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.67
35	452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
	425869	AA524547	Hs.160318	FXYD domain-containing ion transport reg	2.73
	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
40	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.86
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		plakophilin 4	2.94
45	429123	AB011099	Hs.196647	KIAA0527 protein	2.97
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.01
	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.01
	425622	AW360847	Hs.16578	ESTs	3.01
	420195	N44348	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.04
50	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
	407869	AI827976	Hs.24391	hypothetical protein FLJ13612	3.06
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
55	414840	R27319	Hs.23823	hairy/enhancer-of-split related with YRP	3.14
	424651	AI493206		ESTs	3.17
	443932	AW888222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	3.20
60	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.20
	423961	D13666	Hs.136348	periostin(OSF-2os)	3.24
	447384	AI377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.25
	447023	AA356764	Hs.17109	integral membrane protein 2A	3.25
65	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	3.25
	406972	M32053		gb:Human H19 RNA gene, complete cds.	3.26
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	3.29
70	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
	410614	AI091195	Hs.65029	growth arrest-specific 1	3.35
	451529	AI917901	Hs.208641	ESTs	3.35
	430310	U60115	Hs.239069	four and a half LIM domains 1	3.37
	424897	D63216	Hs.153684	frizzled-related protein	3.37
75	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	3.41
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
	407938	AA905097	Hs.85050	phospholamban	3.48
80	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	3.51
	452877	AI250789	Hs.32478	ESTs	3.52
	419577	L36531	Hs.91296	integrin, alpha 8	3.52
	404277			NM_019111*:Homo sapiens major histocompa	3.54

5	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	3.64
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	3.71
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	3.75
10	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	3.77
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.80
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	3.86
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	3.89
15	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.90
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	4.01
20	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	4.09
	421823	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	4.25
25	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	4.26
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	4.29
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.34
	419938	AI076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78065	complement component 7	4.37
30	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	4.41
	452114	N22687	Hs.8236	ESTs	4.43
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
35	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxin)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108623	thrombospondin 2	4.73
40	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
	414290	AI568801	Hs.71721	ESTs	4.98
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416784	AA334592	Hs.79914	lumican	5.20
45	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
	408221	AA912183	Hs.47447	ESTs	5.65
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	5.87
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
50	426406	AI742501	Hs.169756	complement component 1, s subcomponent	7.94
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev9)	9.91

TABLE 70B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
60	412636	1438_1
65		M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE708078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE708045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H00146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE14064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406

			BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 5 454042 30254_1 AJ420458 AI018523 AA708686 BF949633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI654847 AW874199 AI206120 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 10 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366468 N64350 AA779107 AW025969 R49056 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202561 AA788851 AI494436 BF856114 H22570 AW964381 BG007409 BM314056 AA465642 T30661 T33111 Z42834 C04542 BF948152 BF944325 BF58895 AA935284 AI267360 N64249 W67500 F07962 AA322394 BI489987 BE644965 BM313782 AA910364 AI809246 AA836750 BF115228 AA829730 N27413 BM141766 AI742325 AA455261 AA938708 AI420241 AI130039 BF222341 BF941301 AA771807 Z41034 BF447457 BF447426 AW515347 T03874 F02360 F02302 15 N34898 AI678586 AA807824 AA948556 AW204638 BM142045 BF446775 AV648364 AI801368 AA971739 AI017351 AA760722 AI460007 AI458383 AI694152 AA226536 BE467282 N47808 BE348825 BE830581 BE830583 N53009 N59351 N41056 W67501 AA016246 H43293 F21282 R59121 R56280 424651 46029_5 BG435302 BM083687 AA904035 AA468889 W76175 AA761874 H28767 AA910081 AA837086 AI521825 BG986378 AI478562 AA743152 AA746092 H88863 BG986375 AA635644 AI493206 AA696979 BE245127 BG986430 BG986529 BF665873 BG030157 BG622575 AA766495
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TABLE 70C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
404277	1834458	Minus	91665-91946

TABLE 71A: 774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 1A lists 774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 75th percentile of ewing sarcoma to 85th percentile of body map

Pkey	ExAccn	UnigeneID	Unigene Title	R1
104659	AW969769	Hs.105201	ESTs	70.3
101447	M21305		gb:Human alpha satellite and satellite 3	64.7
105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	50.5
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	48.8
121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	46.7
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	46.6
110278	AF061573	Hs.19492	protocadherin 8	46.1
126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	41.4
116752	AL008583	Hs.91622	neuronal pentraxin receptor	40.9
119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	39.6
104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	36.9
110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	35.5
121362	AF050147	Hs.97932	chondromodulin I precursor	34.7
131291	NM_004350	Hs.170019	runt-related transcription factor 3	33.0
101063	D54745	Hs.80247	cholecystokinin	31.7
121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	28.7
122651	AW975398	Hs.293836	ESTs	28.0
100299	D49493	Hs.2171	growth differentiation factor 10	26.5
129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.2
123619	AA602964		gb:nc97c02.s1 NCL_CGAP_Pr2 Homo sapiens	26.1
124006	AI147155	Hs.279727	ESTs; homologue of PEM-3 [Clona savignyi	23.1
116301	AW969706	Hs.293332	ESTs	22.6
121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	22.3
106533	AL134708	Hs.145998	ESTs	22.3
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	21.3
131313	R96290	Hs.75874	ribosomal protein L44	20.8
116790	AW161357		microtubule-associated protein tau	18.7
105316	AI671245	Hs.24835	hypothetical protein FLJ14594	18.2
102123	NM_001809	Hs.1594	centromere protein A (17kD)	17.8
126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	17.8
119791	AA554907	Hs.58291	ESTs	16.7
113003	AW292315	Hs.7215	ESTs	16.3
102836	U94320	Hs.158330	neuropeptide Y receptor Y5	16.3
126799	AW753865	Hs.74376	olfactomedin related ER localized protei	16.3
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	15.5
107160	AA314490	Hs.27669	KIAA1563 protein	14.8
115313	AA808001	Hs.184411	albumin	14.6
123308	C14187	Hs.103538	ESTs	14.2

	126077	M78772	Hs.210836	ESTs	14.0
	100698	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	106821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
	110288	H40665	Hs.31564	ESTs	13.8
5	106498	AI221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;calsyntenin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	128639	AW582962	Hs.102897	CGI-47 protein	13.2
10	125698	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119456	AA248897	Hs.48784	ESTs	12.2
	135155	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	106614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
15	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
	132968	AF234532	Hs.61638	myosin X	11.7
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6616	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
	104968	AI249502	Hs.29669	ESTs	11.1
20	123532	AA608733		gb:ae56f06.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125556	AB033064	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, t	10.6
25	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	10.6
	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
30	110730	N67655	Hs.26411	ESTs	10.3
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (importin) beta 3	10.1
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
40	105091	AA148859	Hs.179909	hypothetical protein FLJ22995	9.6
	106146	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.5
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
45	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
	121910	AI204600	Hs.96978	hypothetical protein MGC10764	9.2
	130625	AF176012	Hs.260720	J domain containing protein 1	9.2
	129755	R42216	Hs.7759	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	9.0
50	111109	AI940675	Hs.20914	hypothetical protein FLJ23056	9.0
	120217	AA862257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-link	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	AI085153	Hs.143764	ESTs, Weakly similar to unknown [H.sapie	8.8
55	113903	AI368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
	105253	AW997484	Hs.5003	KIAA0456 protein	8.6
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
60	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.5
	102725	AB026187	Hs.159156	protocadherin 11	8.5
	130298	AI347487	Hs.132781	class I cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
65	106575	AW970602	Hs.105421	ESTs	8.2
	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	8.1
	119499	AI918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244930	Hs.166895	ESTs	8.0
70	107098	AI823593	Hs.27688	ESTs	8.0
	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894638	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	7.9
75	133063	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.8
	105730	AW377314	Hs.5364	DKFZP564I052 protein	7.8
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	7.8
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	7.8
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	7.7
80	125400	AL110151	Hs.128797	DKFZP586D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AI608657	Hs.95097	ESTs	7.7
	129075	BE250162	Hs.83765	dihydrofolate reductase	7.6

5	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	7.6
	132438	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A (7.6
	118036	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	7.6
	131170	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	7.5
	104548	R39398	Hs.91559	ESTs	7.5
10	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.4
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
	132559	AF119848	Hs.270863	hypothetical protein PRO1580	7.3
15	101050	AU077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW893940	Hs.59698	ESTs	7.1
	105127	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	7.1
	128478	AA708205	Hs.100343	ESTs	7.1
20	110456	H52348	Hs.36636	ESTs	7.1
	118846	AW299598	Hs.50895	homeo box C4	7.1
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	7.1
	128132	AA225632		gb:nc08a07.r1 NCI_CGAP_Pr1 Homo sapiens	7.0
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	7.0
25	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	106213	N45018	Hs.8769	hypothetical protein DKFZp761J17121	6.9
	118013	AI674126	Hs.94031	ESTs	6.9
	120147	AI917116		hemoglobin, beta	6.8
30	118267	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	6.8
	120325	AA195651		AP-2 beta transcription factor	6.8
	133276	AW978439	Hs.69504	ESTs	6.8
	127742	AW293496	Hs.180138	ESTs	6.7
35	127664	AA806164	Hs.116502	ESTs	6.7
	108778	AF133123	Hs.90847	general transcription factor IIIC, polyp	6.6
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	6.6
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.6
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
40	115197	R18656		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
	126967	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937	6.4
	118499	N67274	Hs.50141	EST	6.4
45	105301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AI869372	Hs.17207	Homo sapiens cDNA FLJ11922 fis, clone HE	6.3
	127968	AA830201	Hs.124347	ESTs	6.3
	134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
50	115844	AI373062	Hs.332938	hypothetical protein MGC5370	6.3
	121885	AA934883	Hs.98467	ESTs, Highly similar to AF257737 1 cilia	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
	132256	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	6.2
55	106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	6.2
	135186	U73328	Hs.172648	distal-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
	109261	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	6.1
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	6.1
60	128501	AL133572	Hs.199009	protein containing CXXC domain 2	6.1
	109747	AI223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-5301/15	6.0
	104689	AA420450	Hs.292911	Plakophilin	6.0
65	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121830	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypotheti	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
	109841	H01052		gb:yj32h01.s1 Soares placenta Nb2HP Homo	5.9
	115622	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.8
70	122969	AW821252	Hs.104336	hypothetical protein	5.8
	109872	R65841	Hs.28653	ESTs	5.8
	114208	AL049466	Hs.7859	ESTs	5.8
	113494	T91451	Hs.86538	ESTs	5.8
	127684	AA668631	Hs.159971	KIAA0379 protein	5.8
75	129300	W94197	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
	105909	AA195191		hypothetical protein FLJ20729	5.8
	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
80	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	5.7
	130723	BE247676	Hs.18442	E-1 enzyme	5.7
	107230	AI034467	Hs.34650	ESTs	5.7
	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

	117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
5	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
10	106668	R49390	Hs.254129	KIAA1678	5.4
	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109606	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13675 fis, clone PL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
15	131185	BE280074	Hs.23960	cyclin B1	5.4
	111227	T06701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
20	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
	115121	AI634549	Hs.325422	ESTs	5.3
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.3
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	5.3
25	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (5.3
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040884	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypotheti	5.2
30	120830	AI568170	Hs.96886	ESTs	5.2
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
	103316	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49163	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
35	116680	AW902848	Hs.273829	ESTs	5.2
	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161885	Hs.269745	ESTs	5.1
	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
40	110799	AI089660	Hs.323401	dpy-30-like protein	5.1
	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
45	125321	T86652	Hs.178294	ESTs	5.1
	102627	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
50	116814	H50834	Hs.77899	gb:yp86a10.s1 Soares fetal liver spleen	5.0
	130622	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	5.0
	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127765	AA971146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RU2S	4.9
	120484	AA253170	Hs.96473	EST	4.9
55	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
	129012	R81936		ribosomal protein L44	4.9
	124973	AI476066	Hs.102243	ESTs, Weakly similar to I78885 serine/th	4.9
	124648	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
60	131526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.9
	130637	AA356764	Hs.17109	integral membrane protein 2A	4.8
	126769	AA083456		gb:zn09g08.r1 Stratagene hNT neuron (937	4.8
	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	4.8
	100169	AL037228	Hs.82043	D123 gene product	4.8
65	130262	D63216	Hs.153684	frizzled-related protein	4.8
	109260	AW978515	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
70	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	4.8
	105848	AW954064	Hs.24951	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129706	AA443241		ribosomal protein L44	4.7
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126629	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	4.7
	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW352149	Hs.102314	ESTs	4.7
	126521	AI475110	Hs.203933	ESTs	4.7
	110343	AW136703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

5	113974	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
	103487	AA743603	Hs.172108	nucleoporin 88kD	4.6
	125353	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	4.6
10	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	4.6
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
15	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.5
	104912	AA813192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AI571940	Hs.7549	ESTs	4.5
	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.5
20	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
	106489	AA452054	Hs.119338	ESTs	4.5
	122792	AW188551	Hs.99519	hypothetical protein FLJ14007	4.5
25	112651	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123596	AA421130	Hs.112640	EST	4.5
	125447	AI582222	Hs.128686	ESTs	4.5
	106178	AL049935	Hs.301763	KIAA0554 protein	4.4
30	102250	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334842	tubulin alpha 1	4.4
	127496	AI031650		ESTs	4.4
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	4.4
	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
35	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61939	Hs.103822	ESTs	4.4
	120922	AA481003	Hs.97128	ESTs	4.3
	115167	AA749209	Hs.43728	hypothetical protein	4.3
40	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PRO0659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
	103616	NM_002647	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
45	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	135098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	4.3
	106246	AL036917	Hs.288821	KIAA1638 protein	4.3
50	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
	129650	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
55	106073	AL157441	Hs.17834	downstream neighbor of SON	4.2
	105403	AI473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	4.2
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	4.2
60	106012	AI240665		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.2
	130832	AW838006	Hs.20082	zinc finger protein 3 (A8-51)	4.2
	125960	AI754693	Hs.145968	ESTs	4.2
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
65	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	4.2
	101266	L36645	Hs.73964	EphA4	4.2
70	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.1
	116133	AW449597	Hs.313652	EST, Weakly similar to I38022 hypothetic	4.1
	129001	AA443323	Hs.107812	BPOZ protein	4.1
75	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	4.1
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	4.1
	126107	H75477	Hs.93361	ESTs	4.1
	115333	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	4.1
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	4.1
80	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153746	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	CDC28 protein Kinase 2	4.1
	129948	AI537162	Hs.263988	ESTs	4.1
	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW088276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15069	ESTs	4.1
	118872	AI039201	Hs.283316	ESTs	4.1

5	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retroviru	4.0
	127153	AI732303	Hs.186518	hypothetical protein MGC2599 similar to	4.0
	124105	H11484	Hs.79133	ESTs	4.0
10	100031			AFFX control - DapX-M	4.0
	106897	AF039023	Hs.167496	RAN binding protein 6	4.0
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.0
	126965	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.0
15	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	4.0
	118751	N74210	Hs.50454	ESTs	4.0
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	4.0
	111387	AI244489	Hs.285724	ESTs	4.0
20	118676	N45312	Hs.46506	ESTs	4.0
	107348	AW973753	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	4.0
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
25	115399	AF151534	Hs.92023	core histone macroH2A2.2	4.0
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gb:yy54c08.s1 Soares_multiple_sclerosis_	4.0
	126522	W31912	Hs.21168	gb:zc76d03.s1 Pancreatic Islet Homo sapi	4.0
	131965	W79283	Hs.35962	ESTs	3.9
30	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
	105808	AI133161	Hs.286131	CGI-101 protein	3.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
35	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112996	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
	118967	AI668670	Hs.216756	ESTs	3.9
	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
40	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	3.9
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	3.9
45	131971	BE567100	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.106985	ESTs	3.9
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
	112921	R91095	Hs.4276	KIAA1701 protein	3.9
50	120820	AA347417	Hs.96869	EST	3.8
	106459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
	105476	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.8
	122682	AA984531	Hs.159293	ESTs	3.8
55	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
	129785	H19006	Hs.184780	ESTs	3.8
	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	3.8
60	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H60720	Hs.81892	KIAA0101 gene product	3.8
	106140	AB006624	Hs.14912	KIAA0286 protein	3.8
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
65	103319	X83492	Hs.82359	tumor necrosis factor receptor superfami	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA296874	Hs.77494	deoxyguanosine kinase	3.8
	127262	AA828125		gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens	3.7
	126872	AW450979		gb:UL-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	3.7
70	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.7
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	3.7
	126962	R12014	Hs.20976	ESTs	3.7
	116203	AW137166	Hs.87305	ESTs	3.7
	123377	AW969183	Hs.271297	ESTs	3.7
75	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123654	PCF11p homolog	3.7
	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
	131163	AA099524	Hs.23754	ESTs	3.7
80	126708	AW962593	Hs.135260	ESTs	3.7
	117417	AI241733	Hs.43871	ESTs	3.7
	106272	AW959731	Hs.323099	ESTs	3.7
	110834	AW273860	Hs.5759	ESTs	3.7
	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109260A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W96141	Hs.220687	ESTs	3.7

	130850	AB040922	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
5	105150	AA631977	Hs.155995	KIAA0643 protein	3.6
	103163	AU077018	Hs.3235	keratin 4	3.6
	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW664072	Hs.60136	ESTs	3.6
	113577	AI300699	Hs.111334	PRO0470 protein	3.6
10	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.6
	127563	AB035898	Hs.150587	kinesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.6
	114118	F01598	Hs.175930	ESTs	3.6
15	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.6
	125174	W51835	Hs.231082	EST	3.6
	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	3.6
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	3.6
	135191	X16866	Hs.333497	cytochrome P450, subfamily IID (debrisoq	3.6
20	124367	AI683183	Hs.99348	distal-less homeo box 5	3.6
	113560	T91015		ESTs	3.6
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	3.6
	113988	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88252	ESTs	3.6
25	126600	AA699949	Hs.191385	ESTs	3.6
	127256	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
30	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	115691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
	134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	3.6
	128468	T23625	Hs.150580	putative translation initiation factor	3.6
35	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	3.5
	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	3.5
40	125562	AI494372	Hs.98968	hypothetical protein FLJ23058	3.5
	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.5
	125558	R59305		gb:yh16c10.r1 Soares infant brain 1NIB H	3.5
	117265	AA451966		RAB9-like protein	3.5
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
45	109482	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	3.5
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117613	AW029507	Hs.161102	ESTs	3.5
	100944	L07518		mucin 6, gastric	3.5
50	105226	R58958	Hs.26608	hypothetical protein MGC15880	3.5
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	3.5
	123720	AA609734	Hs.112755	EST	3.5
	128846	AA730767	Hs.285753	SCG10-like-protein	3.5
	116443	AW962196	Hs.339808	LBP protein 32	3.5
55	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
	106918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.5
	131244	AI638429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	insulin receptor substrate 2	3.5
	111223	AA852773	Hs.334838	KIAA1866 protein	3.5
60	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	3.5
	105395	AI580880	Hs.268149	putative methyltransferase	3.5
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	106367	AA504747	Hs.136102	KIAA0853 protein	3.5
	103392	X94563		gb:H.sapiens dbi/acbp gene exon 1 & 2.	3.5
65	101086	AA382524	Hs.250959	histatin 1	3.5
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	3.5
70	114096	AF060219	Hs.27007	chromosome condensation 1-like	3.4
	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
75	109734	AI927212	Hs.3734	ESTs	3.4
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	3.4
	106685	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
80	108687	BE544475	Hs.54347	ESTs	3.4
	113115	AI141426	Hs.8705	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.4
	123110	AA486256	Hs.193510	EST	3.4
	131019	W28614		chorionic somatomammotropin hormone 1 (p	3.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N63753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C186 protein	3.4
5	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	3.4
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	3.4
10	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	3.4
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115506	AB037756	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	3.4
15	106691	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
	105169	BE245294	Hs.180789	S164 protein	3.4
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126638	AA649257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
20	106650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	3.3
	108859	AL121500		ESTs	3.3
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypotheti	3.3
	125693	H23989	Hs.169743	Homo sapiens clone 25121 neuronal olfact	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
25	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.3
	124691	R05835	Hs.110153	ESTs	3.3
	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	gb:ym37a05.r1 Soares infant brain 1NIB H	3.3
30	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 prolina-r	3.3
	107908	AF087999		ESTs	3.3
	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	3.3
35	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
	105463	AA825974	Hs.32646	hypothetical protein FLJ21901	3.3
	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	3.3
40	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
	113283	T66813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133160	N54968	Hs.66309	hypothetical protein MGC11061	3.3
45	134076	AF086215	Hs.78980	gb:Homo sapiens full length insert cDNA	3.3
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
	127728	AW404061		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
	127506	T61039	Hs.76067	ribosomal protein L10a	3.3
50	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
	126666	AA648886	Hs.151999	ESTs	3.3
	130453	U80735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3
	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
55	121292	AA401807		gb:zv65f11.s1 Soares_total_fetus_Nb2HF8_	3.3
	123284	AA488988	Hs.293796	ESTs	3.3
	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
60	114988	AA251089		gb:zs04f05.s1 NCL_CGAP_GCB1 Homo sapiens	3.3
	132867	AF226667	Hs.58553	CTP synthase II	3.3
	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AI521936	Hs.107149	novel protein similar to archael, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
65	111520	AI985369	Hs.301134	ESTs	3.3
	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA768242	Hs.80618	hypothetical protein	3.3
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	3.3
70	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	3.3
	116734	AW900992	Hs.93796	DKFZP586D2223 protein	3.3
	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326683	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
75	129284	AA318224	Hs.296141	ESTs	3.3
	119127	AA708035	Hs.12248	ESTs	3.3
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	118397	BE139479	Hs.161492	ESTs	3.3
80	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
	126735	M69113	Hs.226795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	3.2
	106103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
5	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	3.2
	133761	AF041430	Hs.75922	brain protein l3	3.2
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
10	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
	129673	D38552	Hs.1191	KIAA0073 protein	3.2
	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	126722	N66148	Hs.11125	HSPC033 protein	3.2
	109966	H09103	Hs.30897	EST	3.2
15	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
	109517	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
	105252	AB039670	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
20	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
	134869	AL157518	Hs.90421	PRO2463 protein	3.2
	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
25	129056	AI769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN !!!!	3.2
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
	103038	AA926960		CDC28 protein kinase 1	3.2
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1	3.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	3.2
	132305	AI806090	Hs.44344	hypothetical protein FLJ20534	3.2
30	131136	AB033099	Hs.23413	KIAA1273 protein	3.2
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117639	AA377165	Hs.44833	ESTs	3.2
	127076	AI422951	Hs.146162	ESTs	3.2
35	126153	H85692	Hs.40730	ESTs	3.2
	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypotheti	3.2
	104946	AW242407	Hs.73848	carcinoembryonic antigen-related cell ad	3.2
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
40	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	3.2
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	3.2
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.2
	119651	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108812	hypothetical protein FLJ22004	3.2
45	134964	AI803516	Hs.272891	hippocalcin-like protein 4	3.1
	105551	AW005822	Hs.25292	ribonuclease HI, large subunit	3.1
	119750	AI538880	Hs.94812	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
	104590	AW373062		nuclear receptor subfamily 1, group I, m	3.1
50	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
	116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.1
	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14967 fis, clone TH	3.1
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
	128538	R44214	Hs.101189	ESTs	3.1
55	129179	AW969025	Hs.109154	ESTs	3.1
	108793	AA129395	Hs.71139	ESTs	3.1
	108807	AI652236	Hs.49376	hypothetical protein FLJ20644	3.1
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.1
	132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	3.1
60	134937	AI251449	Hs.171939	ESTs	3.1
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	3.1
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	3.1
	128179	AW293689	Hs.127116	ESTs	3.1
65	117121	H95044	Hs.321386	EST	3.1
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
	128403	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA809672	Hs.123304	ESTs	3.1
	114250	AI914699	Hs.13297	ESTs	3.1
70	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	3.1
	117997	N52090	Hs.47420	EST	3.1
	104558	R56678	Hs.88959	hypothetical protein MGC4816	3.1
	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
75	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
	127521	AW297206	Hs.164018	ESTs	3.1
	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nucleolar protein NOP5/NOP58	3.1
	105024	AA126311	Hs.9879	ESTs	3.1
80	123485	AI308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	LIM domain binding 2	3.1
	115348	AA281562	Hs.766	ESTs	3.1
	117297	AW779829		gb:hn88a05.x1 NCL_CGAP_Kid11 Homo sapien	3.1

5	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
	115188	AK000219	Hs.88367	hypothetical protein FLJ20212	3.1
	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.1
	106472	AI207162	Hs.3815	stathmin-like-protein RB3	3.0
10	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
15	112435	NM_013255	Hs.288791	muskelin 1, intracellular mediator conta	3.0
	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	3.0
	106651	AA460421	Hs.30875	ESTs	3.0
	109597	AA989362	Hs.293780	ESTs	3.0
	132342	AW162758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
20	106057	BE614474	Hs.289074	F-box only protein 22	3.0
	106378	AA824298	Hs.21331	hypothetical protein FLJ10036	3.0
	128660	AA011597	Hs.177398	ESTs	3.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	3.0
25	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	3.0
	126898	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	3.0
	133966	BE280478	Hs.182695	hypothetical protein MGC3243	3.0
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131586	AA460352	Hs.26966	KIAA1171 protein	3.0
30	100237	D30715		Human PAP (pancreatitis-associated prote	3.0
	105515	T24968	Hs.23038	HSPC071 protein	3.0
	123073	AA485061	Hs.105652	ESTs	3.0
	111375	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.0
	130724	AK001507	Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
35	129928	AI338993	Hs.134535	ESTs	3.0
	118922	AW206193		hypothetical protein DKFZp761B2423	3.0
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	3.0
	122219	AA436002	Hs.183161	ESTs	3.0
40	132195	BE018717	Hs.42124	ESTs	3.0
	102298	AA382169	Hs.54483	N-myc (and STAT) interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.0
	126997	AI377150	Hs.150914	ESTs	3.0
45	128902	AA036637	Hs.107052	ESTs	3.0
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	3.0
	106711	BE390125	Hs.143187	hypothetical protein	3.0
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	3.0
50	135029	H58818		hydroxysteroid (17-beta) dehydrogenase 7	3.0
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	3.0
	106735	R77698	Hs.337778	ESTs	3.0
	126628	N49776	Hs.170994	hypothetical protein MGC10946	3.0
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
55	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	3.0
	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	3.0
	129601	AB032964	Hs.115726	KIAA1138 protein	3.0
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	3.0
	128695	NM_003478	Hs.101299	cullin 5	3.0
60	123470	AW303285		Human DNA sequence from clone RP11-110H4	3.0
	109252	BE440157	Hs.85944	ESTs	3.0
	101445	M21259		gb:Human Alu repeats in the region 5' to	3.0
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	3.0
	116475	AA733050	Hs.334612	small nuclear ribonucleoprotein polypept	3.0
65	106573	AA223447	Hs.12835	A kinase (PRKA) anchor protein 7	3.0
	103106	W27172	Hs.1857	phosphodiesterase 6G, cGMP-specific, rod	3.0
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	3.0
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	3.0
	126887	H20832		gb:ym48d03.s1 Soares infant brain 1NIB H	3.0
70	117960	AA310417	Hs.47044	ESTs	3.0
	133626	AW836130	Hs.75277	hypothetical protein FLJ13910	3.0
	113179	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind	3.0
	109968	H09232	Hs.26484	HIRA-interacting protein 3	3.0
75	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

TABLE 71B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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5	108451	13766_27	AA079195 AA084955 AA126308 AA084956 AF087999 N29296 AI928858 AA846757 N20229 AA026894 D80634 AW388923 AW388802 AW388957 AW571771 AW388839 AI686662 AW389079 AA602099 AW134567 AW517843 AI682674 AI474874 AA374167 AA602964 AA609200 AA812434 AI831542 AA766261 AI769894 N63376 AA214392 AA135833 AW605017 AA135965 AW450072 H04812 AA446459 AW439151 AA426273 AI061423 AA558549 Z40087 AI753216 AA743075 AA854268 AA458920 AA843893 AI566516 AI864957 AI566634 AW971760 AA211796 AA430089 M21259 L07518 AW815215 AA451966 NM_016370 AB036693 AL139228 R58124 AI634847 AL119333 W07356 AI334284 H29050 AI192685 AA652438 AW172843 W19794 N21460 AI743862 AW130622 AA991348 AI204553 AA992664 N80848 AA699329 AI824676 R26624 R49653 AW779829 N22494 AI248120 AL121500 AW291763 AI732432 AA129708 AA133309 AI733750 AI225224 W45350 W45406 AW161357 AI879062 AI928938 AW161097 AW161167 BE314465 AA351715 F07096 AA179034 F08510 F00653 AI936671 AA476718 AW772454 AI807773 R44253 AA976667 AI985186 AI650254 H38942 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	123619	371681_1	
10	131495	142008_1	
	101445	1650_5	
	100944	25682_2	
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	117297	647718_1	
	108859	137143_1	
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	116790	19864_1	
25	103038	15024_1	
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	126098	1629789_1	
	125464	168460_1	
45	126127	1205826_1	
	125558	1703083_1	
	126426	110687_1	
50	118644	81501_1	
55			
60	127262	231725_1	
	127315	37938_1	
	103898	187213_3	
65	126769	119008_1	
	120147	386607_2	
	128080	1540039_1	
70	104590	44964_1	
75	126887	1572189_1	
	128132	177108_1	
	128967	169750_1	
80	120325	166688_1	
	112511	17406_2	

5	106012	96214_1	AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 AI360919 H03502 BE208298 R68588 AI350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933 AJ003322 AJ003324 AW404061 R09654 T67160 N50566 N53259 R81936 D78695 D78806 D78780 C17009 AA004406 AA122102 R70625 AA148932 H59583 H81146 H80378 H49863 H21182 H46534 H51478 H20702 H46515 H40200 H50046 H23647 H50439 H18383 H21846 H23849 H40182 R21924 H01290 H01283 H42464 W31947 W39660 AA046219 H03539 H01741 R22008 AA043911 AA156838 D78832 R36616 R66039 AI492481 AA088608 R69918 R36334 H80281 N58483 AI075154 AI086754 AA595787 H81051 H01187 AI057251 T96992 H59584 T47016 R31800 H13647 H01193 N74660 AA156601 H03455 R66040 R81937 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AA327133 AI805980 AA005377 AW611716 T86946 AA369083 R67250 H00240 R32578 W86279 R80248 R23734 H00977 R21732 R78932 AA368675 R16780 R26523 H40161 W93671 R99823 R77956 H61601 R98785 R09738 H78317 H53537 H81056 T53780 H12600 R82345 AA653499 AW953717 R63207 R33888 H54071 H66993 T48748 AI702300 R30775 H68996 AI014957 AA369082 AF075351 AI110886 AI742050 AW954245 AI768458 C19062 AI393674 C18911 C18029 AA708613 AI168432 R67389 AI168453 H00188 R21233 H03055 R53822 AA367558 R75872 W04151 AI220869 AI090290 AA368730 R94434 H81153 H70950 AA367783 H81514 H53536 C16968 C17797 C17677 C17064 AA082581 C17044 D63217 C18791 D78839 D63290 D78838 N91085 H54070 R80360 H78318 H40199 R33887 R02529 H94918 R00900 T87029 AA131924 R99891 AA004267 D78764 D78757 H61600 C18615 H60972 R98784 W86323 R09737 C17492 D78811 R67494 D78775 AA368244 H12650 D79043 AW957062 R82759 C19002 H01715 W28614 W27435 AI983043 AA364395 AW572472 AW190386 AI129278 AI913081 AW473549 AA830713 AI982871 AI638647 AI828466 AW572486 N52583 N89687 AW075567 AI571047 AI887479 AI559469 AI685802 AA805256 AI458777 AA974369 AI866929 AI886032 AI823925 AI823566 AW198135 AI287510 AI565910 AA765775 AI866019 AI263697 AI355825 R42668 AA894603 AW105585 AI824555 AW339175 D20479 NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 AW303285 AW117396 AA888929 BE174517 Z70704 AL042292 H54958 AA310063 AW499643 AW501380 AW501202 AW501293 AW501596 AW630166 AL041326 AA780690 L40517 U21556 AI093182 AW062487 AA883387 AA931302 BE252601 BE258381 AA827330 AL043930 AA356337 AW962830 AW393814 Z70703 AW389484 T62231 AW780049 AL043931 BE149744 AW963292 BE439669 BE091737 BE091657 AA484004 AI673095 AA599106 AW601545 AI538739 AI538730 AI521786 AW366369 AW021010 AA362576 AI289927 AA382592 AA608733 T74884 AA620552 U42359 N57493 H01052 AW206193 AW137594 AI953685 AI919143 AI424371 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AA205307 AW021913 AI687980 AI674198 AI675563 AI417935 AA707350 AA135157 AI434721 AI151036 AI038305 R52643 AA780141 AW207645 D19691 AI474370 AA401739 N22905 N70378 D30715 AA251089 AA598484
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Table 72A shows the Seq ID No, Pkey, ExAccn, UnigeneID, and Unigene Title for all of the sequences in Table 73.

80	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title

Seq ID No: Seq ID number correlation for those sequences in Table 73

	Pkey*	ExAccn	UnigenelID	Unigene Title	Seq ID No
5	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	Seq ID No B1 & B2
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	Seq ID No B3 & B4
	101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	Seq ID No B5 & B6
	447761	AF061573	Hs.19492	protocadherin 8	Seq ID No B7 & B8
	428183	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	Seq ID No B9 & B10
10	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	Seq ID No B11 & B12
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	Seq ID No B13, B14, & B15
	104659	AW969769	Hs.105201	ESTs	Seq ID No B16
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	Seq ID No B17 & B18
	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	Seq ID No B19 & B20
15	100299	D49493	Hs.2171	growth differentiation factor 10	Seq ID No B21 & B22
	116301	AW969706	Hs.293332	ESTs	Seq ID No B23 & B24
	106533	AL134708	Hs.145998	ESTs	Seq ID No B25-B27
	131313	R96290	Hs.75874	ribosomal protein L44	Seq ID No B28 & B29
	105316	AI671245	Hs.24835	hypothetical protein FLJ14594	Seq ID No B30 & B31
20	113003	AW292315	Hs.7215	ESTs	Seq ID No B32
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	Seq ID No B33 & B34
	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	Seq ID No B35-B40
	123308	C14187	Hs.157208	ESTs	Seq ID No B41 & B42
	120147	AI917116		hemoglobin, beta	Seq ID No B43
25	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	Seq ID No B44 & B45
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	Seq ID No B46 & B47
	105301	AW352357	Hs.7457	MAGE1 protein	Seq ID No B48 & B49
	128478	AA708205	Hs.100343	ESTs	Seq ID No B50-B53
	106111	AW875398	Hs.6451	PRO0659 protein	Seq ID No B54 & B55
30	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	Seq ID No B56 & B57
	120830	AI568170	Hs.96886	ESTs	Seq ID No B58 & B59
	127664	AA806164	Hs.116502	ESTs	Seq ID No B60
	102725	AB026187	Hs.159156	protocadherin 11	Seq ID No B61 & B62
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	Seq ID No B63 & B64
35	130637	AA356764	Hs.17109	integral membrane protein 2A	Seq ID No B65 & B66
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	Seq ID No B67 & B68
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	Seq ID No B69 & B70
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	Seq ID No B71 & B72
	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	Seq ID No B73 & B74
40	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	Seq ID No B75 & B76
	420462	AF050147	Hs.97932	chondromodulin I precursor	Seq ID No B77 & B78
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No B79 & B80
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	Seq ID No B81 & B82
	416836	D54745	Hs.80247	cholecystokinin	Seq ID No B83 & B84

Table 72B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

50	Pkey	CAT Number	Accession
	131307	3138_1	NM_000025 X72861 X70811 M29932 X70812 S53291 AW015148 AW581776 AI276134
	131313	93372_1	R96290 H02411 C18327 AA367588 AA367557 H89632 C17954 AA568860 AI752983 AA699451 H04260 AI128118 AW193364 N94503 AA029995 T40536 AA368746 AI189909 BE047384 AA747591 R22855 AI032539 AI151343 AA148534 H63941 T49595 AA694405 H74226 AI200363 R79731 AA702947 AI400076 AI088494 C17938 AA599478 H02962 R77665 C17370 R56618 H73711 R58545 D79189 AW265710 R77664 T52101 AW953745 AW953739 D79107 AA029105 AW953738 AA456487 R67000 AA156623 AA368336 H63662 AW969706 AA456258 AA491881 BE501639 D62113 AW969710 AI591236 AI379869 AW968997 AA040053 AI807206 AW663917 AA454645 AA489238 BE241958 AA743491
60	103080	17092_1	AU077231 AA852219 M74092 X59798 M64349 NM_001758 AA226806 M73554 BE409154 AA160096 BE384352 AA160820 BE382880 BE261734 AA113821 BE407745 AA156380 BE390287 BE390020 AA100854 AA127152 AW794066 AW367101 AW367093 U47703 AI347077 W05266 AI824103 AI499061 AA642944 AI042556 AA906539 W60380 AI571777 AL135581 AA112340 N75459 AA592929 AI085348 AI278890 AA126942 AI023701 AI873252 AA156319 AI190622 W60289 AI274886 R81309 AA100801 AA227161 AI568929 AA160603 AI074344 AI344561 AI150778 AA852218 AA158286 N20142 AA622148 AA864225 AA576367 AW182124 T89175 AI758455 AA780573 N71757 R81200 AI659596 AI674613 AA642544 AW503909 AA128851 W39350 N40420 AA113072 BE168116 AI620604 AI298125 BE075272 N40078 BE075109 BE080779 AI918938 BE168117 BE087369 AW995539 BE080949 BE080727 BE075271 BE075108 BE080955 BE089655 BE081115 AW750304 H66084 AI146884 BE075154 AW992247 AI186525 AI752230 AW263140 W03329 N26056 AA948080 AA113073 H99284 AA227101 AA631077 AA148042 AI740837 BE082728 AA149570 W44495 BE089351 AA375044 N26775 H27771 AA064705 BE091204 R89337 N32676 N27141 BE164704 H98049 W67603 AA425549 W31090 AA807411 BE173280 BE000178 T09020 W23852 AA062709 BE167894 AA076515 R97329 BE541980 N42086 AA102307 AA113772 BE276181 H20622 W44436 W67604 W46412 AW771113 AI700678 AA502628 AA133137 BE274186 BE396090 BE613371 BE612645 W46650 W95203 W92651 AI087288 R76299 AW604781 N55320 AI912334 AA403248 AW169156 H24970 AW298822 AW080962 AI073747 W24123 AA577596 H21715 H27925 H26436 AI288304 AA148043 AA204678 BE047090 W48631 AA908347 AA599485 AI276505 AI953979 AA563710 H25674 H51747 AA425389 AA516104 AI095335 T77237 AA151696 T92084 AI689037 AI624162 W49709 AW514883 AA100676 AI366087 AA069474 AA525859 AW771076 AA029402 AA994114 AI351505 AW770816 AI333594 AI289794 AI346589 AA487700 AI081104 AA613344 AI377520 AI284911 AI311390 AA622062 AI055890 AI660881 AI366117 AA403090 AI272818 AI073353 W46300 AA062689 AI755078 AI753397 AI633564 AI273471 AI339890 AA699584 AA983722 AI079968 AI752231 AA076431 AA113245 AI168564 AA918965 AI066484 AI123599 AI921518 W94586 AA535600 AA064665 AA705388 AA064623 AA962503 AI924926 AW131206 AW275281 AI280632 T29597 W48728 AW954336 W38317 W94768 AI084717 W46567 AI245645 AW302501 N72201 AW510563 AW079132 AA207064 AI143740 AW440672 AA632154 AI290286 AI350704 AI271377 AA025369 AI864756 T77451 H97348 AA852165 AI932951 N98526 AA487486 R92970 AA934071 AI080448 AA063257 C05786 N99099 R42969 AA887065 AA662686 AA533833 AA662304 H51748 BE539444 AI382164 AI814595 BE537043 AI168307 BE408935 AA453606 R89428 AA936527 AA936890 AW369618 AW246002 R18074 AI474189 AW372354 AI094358 R37210 AA948510 AA226909 BE172527 AI086652 BE408324 AW292848 AI768962 BE540703 BE409478 AA931692

5	132520	45737_1	AA257992 AA317029 AA362097 D17042 H48100 AW838107 AW838106 AW838110 AW838231 AW610241 AW838442 AA045061 AW384991 BE000988 AA131806 BE180577 AW838269 AL039831 AI754380 C06051 AA131737 AW838239 AI767465 AI480134 AA610312 AW838190 AA379252 AW838282 AA484027 AI423413 AI685064 BE328307 AI241857 AW838281 AW838284 AI671267 AI814928 AA828367 AI476306 AI270180 AA622362 AI076497 AI635919 AI444994 AI194028 AI669159 AI928131 AA448853 AI350143 AW079289 AW467807 AA480442 AA522935 BE180570 AW380087 AW380109 AI081015 AI690818 AI589485 AI698510 AA642019 AA714366 AI580435 AA985527 AI740475 C21398 AA257993 AI302393 AI689018 AW770194 AW753750 AI079164 BE550338 AA559851 T16108 AI864822 AI932827 AA045095 AA045062 AI954225 AA768569 AA709308 AW958363
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	125770	16581_2	AI457891 AW468784 AI567693 AW884460 AI424892 AA401298 AW244098 AI122936 N24824 AA552932 AA873164 AI308810 N26098 H81852
35	120147	386607_2	N20798 AW263947 AI696267 AA494222 AW877967
	113003	420161_1	AI917116 AA633698 AI580389 Z39483
	104659	82594_1	AW292315 AI090408 AW517041 AI928695 AI092060 AA716741 N98235 T23629
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			AA702310 AA748431 AA749352 C01127 AI003679 T96352
			AW352357 AA852419 T80568 AA332510 AW149659 AA341609 AA809550 AI183690 AA730875 T31719 AW965361 AA779709 T05461
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			AW136277 AA852418 AA240305 T03902 C15551 D52660 H08108 AA844525 AI420648 AI282445 AW068986 AW497637 AA779042 AA298564
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	105782	246361_1	H09748 R61554 AA350215 R40551
	120830	244476_1	AI568170 AA731212 AW294848 AW466878 AA568908 AI281804 AI923633 AA347885 AI718854 AA714940
	128797	20410_1	NM_002975 AF020044 AB009244 BE620464 AA541683 AW000991 AW089850 AW664612 AI636676 AI627854 AI885823 AI864548 AI554122
55			AI499682 AI570905 AI376008 AI871364 AI074230 AI383719 AA905016 AA977446 AA844732 T78922 AW244007 AI924747 AI968230 AI824575
			AI699224 AI569490 AW379856 AW292314 AI016874 AW292037
	106533	305354_1	AL134708 AW206610 AW665919 AW594227 AI917093 AI498361 AA635141 AA453786 D54178 D53224 AI804341 D53111 M78885 AL134707
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	123049	30801_1	BE047680 AF177395 NM_014421 AB033208 AB035181 W55979 AI093106 AI863392 AA715452 AA300480 AW022313 AA648103 AA720544
			D61856 AA481794 AA737112 AW316551 AA714937 AW974378 AI370632 AI184289 AI333962 AA714945
	129703	64196_1	BE388665 AA740614 AI394542 AA484451 AW070675 AA877654 AI360981 AI475799 BE349560 AI037351 N29437 AI246453 AW083444
65			AA844441 AI150871 AI440477 AI889061 AA682422 AA680053 AA740212 AI858728 AA490589 AW243692 AI249450 AI304448 AA534421
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			AA630752 AA115450 NA9944 AW166071 AW769795 AA991877 AA873609 AW083441 H99130 AA910538 AA486199 AW083358 AA151767
70			AI161193 N54945 AA180193 AI423477 AI188387 AI608747 N58900 AI038449 AA136852 AA565913 AA180502 H61741 AA701125 AI127678
			AI278541 R76523 AA666187 H85083 F24755 R77729 AA135137 BE250395 R76239 AW794625 AW794044 H61957 AA308197 AW996031
			AA345524 N52726 AA354360 AA179785 N57375 R16447 AA160645 W21481
	100299	2801_1	D49493 NM_004962 D49492 AA948479 AA993843 AD017558 AA992567 AA912897 AI185363 AA018254 N93253 AA297544 T19187 R53287
			AA069337 AA297489 N62906 AW023929 AA018253 AA017615 W25110 R52085 R52633 W16549 H88916 H89134 AA069338
75	129977	2039_1	NM_000399 AA018140 AF139463 J04076 AW390694 AW361756 AL079830 AI190587 AA731059 AA742743 AI635915 AA878209 AI262612
			AI264201 AA446300 AA715016 AA446027 AI274101 AA593330 AA593338 AW015388 AI681724 AI347984 AL045275 AA970069 AA018188
			AW014396 AW769445 AI588869 AW338296 AI801548 AI367702 AI888410
	123308	322009_1	C14187 AA496211 D80456 AA484051 D80455 AA528446
	101104	26442_2	AW862258 L07615
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			AA169869 AA285240 AA356670 T93146 AA325779 AA357064 AA328151 AA306939 AA306801 N31260 AA306202 AA312530 BE242703
			AA354371 N22599 AL021786 H50965 H38038 AI655965 AI566732 AI953952 AW972835 AI077300 AI948482 AI760966 AA648335 W72197
			N32815 AA768073 AW338181 AW001742 AI819896 AI015666 N58011 AA677584 AI183750 AW105514 W37875 AW301679 AA775257

			AA730357 AI128690 AA630149 AW241515 AI147003 AI183499 N90923 AI968582 AA354145 AI147297 BE550502 AI085777 AI709087 AA773947 AA469192 AI199289 AI127085 H89232 N30719 AI028165 AW029469 AI709314 AA780834 AA778057 H89125 AI654762 T93061 N59622 AI360625 AA719982 AI248242 AA233925 AW262512 AW438666 AA010378 AA484010 AW438790 N22875 AA483718 AI185407 AA736720 AA664587 AA648672 AA503406 AA508123 AA503140 H46638 N75812 AA730938 D60546 AA483039 AA507705 AA480448 AI768654 AA658955 AA730803 AA330312 AW021127 BE172031 AW961052 AA339070 AA648172 BE172892 AA174175 AA492012 AA491590 AW118733 AA484130 AA730783 AA730510 D62577 D62828 AI469294 AI801343 N53447 AA740226 AI831983 AA516146 D79799 AI758212 AA484040 H38039 AI038772 AI039410 AA528387 AA730576 AA527231 AA748111 D62946 U38439 AA721708 H22130 AA559229 H51620 AA283355 AA730970 R01595 N72450 AA469123 AA579389 AA480477 AA283306 AA347822 AA328013 AW248508 AI278454 AI369343 AW291235 AI343946 AI347189 AA970152 AI279668 AI971894 AA664359 AI191039 AA084598 AA081641 AA316181 BE439545 AC005053 AF186249 AW386101 AC004969 AA730199 AA032221 AI686139 AI167942 AA809228 AI184070 AI394674 AW969977 AA032279 AW079284 AA513174 AA888312 AI453179 AA483363 AA528432 AA579511 AU077228 U61145 AL044256 AA206185 AL044975 NM_004456 X95653 AW890905 AA332806 AW965453 BE299226 U52965 BE275009 AA428252 AA769212 AA312778 AA810901 AA461315 AI969286 AI953668 AW296248 AI291422 AA704747 Z44716 BE541235 AW608806 AA588583 AW403788 AW408386 AA053521 T87571 AA581163 BE183241 T97906 R89149 AI808196 BE618521 AI970278 AI652680 AW130143 AI970272 AW197254 BE550449 AI628403 AA010143 AW005107 AA251815 AA805836 N53459 AA055309 AA643678 AI345616 AI345618 AI635728 AI871286 AI018437 AI262514 H75287 AI033155 AI203388 AA205802 AI475265 AW594186 AI696059 AI333312 AW264710 AA876764 AA864892 AA173156 AI292066 T79837 W93995 AA506427 AA815135 AI376342 AA010144 AI310421 AI223350 AA970576 N33926 T89364 AI090913 N55098 AA101673 AA626665 AA251840 N68857 AI890053 H05930 AI474199 AI436166 AA628810 N64452 AI205538 AA055310 BE244495 AI365179 T99536 AI203088 Z40549 AW139858 AA599627 R91847 AA483681 AW068982 H51746 AA091201 H13030 AA459732 T99430 AI051764 R45991 D54745 AU077189 NM_000729 R71188 H87563 R80701 AW956319 AA376289 R82442 H46452 R22481 R64323 AW043690 L00354 AW005571 H19813 AI745597 AI769202 AI205982 AW205841 R64324 AI201975 H46993 C18067 R71189 N29729 AI799838 AI091209 H87455 R82443 AW970995 AW072136 N40841 H13148 AI219052 N30191 T28007 AI817428 AA503602 AF050147 NM_007015 AB006000 AB005999 BE218114 AI703147 AI985891 BE222034 BE549774 BE327618 AI651459 BE549987 AI657194 BE222414 BE046984 AW470357 AW339338 C02526 AW590220 AI298082 AW296998 AI333135 AI867816 AA730514 BE348513 AA405500 AW136179 AA327834 BE327350 BE327366 AW969726 AA424028 AI266636 AI271571 AA423988 AI266634 AA702780 AA452037 AI424866 AA742931 AA483361 AA737106 N35765 N35779 AF086045 N30152 AW374028 AI478237 AA923562 AI382236 AA846668 AI627389 AI371709 H98083 H95983 H26576 H95994 AA745021 AA639180 H26575 AF061573 NM_002590 AA780138 AW135620 AI197884 AA483348 R05468 AW969724 H29216
5			
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	410268	11897_1	
	414761	14860_1	
15			
20	416836	16233_1	
25	420462	19379_1	
	428183	287965_1	
	439221	46993_1	
30	447761	7355_1	

Table 73: Sequences

Seq ID NO: B1 DNA sequence
Nucleic Acid Accession #: NM_053056.1
Coding sequence: 210..1097

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	AGGGAGCGCG	GGGAGCAGCA	AGCGAGAGCC	GAGCGCGGAC	CCAGCCAGGA	CCCAGAGCCC	180
	TCCCCAGCTG	CCCAGGAAGA	GCCCCAGCCA	TGGAACACCA	GCTCCTGTGC	TGCGAAGTGG	240
	AAACCATCCG	CCGCGCGTAC	CCCGATGCCA	ACCTCCTCAA	CGACCGGGTG	CTGCGGGCCA	300
	TGCTGAAGGC	GGAGGAGACC	TGCGCGCCCT	CGGTGTCTTA	CTTCAAATGT	GTGCAGAAGG	360
15	AGGTCTCTGC	GTCCATGCCG	AAGATCGTCG	CCACCTGGAT	GCTGGAGGTC	TGCGAGGAAC	420
	AGAAAGTCCG	GGAGGAGGTC	TTCCCGCTGG	CCATGAACCTA	CCTGGACCGC	TTCTGTGCGC	480
	TGGAGCCCCG	GAAAAAGAGC	CGCCTGCAGC	TGCTGGGGGC	CACCTGCAATG	TTCTGTGGCT	540
	CTAAGATGAA	GGAGACCATC	CCCCTGACGG	CCGAGAAGCT	GTGCATCTAC	ACCGACAACCT	600
	CCATCCGGCC	CGAGGAGCTG	CTGCAAAATG	AGCTGCTCCT	GGTGAACAA	CTCAAGTGGG	660
20	ACCTGGCCCG	AATGACCCCG	CACGATTTCA	TTGAACACTT	CCTCTCCAAA	ATGCCAGAGG	720
	CGGAGGAGAA	CAAAAGATC	ATCCGCAAA	ACGCGCAGAC	CTTCGTGTC	CTCTGTGCCA	780
	CAGATGTGAA	GTTCAATTTCC	AATCCGCCCT	CCATGGTGGC	AGCGGGGAGC	GTGGTGGCCG	840
	CAGTGCACAG	CCTGAACCTG	AGGAGCCCCA	ACAACTTCCT	GTCCCTACTAC	CGCCTCACAC	900
	GCTTCCTCTC	CAGAGTGATC	AAGTGTGACC	CAGACTGCCT	CCGGGCGCTG	CAGGAGCAGA	960
25	TCGAAGCCCT	GCTGAGATCA	AGCCTGCGCC	AGGCCACGCA	GAACATGGAC	CCCAAGGCCG	1020
	CCGAGGAGGA	GGAAGAGGAG	GAGGAGGAGG	TGGACCTGGC	TTGCACACCC	ACCGACGTGC	1080
	GGGACGTGGA	CATCTGAGGG	GCCAGGCGAG	GCGGGCGCCA	CCGCCACCCG	CAGCGAGGGC	1140
	GGAGCCGGCC	CCAGGTGCTC	CCCTGACAGT	CCCTCCTCTC	CGGAGCATTT	TGATACCAGA	1200
	AGGGAAGGCT	TCATTCTCCT	TGTTGTGGT	TGTTTTTCTC	TTTGCTCTTT	CCCCCTTCCA	1260
30	TCTCTGACTT	AAGCAAAAGA	AAAAGATTAC	CCAAAACTG	TCTTTAAAG	AGAGAGAGAG	1320
	AAAAAAGGAT	TTTATACCCC	AATAATCAAC	TCGTTTTTAT	ATTAATGTAC	TTGTTTCTCT	1380
	GTTGTAAGAA	TAGGCATTAA	CACAAAGGAG	GCGTCTCGGG	AGAGGATTAG	GTTCATCCTT	1440
	TTACGTGTTT	AAAAAAGAGC	ATAAAACAT	TTTAAAAACA	TAGAAAAATT	CAGCAAAACCA	1500
35	TTTTTAAAGT	AGAAGAGGGT	TTTAGGTAGA	AAAAATATTT	CTTGCTCTTT	TCTGTATAAA	1560
	GCACAGCTGT	AGTGGGCTTC	TAGGCATCTC	TGTAATTTGC	TTGCTCATAT	GCATGTAGTC	1620
	ACTTTATAAG	TCATTGTATG	TTATTATATT	CCGTAGGTAG	ATGTGTAACC	TCTTCACTCT	1680
	ATTTCATGGC	GAAATCACTT	CTTGGTTACA	GTAGCGTAGC	GTGGCCGTGT	GCATGTCTCT	1740
	TGCGCCTGTG	ACCACCAACC	CAACAAACCA	TCCAGTGACA	AACCATCCAG	TGGAGGTTTG	1800
40	TCGGGCACCA	GCCAGCGTAG	CAGGGTCGGG	AAAGGCCACC	TGTCCCACTC	CTACGATACG	1860
	CTACTATAAA	GAGAAGACGA	AATAGTGACA	TAATATATTC	TATTTTTATA	CTCTTCTAT	1920
	TTTTGTAGTG	ACCTGTTTAT	GAGATGCTGG	TTTTCTACCC	AACGGCCCTG	CAGCCAGCTC	1980
	ACGTCCAGGT	TCAACCCACA	GCTACTTGGT	TTGTGTTCTT	CTTCATATTC	TAAACCATT	2040
	CCATTTCCAA	GCACCTTCAG	TCCAAATAGT	GTAGGAAATA	CGCGTGTTTT	TGTTGTGTGT	2100
45	GCAGGGAGGG	CAGTTTCTCA	ATGGAATGGT	TTGGGAATAT	CCATGTACTT	GTTTGCAGGC	2160
	AGGACTTTGA	GCGAAGTGTG	GGCCACTGTG	GTGGCAGTGG	AGGTGGGGTG	TTTGGGAGGC	2220
	TGCGTGCCAG	TCAAGAAGAA	AAAGGTTTGC	ATTCTCACAT	TGCCAGGATG	ATAAGTTCCT	2280
	TTCTTTTCTT	TTAAAGAAAT	TGAAGTTTAG	GAATCCTTTG	GTGCCAACTG	GTGTTTGAAA	2340
	GTAGGGACCT	CAGAGGTTTA	CCTAGAGAAC	AGGTGGTTTT	TAAGGGTTAT	CTTAGATGTT	2400
50	TCACACCCGA	AGGTTTTTAA	ACACTAAAT	ATATAATTTA	TAGTTAAGGC	TAAAAAGTAT	2460
	ATTTATTGCA	GAGGATGTTT	ATAAGGCCAG	TATGATTTAT	AAATGCAATC	TCCCCTTGAT	2520
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	TACAGATTTA	ATAAGTTTAA	TTTTTAAAGA	TAGATCCTTT	TATAGGTGAG	AAAAAACAAC	2640
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55	ATCTGATTGG	ACAGGCATGG	GTGCAAGGAA	AATTAGGGTA	CTCAACCTAA	GTTGCGTTCC	2760
	GATGAATTCG	TATCCCCTGC	CCCTTCTCTT	AAAAAATTTA	GTGACAAAAT	AGACAATTTG	2820
	CACATCTTGG	CTATGTAAAT	CTTGTAAATT	TTATTAGGA	AGTGTGAAAG	GGAGGTGGCA	2880
	AGAGTGTGGA	GGCTGACGTG	TGAGGGAGGA	CAGGCGGGAG	GAGGTGTGAG	GAGGAGGCTC	2940
	CCGAGGGGAA	GGGCGCGTGC	CCACCCGGG	GACAGGCCGC	AGCTCCATTT	TCTTATTGCG	3000
60	CTGCTACCGT	TGACTTCCAG	GCACGGTTTG	GAAATATTCA	CATCGCTTCT	GTGTATCTCT	3060
	TTACATTTGT	TTGCTGCTAT	TGGAGGATCA	GTTTTTTGTT	TTACAATGTC	ATATACTGCC	3120
	ATGTACTAGT	TTTAGTTTTC	TCTTAGAACA	TGTATTACA	GATGCCTTTT	TTGTAGTTTT	3180
	TTTTTTTTTT	ATGTGATCAA	TTTTGACTTA	ATGTGATTAC	TGCTCTATTC	CAAAAAGGTT	3240
	GCTGTTTCAC	AATACCTCAT	GCTTCACTTA	GCCATGGTGG	ACCCAGCGGG	CAGGTTCTGC	3300
65	CTGCTTTGGC	GGGCAGACAC	GCGGGCGCGA	TCCCACACAG	GCTGGCGGGG	GCCGGCCCCG	3360
	AGGCGCGCTG	CGTGAGAAC	GCGCGCGTGT	CCCCAGAGAC	CAGGCGTGTG	CCCTCTTCTC	3420
	TTCCCTGCGC	CTGTGATGCT	GGGCACTTCA	TCTGATCGGG	GGCGTAGCAT	CATAGTAGTT	3480
	TTTACAGCTG	TGTTATTCTT	TGCGTGTAGC	TATGGAAGTT	GCATAATTAT	TATTATTATT	3540
	ATTATAACAA	GTGTGCTCTA	CGTGCCACCA	CGGCGTTGTA	CCTGTAGGAC	TCTCATTGCG	3600
70	GATGATTGGA	ATAGCTTCTG	GAATTTGTTT	AAGTTTGGG	TATGTTTAAT	CTGTTATGTA	3660
	CTAGTGTCTT	GTTTGTATT	GTTTGTGTTA	TTACACCATA	ATGCTAATTT	AAAGAGACTC	3720
	CAAATCTCAA	TGAAGCCAGC	TCACAGTGCT	GTGTGCCCGG	GTCACCTAGC	AAGCTGCCGA	3780
	ACCAAAGAA	TTTGACACCC	GCTGCGGGCC	CACGTGGTTG	GGGCCCCGCC	CTGGCAGGGT	3840
	CATCTGTGAG	TCGGAGGCCA	TCTCGGGCAC	AGGCCACACC	CGCCCCACCC	CTCCAGAACCT	3900
75	CGGCTCACGC	TTACCTCAAC	CATCTGGCT	GCGGCGTCTG	TCTGAACAC	GCGGGGGCCT	3960
	TGAGGGACGC	TTTGTCTGTC	GTGATGGGGC	AAGGGCACAA	GTCCTGGATG	TTGTGTGTAT	4020
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	CAAGTCTGAG	GGTCTGGGCG	GCGGGCGGCT	GGGTCTGTGC	ATTTCTGGTT	GCACCGCGGC	4140
	GCTTCCACGC	ACCAACATGT	AACCGCATG	TTTCCAGCAG	AAGACAAAAA	GACAAACATG	4200
80	AAAGTCTAGA	AATAAACTG	GTAAACCC	AAAAA	AAAAA		4260

Seq ID NO: B2 Protein sequence
Protein Accession #: NP_444284.1

1 11 21 31 41 51
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MEHOLLCEVE ETIRRAYPDA NLLNDRVLRA MLKAEETCAP SVSYFKCVQK EVLPSMRKIV 60
 ATWMLEVCEE QKCEEEVFPL AMNYLDRFLS LEPVKKSRLQ LLGATCMFVA SKMKETIPLT 120
 AEKLCIYTDN SIRPEELLQM ELLLVNKLKW NLAAAMTPHDF IEHFLSKMPE AEENKQIIRK 180
 HAQTFVALCA TDVKFISNPP SMVAAGSVVA AVQGLNLRSP NNFLSYRLT RFLSRVIKCD 240
 PDCLRACQEQ IEALLESSLR QAQQNMDPKA AEEEEEEEE VDLACTPTDV RDVDI

Seq ID NO: B3 DNA sequence
 Nucleic Acid Accession #: XM_044166
 Coding sequence: 1..1576

1 11 21 31 41 51
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 CGCCCTTCAG CTGGCTCTCG ATCAACTCTG CCTCCTGGGT TTGGGGGAGC CCCCCGCCCC 180
 CAGGGCGGCG GAGGACGGGG GAGGTGGGGG GGGCGGCGCC CCGCGCGAGC CGACAGCCCC 240
 CCGCGAGCGG GCGCGCGCGC GCGCGCCCGC GCGCGCCCGC GCGCGCCCGA CGACGGCCCC 300
 CGCAGCGCAG ACGCCCCAGC CCCCCACCGC CCCCAGAGGG GCGAGCGAGC CCAAGCTCTG 360
 CGCTCTCTAC AAAGAGGGCG AGCTGCGCCT GAAGGGCAGC AGCAACACCA CGGAGTGTGT 420
 TCCGTGCCCC ACCTCGAGC ACGTGGCCGA GATCGTGGGC AGGCAAGGCT GCAAGATTAA 480
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 GTTCATGGTG ACAGGGCGAG GGGAGGACGT GGCCACAGCC GCGCGGAAA TCATCTCAGC 600
 AGCGGAGCAC TTCTCCATGA TCCGTGCTTC CCGCAACAAG TCAGGCGCCG CCTTTGGTGT 660
 GGCTCCTGCT CTGCGCGGCC AGGTGACCAT CCGTGTGCGG GTGCGCTACC GCGTGGTGGG 720
 GCTGGTGGTG GCGCCCAAAG GGGCAACCAT CAAGCGCATC CAGCAGCAAA CCAACACATA 780
 CATTATCACA CCAAGCCGTG ACCGCGACCC CGTGTTCGAG ATCAGCGGTG CCCCAGGCAA 840
 CGTGAGCGCT GCGCGGAGG AGATCGAGAC GCACATCGCG GTGCGCACTG GCAAGATCCT 900
 CGAGTACAA AATGAAAACG ACTTCCTGGC GGGGAGCCCC GACGACGAAA TCGATAGCGG 960
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 GAACAGCCTG GGCTGCATCG GCGAGTTCGG AGTGGACTCT GGCTTTAGAG CCCCACGCGT 1080
 GGGTGAAGCAG GCGCGGGGACT TTGGCTACGG CCGGTACCTC TTTCCGGGCT ATGGCGTGGG 1140
 CAAGCAGGAT GTGTACTACG GCGTGGCCGA GACTAGCCCC CCGCTGTGGG CGGGCCAGGA 1200
 GAACGCCACG CTCGCTGGGG AAGGGGGGAG GGAGGCACTG GTGGCTGGAG GGTGCGCCAC 1260
 CAAGGCCCGC GCTGGGCCCC CCGGCGCACA CCGCTCCCTC GCCACTTCGG CGGGACCCGA 1320
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 TGGGGGCGCG CTGCGGAGCC CCGGCGGCGG GCGGGATTGC ATGGTCTGCT TTGAGAGCGA 1440
 AGTGACTGCC GCCCTTGTGC CCGTGGGACA CAACCTGTTC TGCATGGAGT GTGCAGTACG 1500
 CATCTGCGAG AGGACGGACC CAGAGTGTCC CGTCTGCCAC ATCAGAGCCA CGCAAGCCAT 1560
 CCGAATATTC TCCTAAGCCC CGTGCCCAT GCCTCCGGGG CCGACTCCAC TGGGCCCAAC 1620
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 GAGATACTCG CTCGCTGGGG AAGGGGGGAG GGAGGCACTG GTGGCTGGAG GGTGCGCCAC 1740
 TTTCAAGACC TCTGGTCACC CTGTCTTGA AAGATTGGA GGGGGCCAGA CTGAAAATTT 1800
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 GCTGTGTGTC ACTCCACCCC TTCTTCCGAG GAGGGGGTGG GTAAAAGGGA GAGGGAGAA 1980
 TACCACCTGT ATCTAGAGGT GCTCTTGA ATCCCTAAGC CCTCTGGTCC TGACCTCCGA 2040
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 CTACCAGCCC AGCTTTGGGG ACACCATCCT TCTGGGGAGA AGTAGGGGGA GGAATATTG 2160
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 TAGTTCTTGG GCTGGATTTC CTGGTTTGGG AAGTGGGGGC GCCAGAGTAG TGTGTCTGCT 2400
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 CTTCACCCCC CTGTGCTGCT TCCCTCTGTC TCATTGTTGGG CTGCCACAG CTCTCCACCC 2760
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 GGAAGGAGGT CACAGCCAAG AAACTGCCCC TGTGACGACT TCCCTCTCTC CCGCTATGT 3060
 GAGCCATCCT GAGATGTCTG TACAATAGAA ACCAAACCAA ATGGGCACCC TCGGTTGCCG 3120
 GGGGGCAGGT GGGGAGGGGG GTGGGAAGAA GGGATGTCTG TCTGTCGTCC CCTTCCCCCT 3180
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 AAAATAGAG AGAGAAAGAG AGCATGAGAG GGAGCGAGC AGGCGACCAA CACAGAGGAG 3360
 AGAAAACAAA AATAGCAAAA AAAAAAATAA AAAGCAGTTC TTTATAATT AATATTCTAT 3420
 TTTAATAAAG GCGTTTATTA CCATATAAAT GTAGCAAGA ACCTGGGCTA ATATGAA

Seq ID NO: B4 Protein sequence
 Protein Accession #: XP_044166.2

1 11 21 31 41 51
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 ALYKEAELRL GSSNTTECV PVPTSEHVAE IVGRQCKIK ALRAKTNTYI KTFVRGEEPV 180
 FMVTGRREKV ATARREISA AEHFSMIRAS RNKSGAAGV APALFGQVTI RVRVPRVVG 240
 LVVGPKGATI KRIQQQNTNY IITPSRDRDP VFEITGAPGN VERAREEIEI HIAVRTGKIL 300
 EYNNENDFLA GSPDAIDSR YSDAWRVHQP GCKPLSTFRQ NSLGCIGECG VDSGFAPRL 360
 GEQGGDFGYG GYLFPYGVQ KQDVVYGVAE TSPPLWAGQE NATPTSVLFS SASSSSSSSA 420

KARAGPPGAH RSPATSAGPE LAGLPRRPPG EPLQGFSLKG GGGLRSPGGG RDCMVCFESE 480
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Seq ID NO: B5 DNA sequence
Nucleic Acid Accession #: NM_000909.1
Coding sequence: 209..1363

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    AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTTGTCTAAA 180
    ATAATCTATA ACAACCAAAC CAATCAAAAT GAATTCACAA TTATTTTCCC AGGTTGAAAA 240
    TCATTTCAGT CACTCTAATT TCTCAGAGAA GAATGCCCCAG CTTCTGGCTT TTGAAAATGA 300
15  TGATTGTCTC CTGCCCTTGG CCATGATATT TACCTTAGCT TTGCCTTATG GAGCTGTGAT 360
    CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATATC ATCTTGAAAC AAAAGGAGAT 420
    GAGAAATGTT ACCAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTTGCCAT 480
    CATGTGTCTC CCCTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC 540
    GATGTGTAAG TTGAATCCTT TTGTGCAATG TGTTTCAATC ACTGTGTCCA TTTTCTCTCT 600
20  GGTTCCTATT GCTGTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGCT GGAGACCAAA 660
    TAATAGACAT GCTTATGTAG GTATTGTGCT GATTGGGGTC CTTGCTGTGG CTTCTTCTTT 720
    GCCTTTCCTG ATCTACCAAG TAATGACTGA TGAGCCGCTC CAAAATGTAA CACTTGATGC 780
    GTACAAAGAC AAATACGTGT GCTTTGATCA ATTTCCATCG GACTCTCATA GGTGTCTTAA 840
    TACCACTCTC CTCTTGGTGC TGCAGTATTT TGGTCCACTT TGTTTATAT TATTTTGCTA 900
25  CTTCAAGATA TATATACGCC TAAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA 960
    TAAGTACAGG TCCAGTGAAG CCAAAGAAGT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020
    ATTTGCACTC TGCTGGCTCC CTCTTACCAT CTTTAACTAT GTGTTTGATT GGAATCATCA 1080
    GATCATTTGT ACCTGCAAC ACAAATCTGT ATTCTGTCT TGCCACCTCA CAGCAATGAT 1140
    ATCCACTTGT GTCAACCCCA TATTTTATGG GTTCCTGAAC AAAAAGTCTC AGAGAGACTT 1200
30  GCAGTTCTTC TTCAACTTTT GTGATTTCCG GTCTCGGGAT GATGATTATG AAACAATAGC 1260
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    ATTTAAAAAA ATCAACAACA ATGATGATAA TGAAAAAATC TGAAACTACT TATAGCCTAT 1380
    GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT 1440
    TCTCCCAAGG AATGGGGTTG AAATCATTTG AAAATGACTA AGATTTTCTT GTCTTGCTTT 1500
35  TTACTGCTTT TGTGTAGTT GTCCATAATTA CATTTGGAAC AAAAGGTGTG GGTCTTGGGG 1560
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    TTAGATTAGA TTAGATTCTG AACGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800
40  TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860
    GAAGTCATTC AGAAGTGGTT TGAGGTTTCT GTTTTTTGGT GGTTTTTGTT TGTTTTTTTT 1920
    TTTTTTCACC TTAAGGGAGG CTTTCATTTC CTCCGACTG ATGTGCACTT AAATCAAAAT 1980
    TTAAAAATGA ATAAAAAGAC ATACTTCTCA GCTGCAAAATA TTATGGAGAA TTGGGCACCC 2040
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45  AGAGCATTTT AGAGTAAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT 2160
    TATATTTATT TGAATTGATG GTCAGAGAT TTTCCATTTT TTTTACAGAC TGTTCAGTGT 2220
    TTGTCAAGCT TCTGCTCTAA TATGTACTCG AAAGACTTTC CGCTTACAAT TTGTAGAAAC 2280
    ACAAAATATG TTTTCCATAC AGCAGTGCTT ATATAGTGAC TGATTTTAAAC TTTCAATGTC 2340
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50  AGGGAAAAAT ACACAAAAAC TGCAGATACT TCATATAGCC CATTTTAACT TGTATAAACT 2460
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    GTTAATGTGC CTAATTTTCA GTATCTTGTA ATCATGATTG AGCCTCAGAA TCATTGGAG 2580
    AAACATATAT TAAAGAGACA AGACATACTT CAATGTATTA TACAGATAAA GTATTACATG 2640
    TGTTTGATTT TAAAGGGGCG GACATTTTAT TAAATCAAT ATTGTTTTTG CTTTTTCTGA 2700
55  GGAGTCTCTT TCAGTTTCTT TTTTCTCAT CCCATGACTT CCCTCCGATG GT

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Seq ID NO: B6 Protein sequence
Protein Accession #: NP_000900.1

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    CVSITVSIFS LVLIIVERHQ LIINPRGWRP NNRHAYVGIA VIWVLAVASS LPFLIYQVMT 180
65  DEPFQNVITLD AYKDKYVCFD QFPSDSHRLS YTTLLLVLYQ FGPLCFIFIC YFKIYIRLKR 240
    RNNMMDKMRD NKYRSSETR INIMLLSIVV AFVWCWLPIT IFNTVFDWNH QIIATCNHNL 300
    LFLLLCHLTAM ISTCVNPIFY GFLNKNFQRD LQFFNFCD FRSRDDDYETI AMSTMHTDVS 360
    KTSLKQASPV AFKKINNNDD NEKI

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Seq ID NO: B7 DNA sequence
Nucleic Acid Accession #: NM_002590.2
Coding sequence: 204..3416

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    TTCCGAGAGC CTGAGACTGA CGCCCGACCT GGAAACAGAG GAAGACTTCC TTAGCCTTTC 180
    GGATCGCACT TGAGGCTGGA GGCATGAGTC CTGTGAGGCG TTGGGGCAGC CCCTGCCTTT 240
    TCCCCTTGCA GCTCTTCAGC CTCTGCTGGG TGCTCTCAGT GGCCCAAGAG AAAACAGTCC 300
80  GATACAGCAC CTTCAGGAGG GATGCCCCCG GCACGGTCAT CGGGACCTTG GCCGAGGACC 360
    TGATATGAA AGTATCGGGT GACACAAGCT TCCGCTGAT GAAGCAATTC AACAGCTCTC 420
    TGCTCCGGGT GCGCAAGGC GACGGGCAGC TGACCGTCCG GGACGCCGCG CTGACCGCG 480
    AGCGGCTGTG TGGCCAGGCC CCGCAGTGCG TGCTGGCTTT CGATGTGGTC AGCTTCTCGC 540

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AGGAGCAGTT CCGGCTGGTG CACGTGGAGG TAGAGGTGAG GGACGTCAAC GACCACGCGC 600
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 CCGACGAGGG ACCTAACGGC GACGTGGTGT TCGCATTGG CGCCCGCACC CGCCCGGAGG 1080
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 ACTACGAGCG TCAGGACACC TACGAGCTGG ACGTGGCGGC GCAGGACCGC GGACCCGGGC 1200
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Seq ID NO: B8 Protein sequence
 Protein Accession #: NP_002581.2

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75
80

1 11 21 31 41 51
 MSPVRRWGSP CLFPLQLFSL CWVLSVAQSK TVRYSTFEED APGTVIGTLA EDLHMKVSGD 60
 TSFRLMKQFN SSLLRVREGD QQLTVGDAGL DRERLCGQAP QCVLAFDVVS FSQEQFRLVH 120
 VEVEVRDVND HAPREFPRAQI PVEVSEGA AV GTRIPLEVPV DEDVGANGLQ TVRLAEPHSP 180
 FRVELQTRAD GAQCADLVLL QELDRESQAA YSLELVADQG GRPPRSATAA LSVRVLDAND 240
 HSPAPFPQGA AEVELAEDAP VGSLLLDLDA ADPDEGPNGD VVFAFGARTP PEARRLFRLD 300
 PRSGRLTLAG PVDYERQDTY ELDVRAQDRG PGPRAACTKV IVRIRDVNDN APDIAITPLA 360
 APGAPATSPF AAAAAAALG GADASSPAGA GTPEAGATSL VPEGAARESL VALVSTSDRD 420
 SGANGQVRCA LYGHEHFRLO PAYAGSYLVV TAASLDREI AEYNLTVAE DRGAPFLRTV 480
 RPYTVRVGDE NDNAPLFTFP VYEVSVRENN PPGAYLATVA ARDRDLGRNG QVTYRLLAE 540
 VGRAGGAVST YVSVDPATGA IYALRSFDYE TLRQLDVRIQ ASDGSGPQLS SSALVQVRVL 600
 DONDHAPVLV HPAPANGSL E VAVPGRTAKD TVVARVQARD ADEGANGELA FELOQQEPRE 660
 APAIGRRITGE ILLTGDSLQE PPGRVFRALL VISDGRPPL TTTATVSVFV TAGGGRGPAA 720
 PASAGSPERS RPPGSRGLVS GSVLQWDTPL IVIIVLAGSC TLLLAIIAI ATTNRKKKE 780
 VRKGALREE RPGAAGGAS APGSPPEEAR GAGPRPNMFD VLTFFGTGKA PFGSPAADAP 840
 PPAVAAAEVP GSEGGSATGE SACHFEGQOR LRGAHAEPYG ASPFGKEPA PPVAVWKHGS 900
 FNTISGREAE KFSKDSKSGK DSDFNDSDD ISGDALKKDL INHMQSGLWA CTAECKILGH 960
 SDRCWSPSCS GPNAPHPSPHP PAQMSTFCKS TSLPRDPLRR DNYQAQLPK TVGLQSVYEK 1020
 VLHRDYDRTV TLLSPRPFRGR LPDLQIEGVP LYQSPFGRYL SPKKGANENV

Seq ID NO: B9 DNA sequence
Nucleic Acid Accession #: AL121939.12
Coding sequence: 185..1426

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5      1      11      21      31      41      51
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GCTCAGGCTG GCTGAGAGGC TCCCAGCTGC AGCGTCCCCG CCCGCCCTCT CGGGAGCTCT 120
GATCTCAGCT GACAGTGCCC TCGGGGACCA AACAAAGCCTG GCAGGACAAA ATTAGAAGAT 180
10     CAAAATGGAA AATATGCTGC TTTGGTTGAT ATTTTTCACC CTGGGTGGA CCCTCATTGA 240
TGGATCTGAA ATGGAATGGG ATTTTATGTG GCACTTGAGA AAGGTACCCC GGATTGTCAG 300
TGAAAGGACT TTCCATCTCA CCAGCCCCGC ATTTGAGGCA GATGCTAAGA TGATGGTAAA 360
TACAGTGTGT GGCATCGAAT GCCAGAAAGA ACTCCCAACT CCCAGCCTTT CTGAATTGGA 420
GGATTATCTT TCCTATGAGA CTGCTTTTGA GAATGGCACC CGAACCTTAA CCAGGGTGAA 480
15     AGTTCAAGAT TTGGTTCTTG AGCCGACTCA AAATATCACC ACAAAGGGAG TATCTGTAG 540
GAGAAAGAGA CAGGTGTATG GCACCGACAG CAGGTTGAGC ATCTTGAGCA AAAGGTTCTT 600
AACCAATTTT CCTTTTCAGCA CAGCTGTGAA GCTTTCCACG GGCTGTAGTG GCATTCTCAT 660
TTCCCTTCAG CATGTTCTAA CTGCTGCCCA CTGTGTTTCA GATGGAAGG ACTATGTCAA 720
AGGGAGTAAA AAGCTAAGGG TAGGGTTGTT GAAGATGAGG AATAAAAGTG GAGGCAAGAA 780
20     ACCTCGAGGT TCTAAGAGGA GCAGGAGAGA AGCTAGTGGT GGTGACCAAA GAGAGGGTAC 840
CAGAGAGCAT CTGCAGGAGA GAGCGAAGGG TGGGAGAAGA AGAAAAAAAT CTGGCCGGGG 900
TCAGAGGATT GCCGAAGGGA GGCTTCCTT TCAGTGGACC CGGGTCAAGA ATACCCACAT 960
TCCGAAGGGC TGGGCACGAG GAGGCATGGG GAGCCTACC TTGGACTATG ACTATGCTCT 1020
TCTGGAGCTG AAGCGTGTCT ACAAAAAGAA ATACATGGAA CTTGGAATCA GCCCAACGAT 1080
25     CAAGAAAATG CCTGGTGGAA TGATCCACTT CTCAGGATTT GATAACGATA GGGCTGATCA 1140
GTTGGTCTAT CGGTTTTCGA GTGTCTCYGA CGAATCCAAT GATCTCCTTT ACCAATAYTG 1200
CGATGCTGAG TCGGGCTCCA CCGGTTCCGG GGTCTATCTG CGTCTGAAA ATCCAGACAA 1260
AAAGAATTGG AAGCGCAAAA TCATTGCGGT TACTCAGGG CACCAGTGGG TGGATGTCCA 1320
CGGGTTTCAG AAGGACTACA ACGTTGCTGT TCGCATCACT CCCCTAAAAT ACGCCAGAT 1380
30     TTGCTCTGG ATTCAACGGA ACGATGCCAA TTGTGCTTAC GGCTAACAGA GACCTGAAAC 1440
ATGGCGGTGT ATCATCTAAA TCACAGAGAA AACCAGCTCT GCTTACCSTA GTGAGATCAC 1500
TTCATAGGTT ATGCTCTGAC TTGAACCTCT TCAATAGCAT TTCWACATTT TTCAAAATCA 1560
GGAGATTTTC GTCCATTTAA AAAATGTATA GGTGCAGATA TTGAAACTAG GTGGGCACTT 1620
CAATGCCAAG TATATACTCT TCTTTACATG GTGATGAGTT TCATTGTAGT AAAAAATTTG 1680
35     TTGCTCTTT AAAAATTAGA CACACTTTAA ACCTTCAAAC AGGTATTATA AATAACATGT 1740
GACTCCTTAA TGGACTTATT CTCAGGGTCC TACTCTAAGA AGAATCTAAT AGGATGCTGG 1800
TTGTGTATTA AATGTGAAAT YGCATAGATA AAGGTAGATG GTAAAGCAAT TAGTATCAGA 1860
ATAGAGACAG AAAGTTACAA CACAGTTTGT ACTACTCTGA GATGGAYCCA TTCAGCTCAT 1920
GCCCTCAATG TTTATATTGT GTTATCTGTT GGGTCTGGGA CATTTAGTTT AGTTTTTTTG 1980
40     AAGAATTACA AATCAGAAGA AAAAGCAAGC ATTATAACA AAACATAATA CTGTTTACT 2040
GCTTTAAGAA ATAACAATTA CAATGTGTAT TATTTAAAAA TGGGAGAAAT AGTTTGTCT 2100
ATGAAATAAA CCTAGTTTAG AAATAGGGAA GCTGAGACAT TTTAAGATCT CAAGTTTTTA 2160
TTTAACATAT ACTCAAATA TGGACTTTTC ATGTATGCAT AGGGAAGACA CTTCAAAAT 2220
TATGAATGAT CATGTGTTGA AAGCCACATT ATTTTATGCT ATACATTCTA TGTATGAGGT 2280
45     GCTACATTTT TAGGACAAAG AATTCTGTAA TCTTTTTCAA GAAAGAGTCT TTTTCTCCTT 2340
GACAAATCC AGCTTTTGTG TGAGGACTAT AGGGTGAATT CTCTGATTAG TAATTTTAGA 2400
TATGTCCTTT CCTAAAATG AATAAAATT ATGAATATGA CTTAAAAAAA AARWCGACG 2460
CGGCCCGGAA TTTAGTAGTA GTAGTCGACC CGGGAATTCC GGACCGGTAC CTGCAGGCGT 2520
ACCAGC

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Seq ID NO: B10 Protein sequence
Protein Accession #: CAC35071.1

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55     1      11      21      31      41      51
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MENMLLWLIF FTPGWTIDG SEMEWDFMWH LRKVPRIVSE RTFHLTSPAF EADAKMMVNT 60
VCGIECQKEL PTPSLSELED YLSYETVFEN GTRTLTRVKV QDLVLEPTQN IITKGVSVRR 120
KRQVYGTDSR FSILDKRFLT NFFSTAVKL STGCSGILIS PQHVLTAACH VHDGKDYVK 180
60     SKLRLVGLLK MRNKGSGKKR RGSKRSRREA SGGDQREGTR EHLRERAKGG RRRKKSRRGQ 240
RIAEGRPSPQ WTRVKNTHIP KGWARGMGMD ATLDYDYALL ELKRAHKKKY MELGISPTIK 300
KMPGGMIHFS GFDNDRADQL VYRFCSVSDE SNDLLYQYCD AESGSTGSGV YLRKLDPKDK 360
NWKRKIIAVY SGHQWVDVHG VQKDYNAVVR ITPLKYAQIC LWHGNDANC 420

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Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: NM_002035.1
Coding sequence: 108..1106

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70     1      11      21      31      41      51
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AGGCGCCCGC CCGCCGCGCG TGATTCTCGC CTCGCCCGAG CCCAGCCCTG CGCGCCTTGC 60
CCGGCGCGCC CCGCCGCGCC GCTCCGCGCC CCTGGCCCCG CGGAGCGATG CTGCTGCTGG 120
CTGCCGCTTT CCTCGTGGCC TTCGTGCTGC TGCTGTACAT GGTGTCTCCG CTCTAGCACC 180
75     CCAAGCCCTT CGCCCTGCCC GGGGCGCATG TGGTGGTTAC AGGAGGTTCC AGTGGCATCG 240
GGAAAGTGAT TGCTATCGAG TGCTATAAAC AAGGAGCTTT TATAACTCTG GTTGACAGAA 300
ATGAGGATAA GCTGCTGCAG GCAAGAAAG AAATTGAAAT GCACTCTATT AATGACAAAC 360
AGGTGGTGCT TTGCATATCA GTTATGTAT CTCAAGACTA TAACCAAGTA GAGAATGTCA 420
TAAAAACAAGC ACAGGAGAAA CTGGGTCCAG TGGACATGCT GGTAAATTGT GCAGGAATGG 480
CAGTGTGAGG AAAATTGAA GATCTTGAAG TTAGTACCTT TGAAAGGTTA ATGAGCATCA 540
ATTACTGGG CAGCGTGAC CCCAGCCGGG CCGTGATCAC CACCATGAAG GAGCGCCGGG 600
80     TGGGCGAGAT CGTGTGTTG TCCTCCACAG CAGGACAGTT GGGATTATTC GGTTCACAG 660
CCTACTCTGC ATCCAAGTTT GCCATAAGGG GATTGGCAGA AGCTTTGAG ATGGAGGTGA 720
AGCCATATAA TGTCTACATC ACAGTTGCTT ACCCACCAGA CACAGACACA CCTGGCTTTG 780
CCGAAGAAAA CAGAACAAAG CCTTTGGAGA CTCGACTTAT TTCAGAGACC ACATCTGTGT 840
GCAAAACCAGA ACAGGTGGCC AAACAAATTG TTAAAGATGC CATAAGAGGA AATTCTGAAC 900

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GTTCCCTTGG CTCAGATGGG TACATGCTCT CGGCCCTGAC CTGTGGGATG GCTCCAGTAA 960
 CTCTATTAC TGAGGGGCTC CAGCAGGTGG TCACCATGGG CCTTTTCCGC ACTATTGCTT 1020
 TGTTTTACCT TGAAGTTTT GACAGCATAG TTCGTCGCTG CATGATGCAG AGAGAAAAAT 1080
 CTGAAAATGC AGACAAAAC CTCTAATCTT CTTACCCCTT GGAAGAAGAC TGTTCCTCAA 1140
 TAAATTTGAAC AGCTTGCTGC TAAATGGGAC CCAATTTTGG GCCTATAGAC ACTTATGTAT 1200
 TGTTCCTGAA TACGTTCAGT TGGACCATGG CTCTTCAGGA ATGTGGCTGC AAGCAAGGGG 1260
 CTAGAAGTTC ACCTCCTGAC AGTATTATTA ATACTATGCA AATATGGAAT AGGAGACCAT 1320
 TTGATTTTCT AGGCTTTTGT GTAGAGAGGT GAAGGTATGA GAATTAATAG CGTGTGAACA 1380
 AAGTAAAGAA CAGGATTCCA GAATGATCAT TAAATTTGTT TCTATTATT CTTTTTGGCC 1440
 CCCCTAGAGA TTAAGTCCAG AATGTACTT TCTGGCACAT AAAGAAATCT TGAGGACTTT 1500
 GTTTAAACCT TCCATAAAAA AACAAATTTT GGTTCCTCGG GTTCCTCTCT TCTGTCTCTC 1560
 TGTCTCTCTG TCTCTCTGTC TCTCTGTCTC TCTCTCTCTC TCTCTTCTT TCTTTGTGTA 1620
 TTTTATTCAA GATGAGTTGG ACCCATGGCC AGTGAGTCTG AATGTCACTG ACAGCCCTGT 1680
 GTTGTGCTCA GGAATCACTC TGCTGCTGGT GGAAACTCAT GGCTTCTCTC TCTCTTTGAT 1740
 CCCATAAAGC TACGAGGGGG ACCGGAGAGG GCAGTGCAAT GGAAGTAA GAGATATTTT 1800
 CCAGTAGGAA AAGCAATGCT TTCTGTCTT TAGACTCAAA TGCTTAGGGA ACCTTTTCATT 1860
 TCTCATTGAT GGGGAAAGGC AGCCTCCTTA AATGTTTCTT GAAGAGCGGT AAAATCTAGA 1920
 AGCTTAAGAA TTTACAGTTC CTTCAATAAC CATGATGACC TGAAGTTCAC CTATCCCAT 1980
 TTAGCATCTA CTTGTTTTTC CCATCTCTTC CTTTCCAATT TTGCTTATAC TGCTGTAATA 2040
 TTTTGTGAAA AAAAAAATAA AAGGAAAAAA AAGACCAGCT AAAATTTTCC ACTTGACTTT 2100
 TTAACCTAAC TCATGAAATTA ATTAAGCAA ATGAAAAAAT TAAAAAGTGT GACTTTTCT 2160
 CGGAGCATAT ATGTAGCTTT TAGGAAAGGC TGATGATGGT ATAAAGTTTG CTCATTAAGA 2220
 AAAAAAGACA AGGCTGATTT TGAAGAGAGT TGCTTTTGAA ATAAATGAT CA

Seq ID NO: B12 Protein sequence
 Protein Accession #: NP_002026.1

1 11 21 31 41 51
 MLLLAAPLV AFVLLLYMVS PLISPKPLAL PGAHVVTGG SSGIGKCIAT ECVKQGAFFIT 60
 LVARNEKLL QAKKEIEMHS INDKQVLCI SVDVSQDYNQ VENVIKQAE KLGPDVMDLVN 120
 CAGMAVSGKF EDLEVSTFER LMSINYLGSV YPSRAVITM KERRVGRIVF VSSQAGQLGL 180
 FGFTAYSASK FAIRGLAEAL QMEVKPYNVY ITVAYPPDTD TPGFAENRT KPLETRLISE 240
 TTSVCKPEQV AKQIVKDAIQ GNFNSSLGSD GYMLSALTGC MAEVTSITEG LQQVVTMGLF 300
 RTIALFYLGS FDSIVRRMM QREKSENADK TA

Seq ID NO: B13 DNA sequence
 Nucleic Acid Accession #: CAT Cluster

1 11 21 31 41 51
 CTTGGGATGC ATTATATATT GCATTATATT TGCCGGTAAA ACTCGGTAA TTTTAAAAAT 60
 CGGCAAAATA TTGGTGCTT TCCCGAAATT TGCTCCGGG CTCCCTTATA GGATAATTGG 120
 TTTGGATTGG TTAAGTCCAA TTATTAAATG CTGCGGTTTC AAATTCCAG CTGGAAGGAC 180
 CACCCATTTA AAAACTTCAG AAGGCAGGAT CCTGCTCAAT TTATAAGGCT TTGGAAAAAT 240
 CCAGGCATTG GTTTGACATA TTTCCAGAGC TCAAACTGTC AGTGTTCCAC ATGCACATAC 300
 AAGATCCAGA GTCTCATGTT AAATCACTT ACATACCAG AAAGACCACC ACTTTGCAGG 360
 TATAATATTG TACTTAAAGA CAGAGAGGAA GTGTTTCTTA ATCCAAACAC ATGTACACCA 420
 AAGAACACAT AAGATGCTT CTTCATCAA ATGCACCTGC TTGTGAATTA ATGGACTTGT 480
 AATGAAACA ATGCAATCAG TCTTTTATAA TGCACTGTTT AATTGAGAT TCAAGTATTT 540
 CTATTTCTTG GAAAAAATTT TAAGAATCAA AATAAAGAA AATAAAAGT GCATACAGTT 600
 AAACATTCCA AAAAAAAAAA AA

Seq ID NO: B14 DNA sequence
 Nucleic Acid Accession #: XM_086767.1
 Coding sequence: 276..611

1 11 21 31 41 51
 CTTGTTTCATG GCATCTTTAG AAACAACTG CAATTTTATT TCATTTCCTT GTCGTTTATA 60
 CAAAGATTAC AAGACTAGCT TATGTGTGGA CTGTGACTGT TTTAAGGAAA AATCATGTCC 120
 TCGGCTGGGT TATCAAGCCA AGCTATTTAA AGGTGTTTAA AAAGAAAGGA TGGAAAGGAG 180
 ACCTCTTAGG ACCACTGTGT TTTTGGATAC AAGTGGTACA TATCCATTCT GTAGCCTATT 240
 ATTTTGTCTT CAGTATAATT GTTCCAGATA AAACATGAT GGATGGCTCG TTTTCATTTA 300
 AATTATTAAA TCAGCTTGGA ATGATTGAAG AGCCAAGGCT TTATGAAAAG AACAAACCAT 360
 TTTATAAATC TCAAGAAGTC AAGATTCTTG CTCAATTTTA TAATGACTTT GTAATATTT 420
 CAGCATTTGG TTTGACATAT TTCCAGAGCT CAAATCTGCA GTGTTCCACA TGCACATACA 480
 AGATCCAGAG ACTCATGTTA AAATCACTTA CATACCCAGA AAGACCACCA CTTTGCAGGT 540
 ATAATATTGT ACTTAAAGAC AGAGAGGAAG TGTTCCTTAA TCCAAACACA TGTACACCAA 600
 AGAACACATA AGATGCTTTC TTCCATCAA TGCACCTGCT TGTGAATTAA TGGACTTGTA 660
 AATGAAACA TGCAATCAGT CTTTATAAT GCACTGTTCA ATTTGAGATT CAAGTATTTT 720
 TATTTCTTGG AAAAAATTTT AAGAATCAA AATAAAGAAA ATAAAAAATG CATACAGTTA 780
 AACATTCC

Seq ID NO: B15 Protein sequence
 Protein Accession #: XP_086767.1

1 11 21 31 41 51
 MMDGSFSEFL LNQLGMIEEP RLYEKNKPFY KLQEVKILAQ FYNDFVNISS IGLTYFQSSN 60
 LQSTCTCYKI QRIMLKSLTY PERPPLCRYN IVLKDREEVF LNPNTCTPKN T

Seq ID NO: B16 DNA sequence

Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
5	TTTTTTTTTT	TTTTTTTTTT	TTAAATGCAA	AGGAGCAACA	AAATTTATTG	ACTGAATTAA	60
	ACACAACAGT	AAAATGGCAG	TGTTGTAATT	TCATTTTCAG	ATGTTTGAAT	GGAACAAGAA	120
	AAGTGCTATT	AGCCCAAGCT	TCTTACATTC	ATTAAAGAG	TGACTATCAA	AAACAGCAAC	180
	ATGCACAATG	GTACATATGC	ACAAAATGGA	ATTATATCAA	CAAATATACA	AAATACCCAA	240
	AATAAAATAT	TTACAGGTTT	AAAAATATAA	ACATTGATTC	CTCTATCCCA	TTAAACCATT	300
10	GGAGTGGAGA	AAGGAGGAAA	GACCCATTG	CTATTTAGAA	TCCTTTTAA	AACAAGTTTT	360
	TAAACATAG	AATTAGTTCT	AGGAGACAAT	TTTTGATGTT	TTTCAGGGGT	TTACATTCT	420
	ATTATAAAAA	TAACATCTAT	AAACCTACTA	ACAATTTTCC	TCCTGTGCAC	AAAAATAATA	480
	CTGCCAAAAC	CTGTCTCTCA	AGACATGCCT	GACTTTCAGG	AAAGCTAATT	ATGGAAATGG	540
	AGTTTCTCGT	TTGGGTTATC	TTTGTTACTA	TTTTCAAATA	ACCAGCAACT	CCCTATATTA	600
15	CACGTAGATA	CTTTATATAA	ATAACGTGGG	CGAAACCTGA	AGTTCACAAT	GAGCCTGCTA	660
	GGTAGCTGGT	GTCAAGTACA	AATGATAGGA	ATTGACTTTG	CCAACAACAT	CAAAAGCATT	720
	TTCCCTGATA	TTCTGTATAG	ACCTACCACT	ATCAGATCCT	CCATATTCAA	TAAGATTAT	780
	CCTGGAAGCA	ATGAAATGT	TAAATATTAC	TTTGCTAGAG	TTTCTCCTCC	TTTATTTAGA	840
20	AATAAATGTG	TAGTGGGGAC	CAGTGGTTGT	AATGTAGATA	CTTGAGAAGT	TTCATTGATT	900
	CCTTCAGACC	CATGCCG					

Seq ID NO: B17 DNA sequence

Nucleic Acid Accession #: NM_022898.1

Coding sequence: 268..2739

	1	11	21	31	41	51	
25	TTTTCTTGCT	TTTCTTCCCT	TTTTTTTCTT	TTTGCAACA	AAACAAAAAA	CAGCATAGAA	60
	GAAAGAGCAA	AATAAAGAA	AAGAAGAGGA	GGAAGAGAGG	GAAAGAGAGG	AAGGGAAAAA	120
30	AAACACCAAC	CCGGGCAGAG	GAGGAGGTGC	GGCGGCGGCG	GCGGCGGCGG	CAGCGGCGGC	180
	AGCGGCGCGG	CGGCGGCTCG	GACCCCTCC	CCCGGCTCCC	CCCATCAGTG	CAGCTCTCCG	240
	GGCGATGCCA	GAATAGATGC	CGGGGCAATG	TCCCGCCGCA	AACAGGGCAA	CCCGCAGCAC	300
	TTGTCCCAGA	GGGAGCTCAT	CACCCAGAG	GCTGACCATG	TGGAGGGCCG	CATCCTCGAA	360
	GAAGACGAGG	GTCTGGAGAT	AGAGGAGCCA	AGTGGCCTGG	GGCTGATGGT	GGGTGGCCCC	420
35	GACCCTGACC	TGCTCACCTG	TGGCCAGTGT	CAAAATGAACT	TCCCTTGGG	GGACATCCTG	480
	GTTTTTATAG	AGCACAAGAG	GAAGCAGTGT	GGCGGCAGCT	TGGGTGCTCG	CTATGACAAG	540
	GGCCTGGACA	AGGACAGCCC	GCCACCCCTC	TCACGCTCCG	AGCTCAGGAA	AGTGTCCGAG	600
	CCGGTGGAGA	TCGGGATCCA	AGTCACCCCC	GACGAAGATG	ACCACCTGCT	CTCACCCACG	660
	AAAGGCATCT	GTCCCAAGCA	GGAGAACATT	GCAGGTAAG	ATGAGCCTTC	CAGCTACATT	720
40	TGCACAACAT	GCAAGCAGCC	CTTCAACAGC	CGCTGGTTCC	TGCTGCAGCA	CGCGCAGAAC	780
	ACGCACGGCT	TCCGCATCTA	CCTGGAGCCC	GGGCGCGCCA	GCAGCTCGCT	CACGCCGCGG	840
	CTCACCATCC	CGCCGCGCTG	CGGCGCGGAG	GCCGTGGGCG	AGTCCCGCT	CATGAATTTC	900
	CTGGGCGACA	GCAACCCCTT	CAACCTGCTG	CGCATGAOCG	GCCCATCCT	GCGGGACCAC	960
	CCGGGCTTCG	GCGAGGGCCG	CCTGCCGGGC	ACGCCGCCCT	TCTTCAGTCC	CCCGCCGCGC	1020
45	CACCACTGG	ACCCGCACCG	CCTCAGTGCC	GAGGAGATGG	GGCTCGTCGC	CCAGCACCCC	1080
	AGTGCCTTCG	ACCGAGTCAT	GCGCCTGAAC	CCCATGGCCA	TCGACTCGCC	CGCCATGGAC	1140
	TTCTCGCGCG	GGCTCCGCGA	GCTGGCGGGC	AACAGCTCCA	CGCCGCGGCC	CGTGTCCCGG	1200
	GGCCGCGGCA	ACCCTATGCA	CCGGCTCCTG	AACCCCTTCC	AGCCCAAGCC	CAAGTCCCGG	1260
	TTCTTGAGCA	CGCCGCGCTG	CGCGCCCATG	CCCCCTGGCG	GCACGCGCGC	CCCGCAGCCG	1320
50	CCAGCCAAGA	GCAAGTCGTG	CGAGTTCTGC	GGCAAGACCT	TCAAGTTCCA	GAGCAATCTC	1380
	ATCGTGCAAC	GGCGCAGTCA	CACGGGCGAG	AAGCCCTACA	AGTGCCAGCT	GTGCGACCAC	1440
	GCGTGCTCGC	AGGCCAGCAA	GCTCAAGCGC	CACATGAAGA	CGCACATGCA	CAAGGCGCGC	1500
	TCGCTGGCCG	GCCGCTCCGA	CGACGGGCTC	TCGGCCGCCA	GCTCCCCCGA	GCCCGGCACC	1560
	AGCGAGCTGG	CGGGGCGAGG	CCTCAAGGCG	GCCGACGGTG	ACTTCCGCCA	CCACGAGAGC	1620
55	GACCCGTCCG	TGGGCCACGA	GCCGGAGGAG	GAGGACGAGG	AGGAGGAGGA	GGAGGAGGAG	1680
	GAGCTGCTAC	TGGAGAACGA	GAGCCGCGCC	GAGTCGAGCT	TCAGCATGGA	CTCGGAGCTG	1740
	AGCCGCAACC	CGGAGAACGG	CGGTGGTGGG	GTGCCCGGGG	TCCCGGGCGC	GGGGGGCGGC	1800
	GCGGCCAAGG	CGCTGGCTGA	CGAGAAGGCG	CTGGTGCTGG	GCAAGGTCAT	GGAGAACGTG	1860
	GGCCTAGGCG	CATGCGCGCA	GTACGCGGAG	CTCCTGGCCG	ACAAGCAGAA	GCGCGGCGCC	1920
60	TTCTGTAAGC	GTGCGGCGGG	CGCGGGGAC	CGGGGCGAGC	ACGACGACGC	GGGCGGCTGC	1980
	GGGGACGCGG	CGCGGGGCGG	CGCGGTCAAC	GGGCGCGGGG	GCGGCTTCGC	GCCAGGCACC	2040
	GAGCCCTTCC	CCGGGCTCTT	CCCGCGCAAG	CCCGCGCCGC	TGCCAGCCCC	CGGGCTCAAC	2100
	AGCGCCGCCA	AGCGCATCAA	GGTGGAGAA	GACCTGGAGC	TGCCGCCCCG	CGCGCTCATC	2160
	CCGTCCGAGA	ACGTGTACTC	GCAGTGGCTG	GTGGGCTACG	CGGCGTCGCG	GCACTTCATG	2220
65	AAGGACCCCT	TCCTGGGCTT	CACGGACGCA	CGACAGTCGC	CCITCGCCAC	GTGCTCCGAG	2280
	CACTCGTCCG	AGAACGCGAG	CCTGCGCTTC	TCCACGCGCG	CCGGGGACCT	GCTGGACGGC	2340
	GGCCTCTCGG	GCCGCGAGCG	CACGGCCAGC	GGAGGCGAGC	CCCCGCACCT	GGGCGGCCCC	2400
	GGCCCGGGCG	GCCCGAGCTC	CAAGGAGGGC	CGCCGCGAGC	ACACGTGCGA	GTACTGCGGC	2460
70	AAGGTGTTCA	AGAAGTGCAG	CAACTTGACG	GTGCACCGGC	GGAGCCACAC	CGGCGAGCGG	2520
	CCTTACAAGT	GCGAGCTGTG	CAACTACGCG	TGCGCGCAGA	GCAGCAAGCT	CACGCGCCAC	2580
	ATGAAGAGCG	GTCAAGTCTG	CGGCAAGGAG	GTGTACCGCT	GCGACATCTG	CCAGATGCCG	2640
	TTCAGCGTCT	ACAGCACCTT	GGAGAAACAC	ATGAAAAAGT	GGCACGGCGA	GCACTTGCTG	2700
	ACTAACGACG	TCAAAATCGA	GCAGGCCGAG	AGGAGCTAAG	CGCGCGGGCC	CCGCGGCCCC	2760
75	GCACCTGTAC	AGTGGAAACG	TTGCCAACCG	AGAGAAATGT	GACCTGACTT	GCCTCCGTGT	2820
	CACCGCCACC	CCGCAACCCG	CGTGTCCCGG	GGGCCCCAGG	GAGGCGGCAC	TCCAACCTAA	2880
	CCTGTGTCG	CGAAGTCTTA	TGGAAACCCG	AGGGTTGATT	AAGGCAGTAC	AAATTGTGGA	2940
	GCCTTTTAAC	TGTGCAATAA	TTTCTGTATT	TATTGGGTTT	TGTAATTTT	TTGTCATGTG	3000
	CAGGTACTTT	TTATTATTAT	TTTTTCTGTT	TGAATTCCTT	TAAGAGATT	TGTTGGGTAT	3060
	CCATCCCTTC	TTTGTTTTTT	TTTTAACCCG	GTAGTAGCCT	GAGCAATGAC	TCGCAAGCAA	3120
80	TGTTAGAGGG	GAAGCATATC	TTTTAAATTA	TAATTTGGGG	GGAGGGGTGG	TGCTGCTTTT	3180
	TTGAAATTTA	AGCTAAGCAT	GTGTAATTTT	TTGTGAAGAA	GCCAACTCTC	AAATGACTTT	3240
	TAAAGTTGTT	TACTTTTCTA	TTCTTCTCTT	TTTTTGTGTC	TGAAATAAAA	AGTGGCATGC	3300
	AGTTTTTTTT	TAAATATTAT	TTAATTTTTT	TTTTTGGTTT	TGTTTTTTGG	GGTGGGGGGT	3360
	GTGGATGTAC	AGCGGATAAC	AATCTTTCAA	GTCGTAGCAC	TTTGTTCAG	AACTGGGAATG	3420

5 GAGATGTAGC ACTCATGTCG TCCCAGTCA AGCGGCCTTT TCTGTGTTGA TTTCGGCTTT 3480
 CATATTACAT AAGGGAAACC TTGAGTGGTG GTGCTGGGGG AGGCACCCCA CAGACTCAGC 3540
 GCCGCCAGAG ATAGGGTTT TGGAGGGCTC CTCTGGGAAA TGGCCCGACA GCATTCTGAG 3600
 GTTGTGCAATG ACCAGCAGAT ACTATCCTGT TGGTGTGCCC TGGGGTGCCA TGGCTGCTAT 3660
 TCGCTGTAGA TTAGGCTACA TAAATGGGC TGAGGGTACC TTTTGGGGA GATGGGGTGG 3720
 CCTGCAGTGA CACAGAAAGG AAGAACTAG CGGTGTTCTT TTAGGCGTTT TCTGGCTTGA 3780
 CGGCTTCTCT CTTTTTTTAA ATCACCCCCA CCACATAAAT CTCAAATCCT ATGTTGCTAC 3840
 AAGGGGTCAT CCATCATTTT CCAAGCAGAC GAATGCCCTA ATTAATTGAA GTTAGTGTTC 3900
 TCTCATTTAA TGCACACTGA TGATATTGTA GGGATGGGTG GGGTGGGGAT CTGCAAAAT 3960
 10 TCTATTCTCT TTTACTGAAA AAGCAGGGGA TGAGTTCCAT CAGAAGGTGC CCAGCGCTAC 4020
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 CTGTTAAGAT TAGACATTGT AATTCTGTG ACCCGCACTT TAAAGCTTTT GTTTGCATT 4140
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 15 GTTAAACTGT AAGGGACAGC TGAGATTGAG TGTCAGTATT GCTAAGCGTG GCATTACAA 4260
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 TTCAATTGTA TGTGAGTGC TTGAAAAC TGCTTCTAT TTGAGTCTCT TGAGACAAAT 4380
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 20 AGATAGAGGA TATGAAATGC CATAAGACCC AATCAAAATGA AGAAATAAAC CCAGCACAAC 4560
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 30 TAACGTGAAA GTCGGAGTTT TAGTAAATTT TTTTCTGCTT TGGGTGTGTA ATTTTATTT 5160
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 60 CTCTGTGACT GCAGAGAAGA GAGAATTTG CTTCTGTTT GTGTTTAAAA AACCAACACG 6900
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 65 TGATTTAAGT TGTTTGCAAT TGTACTGGCA AGGCAAAATA TTTTATTAT CTTTCTATT 7260
 ACTTATTGTA TGAGCTTTTG TTGTTTACTT GGAGGTTTGT TCTTTTACTA CAAGTTTGGG 7320
 ACTATTTATT ATTGCTTGGT ATTTGTGCTC TGTTTAAGAA ACAGGCACCT TTTTATTA 7380
 TGGATAAAAT GTTGAGATGA CAGGAGGTCA TTTCAATATG GCTTAGTAAA ATATTTATTG 7440
 70 TTCTTTTATT CTCTGTACAA GATTTTGGGC CTCCTTTTCT CTTAATGTC ACAATGTTGA 7500
 GTTCAGCATG TGTCTGCCAT TTCATTTGTA CGCTTGTTCA AAACCAAGTT TGTCTGGTT 7560
 TCAAGTTATA AAAATAAATT GGACATTTAA CTGATCTCC AAA

Seq ID NO: B18 Protein sequence
 Protein Accession #: NP_075049.1

75 1 11 21 31 41 51
 MSRRKQGNPQ HLSQRELITP EADHVEAAIL EEDEGLEIEE PSGLGLMVGG PDPDLLTCGQ 60
 QMNFPLGDI LVFIEHKRQK CGGSLGACXD KALDKDSPPP SSRSELKVS EPVEIGIQVT 120
 80 PDEDDHLLSP TKGICPKQEN IAGKDEPSSY ICTCKQPFN SAWFLQHAQ NTHGFIYLE 180
 PGPASSSLTP RLTIPLPLPG EAVAQSLPMN FLGDSNPFNL LRMTGFILRD HPGFGEGRLP 240
 GTPPLFSPPP RHHLDPHRLS AEEMGLVAQH PSAFDRVMRL NPMAIDSPAM DFSRRLRELA 300
 GNSSTPPFVS PGRGNPMHRL LNPFQPSPKS PFLSTPPLPP MPPGCTPPPQ PPAKSKSECF 360
 CGKTFKFQSN LIVHRSHTG EKPYKCQLCD HACSQASKLK RHMKTHMHKA GSLAGRSDDG 420
 LSAASSPEPG TSELAGEGLK AADGDFRHE SDPSLGHEPE EDEDEDEEEE BELLLENESR 480

PESSFSMDSE LSRNRENGGG GVPVPGAGG GAAKALADEK ALVLGKVMEN VGLGALPQYG 540
 ELLADKQKRG AFLKRAAGGG DAGDDDDAGG CGDAGAGGAV NGRGGGFAPG TEPFPGLFPR 600
 KPAPLPSPGL NSAAKRIKVE KDLELPPAAL IPSENVYSQW LVGYAASRHF MKDPFLGFTD 660
 ARQSPFATSS EHSSENGSLR FSTPPGDLDD GGLSGRSGTA SGGSTPHLGG PGPGRPSSKE 720
 GRRSDTCEYC GKVFKNCSNL TVHRRSHTE RPYKCELCNY ACAQSSKLTR HMKTHGQIGK 780
 EVYRCDICQM PFSVYSTLEK HMKKWHGEHL LTNDVKIEQA ERS

Seq ID NO: B19 DNA sequence
 Nucleic Acid Accession #: NM_000399.2
 Coding sequence: 339..1769

1 11 21 31 41 51
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 15 TAACTGAGCG AGGAGCAATT GATTAATAGC TCGGCGAGGG GACTCACTGA CTGTTATAAT 60
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 CTGTGTGATTT TTTTCTCTTG GTGTGTGTGG TGGTTGTTTT TAAGTGTGGA GGGCAAAAGG 240
 AGATACCATC CCAGGCTCAG TCCAACCCCT CTCCAAAACG GCTTTTCTGA CACTCCAGGT 300
 20 AGCGAGGGAG TTGGGTCTCC AGGTTGTGCG AGGAGCAAAT GATGACCGCC AAGGCCGTAG 360
 ACAAAATCCC AGTAACCTCT AGTGGTTTTG TGCACCACTG GTCTGACAAC ATCTACCCGG 420
 TGGAGGACCT CGCCGCCACG TCGGTGACCA TCTTTCCTAA TGCCGAACCTG GGAGGCCCTT 480
 TTGACCAGAT GAACGGAGTG GCCCGAGATG GCATGATCAA CATTGACATG ACTGGAGAGA 540
 AGAGGTCGTT GGATCTCCCA TATCCAGCA GCTTTGCTCC CGTCTCTGCA CCTAGAAACC 600
 25 AGACCTTCAC TTACATGGGC AAGTTCTCCA TTGACCTCCA GTACCTTGGT GCCAGCTGCT 660
 ACCCAGAAGG CATAATCAAT ATTGTGAGTG CAGGCATCTT GCAAGGGGTC ACTTCCCCAG 720
 CTTCAACCAC AGCCTCATCC AGCGTCACTT CTGCCTCCCC CAACCCACTG GCCACAGGAC 780
 CCCTGGGTGT GTGCACCATG TCCACAGACC AGCCTGACCT GGACCACTGT TACTCTCCGC 840
 CACGCGCTCC TCCTCCTTAT TCTGGCTGTG CAGGAGACCT CTACCAAGGAC CCTTCTGCGT 900
 30 TCCTGTGAGC AGCCACCACT TCCACCTCTT CCTCTCTGGC CTACCCACCA CCTCCTTCTT 960
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 GATTCTTTCC ATCTCAGTGC CAGAGAGACC TACATGGTAC AGCTGGCCCA GACCGTAAGC 1080
 CCTTTCCCTG CCCACTGGAC ACCCTGCGGG TGCCCCCTCC ACTCACTCCA CTCTCTACAA 1140
 TCCGTAACCT TACCTTGGGG GGGCCCACTG CTGGGGTGAC CGGACCAGGG GCCAGTGGAG 1200
 35 CGAGCGAGGG ACCCGGCTG CCTGGTAGCA GCTCAGCAGC AGCAGCAGCC GCCGCGCGCG 1260
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 ACAGACCCAG CAAGACGCGG GTGCACGAGA GGCCCTACCC GTGCCACGA GAAGGCTGCG 1380
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 AGCCCTTCCA GTGTGCGATC TGCATGCGCA ACTTCAGCCG CAGTGACCAC CTCACCACCC 1500
 40 ATATCCGCAC CCACACCGGT GAGAAGCCCT TCGCCTGTGA CTACTGTGGC CGAAAGTTTG 1560
 CCCGGAGTGA TGAGAGGAAG CGCCACACCA AGATCCACCT GAGACAGAAA GAGCGGAAAA 1620
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 AGCCTGGGGG TACCCGTGTG AGCAGTAACA GCAGCAGTCT TGGCGGAGGG CCGCTCGCCC 1740
 CTTGCTCCTC TCGGACCCCG ACACCTTGAG ATGAGACTCA GGCTGATACA CCAGCTCCCA 1800
 45 AAGGTCCCGG AGGCCCTTTG TCCACTGGAG CTGCACAACA AACACTACCA CCCTTTCCCTG 1860
 TCCTCTCTC CCTTTGTTGG GCAAAGGGCT TTGGTGGAGC TAGCACTGCC CCCTTTCCAC 1920
 CTAGAAGCAG GTTCTTCTTA AAACCTAGCC CATTCTAGTC TCTCTTAGGT GAGTTGACTA 1980
 TCAACCAAG GCAAAGGGGA GGCTCAGAAG GAGGTGGTGT GGGGATCCCC TGGCCAAGAG 2040
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 50 CTATTTTTGA CCCATCACAG GTTTTGTGACC CTGGATGTCA GAGTTGATCT AAGACGTTTT 2160
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 55 AACCTTGAA GCAATATGTA TTATATACTC AGAGAACAGA AGTGCAATGT GATGGGAGGA 2400
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 60 TGATGTAGAC AAATGTTACA AGGCTGCATG TAAATGGGTT GCCTTATAT GGAGAAAAAA 2700
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 TAGAAAGTAT ATTTTGTGAT GCTTTGTTT GTGACTTAAA AGTGTACCT TTGTAGTCAA 2820
 ATTTAGATA AGAATGTACA TAAATGTACC GGAGCTGATT TGTGTTGTCA TTAGCTCTTA 2880
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 TGGATGGTTT GTGACTATAG TGTAATAAAA TACTTTTCAA CAAT

Seq ID NO: B20 Protein sequence
 Protein Accession #: NP_000390.2

1 11 21 31 41 51
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 70 MMTAKAVDKI PVTLSGFVHQ LSDNIYPVED LAATSVTIFP NAEELGGPFDQ MNGVAGDGM 60
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 LQGVTSAPT TASSSVTSAS ENPLATGPLG VCTMSQTQPD LDHLYSPPPP PPPYSGCAGD 180
 LYQDPSAFLS AATTSTSSSL AYPPPPSYPS PKPATDPGLF PMIPDPYGF FSPQQRDLHG 240
 75 TAGPDRKFPF CPLDTRLVPP PLTPLSTIRN FTLGGPSAGV TGPASGSGSE GPRLPSSSSA 300
 AAAAAAAYY NQHILPLRPI LRPRKYPNRP SKTPVHERPY PCPAEGCDRR FSRSDDELTRH 360
 IRIHTGHPKF QCRICMRNFS RSDHLTHIR THTGKPFAC DYCGRKFARS DERKRTKIH 420
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Seq ID NO: B21 DNA sequence
 Nucleic Acid Accession #: NM_004962.2
 Coding sequence: 457..1893

1 11 21 31 41 51
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5 CACACACGGG CGCACGCACA CGGCAGCCGG GCCAGGGACG ACCCTGTCAG CTGCAGCCCC 60
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 CCTCGAAGCA GCCGGGCCGG GCGCGCAGTG GGCTACAAAC TTTGCGCAGC CGAGTCCGCC 180
 AAGGCAGCGC GCCGACTCGG GCTCGGCTCG GCTCTGCGCT GCTCCGACG GCTGTGACCG 240
 CTGGCGGGGG GCTCGGGCGC CGGTACCACA CGGACCGGCG GCCCGGGTGC CTGCTCCGCT 300
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 AGCCCGGGAC CCGGGCCCCA GCTGCTGCTG CTGCTGCTGC CGTTGTTTCT GCTGTTGCTC 540
 10 CGGGATGTGG CCGGCAGCCA CAGGGCCCCC GCCTGGTCCG CACTGCCCGC GGCCGCCGAC 600
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 CAGGGCGCGC GGCCGGGAGG GGGCAACACG GTCCGCAGCT TCAGGGCCAG GCTGGAAGTG 780
 15 GTCGACCAGA AGGCCGTGTA TTTCTTCAAC CTGACTTCCA TGCAAGACTC GGAATGATC 840
 CTTACGGCCA CTTTCCACTT CTACTCAGAG CCGCCTCGGT GGCTTCGAGC GCTCGAGGTG 900
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 20 ATCGTCAAGG CGGCCCGCGG GGATGGCGAG CTGCTCCTCT CCGCCAGCT GGATTCTGAG 1140
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 AACGATCTGG CCATCTCGGA GCCCAACAGC GTGGCAGTGA CGCTGCAGAG ATACGACCCC 1260
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 25 AGGCCGCGCG CGGCCACGCG ACAGCACTTC CACAAGCACC AGCTGTGGCC CAGCCCTTC 1440
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 30 TGTGAGTTCC CACTGCCTAA GATCGTTCGT CCATCCAACC ATGCCACCAT CCAGAGCATT 1740
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 AACATGTCCG TGGACACCTG TGCCTGCCG TGAGACCACT CCAGGGTGGA AAGAAGCCAC 1920
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 35 CACAGAGCAC AGCTCATGGT CAACATCACT GGGGCCCAGA GAGAGCTGTC CGCCAGTGCA 2040
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 45 ATATTTTGT AAATTATACT TTCTATACTG TAGATTGTGT ATGTTATGTG TTTTATGGA 2640
 AAGCTAATAA ATTAAAGTA CAGTGGTATC TTGA

Seq ID NO: B22 Protein sequence
 Protein Accession #: NP_004953.1

50 1 11 21 31 41 51
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 MAHVPARTSP GPGPQLLLLL LPLFLLLLRD VAGSHRAPAW SALPAAADGL QGDRDLQRHP 60
 GDAAATLGPS AQDMVAVMHM RLYEKYSRQG ARPGGGNTVR SFRARLEVVD QKAVYFFNLT 120
 55 SMQDSEMLT AFHFYSEPL RWPRALEVLC KPRAKNASGR PLPLGPPTRO HLLFRSLSQN 180
 TATQGLLRGA MALFPFPRGL WQAKDISPIV KAARRDGELL LSAQLDSEER DPGVPRPSPY 240
 APYILVYAND LAISEPNSVA VTLQRYDFPF AGDPEPRAAP NNSADPRVRR AAQATGPLQD 300
 NELPGLDERP PRAHAQHFKH QLNWPSPFRA LKPRFGRKDR RKKQGEVFMA ASQVLDLDEK 360
 TMQKARRKQW DEPRVCSRRY LKVDFAIDGW NEWIISPKSF DAYYCAGACE FPMPIKIVRS 420
 60 NHATIQSIVR AVGIIPGIPE PCCVPDKMNS LGVLFLENR NVVLKVYFNM SVDTCACR

Seq ID NO: B23 DNA sequence
 Nucleic Acid Accession #: AK026322.1

65 1 11 21 31 41 51
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 70 TAGCATMTT GGAGTGACTG CTTTTCAGT TGCCTTTAAA AGTATTGGAC TTCGTTTGA 240
 TAGTTGAATT ACTTGCAAA CAGCTTGATC ATTCTGAGAC TTGTTTAA CTTTGTGCGA 300
 AAAGGCTATG CTACTTCAAG TATAATAAAA CCTAGTTTGA GTTTTATCCT ATAACAAAGG 360
 CATGTGTTCA ATTTGAATGT CTCCAACCT GTGTGAAC TCAGTCTCCA 420
 ATTTGCGAGT AATTTTCTT GTTCAGCCTT GCAGTCTCAT CTAATCAAG TGTGGCTCTG 480
 75 TATCCAACAA CAGTCTTGGA GATCTCATGA AGATTCTGA AACTTTTGCT CTGCAGGATA 540
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 80 TTTCTTGTGA CAGGAGCCTC CATTACTTTT CAAACAGTAA TGCAGTTGCA GTTGCTCTCT 840
 CTTTCTTCA TTATGTGTTT ATCTCTGGCA GTTTGAGCCA AGAGAGGGCA CGGAGAAGTA 900
 CAATGACTAG AGAGCACTT TGTGAGGCT CATTATTGA CCCCTACCCC AGTGTCTTAT 960
 GAATGTGTGC TGCAGATGTC ATACAGCATC ACAGCTTCTT CTTAATTTA TGAGGCATAA 1020
 TTTTCTTTT TGTATTTTAA TTGTATTACC TGCTTGGTTG CAAGAGGATG ATGAGGAGGA 1080
 CTACTATAGG ATAAATTTGT TTTTATAGAG CAATTCTCA TGGGTACGA GGGATAGTAC 1140

TCCATTTTCC TCACTGATAT CGGCTTGATC ATCTGAGTCA GTGGGCTCAT TGTGGAAACA 1200
 TATGGAATCC TTTATGCTTT TTCTCAGGCT GCTTCTGTGA CATGAAATAA AGCCAGAGTT 1260
 GATTGTGAAA AAAAAAAAAA AAAA

5 Seq ID NO: B24 DNA sequence
 Nucleic Acid Accession #: cat cluster

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	CTTTCCTCACT	CTGATGATTT	GTGCTCTTAT	TTTTCTCTAGA	TTTACCTCAT	CTAGGGCATA	180
	TTCTTTTCCC	TCTTCTCTTT	TACCTTTCCCT	GGTCTGTATC	CCTCTGTACT	CAGTTCCCTT	240
15	AAATTATTGG	ACTACAAACT	AATATACTAG	AAAAGCATAC	ACTTATTTTA	TTTGAATGCA	300
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	TTAACACTGT	AACCTTCAGT	ATTCCCCAGT	TAGCGTACCT	AACCTCTCTG	TGGGTATATG	420
	TAATTCCTAT	TAGACTACTA	GAGAAAAACC	AACCTGGCAGT	TTGCTAAGCA	TATCTACTGG	480
	TGTTGTTTCT	GCGCCCTCTT	TTGGCTAATT	GATGTAATTA	TACTGGCTCT	AAAGATTAC	540
20	TGCCCATATA	GTAATAGTA	TAGCCACATT	CTGAACATAT	CAAAAGTACA	AACCTAGGAG	600
	GAGTGTATGT	ACAAATATGT	AAAATTTTAT	GAAAATGAAC	ATGTTTTTAT	GATGTTATTT	660
	CTAGTTCATA	AGAATGTGAT	GACTGCTTTG	CTTCATTAT	GTACGTTCCC	ATTATATTCT	720
	TGCTGTCAAT	CAATCACAAA	TTTATATCAG	ATTAGGATAA	ACTAAGCCAT	TTTATGTATT	780
	TTATTTTAAA	CCTTATTTTG	GCAGAGTAAT	TCCTTAGAAT	TGGAAAAGCT	GTTACTTTGA	840
25	AATTACCAAT	TTATTACAAA	ACATAGAAAT	GTATTGTAGC	TACAAAGACA	ACCAAGCATT	900
	TTCTGTGTTT	TAATGAATAT	CTAAAAAAT	ACATTTAGTT	TATTTTACTC	AGTTTGTAAA	960
	TGATTTTTTT	ACTGGCTCTA	TTGCCCTTAA	ATACTAAGA	GATTAATGAT	TCTTTGTATA	1020
	ATTTTCCTTT	TCTTTGTTCT	TTTTTTTACA	TTTCGCAGAG	TTATATCTAT	AGTTTTAGTA	1080
	ACAAATTTCT	ATGATTTCTG	GATAACTGAA	AACAACATAA	GGTGTGGGCG	ATTAGAAAAA	1140
30	AATTGTGAGC	AGTAAGATTA	CTGATGTAAT	ATGTATGTTG	GACTGAAGTA	TTTCTTTATA	1200
	AACATTCTAT	TTGATTTTAA	GCAAAATGTA	TGTTAAAGCA	TGTTTTTACA	TCAGTAAAGT	1260
	CATTTGTGCA	CCTTCTGGAA	ATGAAAGGTT	TTTACCTAGA	TACTGTAAGT	TACACCTCCT	1320
	TAACAATCAT	ATTTGTCTAT	GTGTTTTTCT	GCAACAAAAA	ATGTTTATGG	GCTTCATGTA	1380
	GGCTTAAGAT	TGTAGGCAAA	AATGGACTGA	GTTCAAGACC	CTTCAAGCAG	TAGGCATTCA	1440
35	GTTACAGAGC	AGTTGGTACT	TTGTAACCCA	GACTTACAGT	TTAAAAATAT	CAAGTTAGCT	1500
	GATGTTTCAT	TATAATAAAA	ATACTATTTT	GCTTAAGAGT	TGTATTACAA	ATATTTGTGC	1560
	TTAACATTAG	AAATAGCTGT	TTTAAATTGT	AGTTTAACATA	TTAACTTTT	CAGAAAAAAA	1620
	GCATGGTTTA	TTTTTAATAA	TGAAATAGAG	AACATAATAC	GTAATGTTCA	GTATAACAGC	1680
	TGAGTTAAAA	CATCGCCAG	GATTAACATC	AGTGCCTTTT	TGCCAATGCA	TAGAGGCATT	1740
40	TTTCTCTAAG	TATGATGGCT	AATGATAACT	ATTCCTTTGT	ACACATTCOA	GTCACTCCCA	1800
	TACAAGTAAC	TAGTGGGTGA	TATGTTTCAC	TCCAAGGGT	GTATTAATTC	TGAAATGCTAA	1860
	TCATGAAGAC	TTAAGTTAGG	ACAACACTTC	AAACCAGGAA	GTGTGAACCTG	ATTTA	

Seq ID NO: B25 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1144

	1	11	21	31	41	51	
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	AAGAGCCTGA	GCGCCTCCAC	CTCCAAGCGC	TTGGAAGCGG	CTTCCGCTC	CACGCCCCCG	120
	GGCATGGACC	TGTCCCTGGC	GCCGCCGCCCT	CGGGAACGCC	CGGCGTCCCT	CTCCTCGTCG	180
	CCCTCTGGCT	GCTTCGAGCC	GGCTGACCCC	GAGGGGGCAG	GGCTGCTGTT	GCCGCCGCCCT	240
	GGAGGAGGCG	GCGGCGGAGC	GCGGGGAAGT	GCGGCGGCGG	GCGGCGGCGG	GGTGGGTGTC	300
55	CCCGGGCTGC	TAGTAGGTTT	AGCGGCGGTT	GGGGGGCAGC	CTAGCCTAAG	CAGCCTGCCG	360
	GCCGGGGCGG	CCCTTTGCCT	CAAGTACGGC	GAAAGCGCGA	GCCGGGGCTC	GGTGGCCGAG	420
	AGCAGCGGCG	GCGAGCAGAG	CCCAGACGAC	GACAGCGACG	GTGCTGCGCA	GCTCGTCTG	480
	CGGGCCGGAG	TAGCCGACCC	GCGGGCCTCC	CCGGGAGCGG	GAGGTGGTGG	GCGGAAGGCA	540
	GCCGAGGGCT	GCTCCAATGC	CCACCTCCAC	GCGGCGGCCA	GCGTCCCCCC	GGGGGGCCTG	600
60	GGCGGCGGCG	GCGGCGGGGG	TAGCAGCAGC	GGTAGCAGTG	GCGGCGGTGG	CGGTAGCGGT	660
	AGCGGCAGCG	GCGGCAGCAG	CAGCAGCAGC	AGCAGCAGCA	GCAAGAAATC	CAAAGAGCAA	720
	AAGGCGCTGC	GGCTTAACAT	CAATGCCCGA	GAGCGCCGGC	GGATGCACGA	CCTGAACGAC	780
	GCGCTGGACG	AGCTGCGGCG	GGTGATCCCC	TACGCGCACA	GCCCTCGGT	GCGAAAGCTC	840
	TCCAAGATCG	CACGCTGCT	GCTCGCCAAG	AACTACATCC	TCATGCAGGC	GCAGGCCCTG	900
65	GAGGAGATGC	GGCGCCTAGT	CGCCTACCTC	AACCAGGGCC	AGGCCATCTC	GGCTGCCTCC	960
	CTGCCAGCT	GCGCGGCTGC	AGCGGCAGCA	GCTGCTGCCC	TGCACCCGGC	GCTCGGCGCC	1020
	TACGAGCAGG	CAGCCGGCTA	CCCCTTCAGC	GCCGGAAGTG	CCCCGGCTGC	CTCCTGCCCG	1080
	GAGAAGTGC	CCCTGTTTAA	CAGCGTCTCC	TCCAGCCTCT	GCAACAGTGC	CACGGAGAAG	1140
	CCTT						

70 Seq ID NO: B26 Protein sequence
 Protein Accession #: FGENESH predicted

	1	11	21	31	41	51	
75	MERGMHLGAA	AAGEDDLFLH	KSLSASTSKR	LEAAFRSTPP	GMDLSLAPPP	RERPASSSSS	60
	PLGCFEPADP	EGAGLLPLPP	GGGGGGSAGS	GCGGGGGVGV	PGLLVGSAGV	GDDPSLSLPP	120
	AGAAALCLKYG	ESASRGSVAE	SSGGEQSPDD	DSDBGRCCLVL	RAGVADPRAS	PGAGGGGAKA	180
	ABGCRNAHLH	GGASVPPGGL	GGGGGGGSSS	GSSGGGGGSG	SGSGGSSSSS	SSSSKKSKEQ	240
	KALRLNLINAR	ERRRMHDLND	ALDELRAVIP	YAHSPSVRKL	SKIATLLLLAK	NYILMQAAL	300
80	EEMRRLVAYL	NQGQAISAAS	LPSSAAAAAA	AAALHPALGA	YEQAAGYPFS	AGLPPAASCP	360
	EKCALFNSVS	SSLCKQCTEK	P				

Seq ID NO: B27 DNA sequence
 Nucleic Acid Accession #: cat cluster

	1	11	21	31	41	51	
5	TTTTTTTTTT	TTTTTTTAA	ATGTTTGATC	AAAATATTTT	AATAAAGATT	CTTCTGACA	60
	TAGATACACA	TACAAATGGT	CGTACATAGC	TGTCATAGTC	TGATTGACCT	ATTTAATATA	120
	TATATCATTC	TTTACACATC	CAAAACCCGC	CAACAGATCC	ATCACAGCTC	CCAACCTACC	180
	ATCCAACTG	ACAAACTGAA	TTTGTATTAT	CTGCAAGGAG	TGGAAAATAG	CAGGACTCCA	240
	TTTTTAAAAA	AGATTTTCTT	GATTTTTCATA	GGGCGGAAAG	GCAGTCAAA	AGCCATGCAG	300
10	AACTAAAACT	GAAAGCTCAC	TTTGGGTAAA	TAGCTTCTTG	TTCTTCCTTA	GTTTTCTTTC	360
	TTTTTAAATT	TTATTTTTTT	AGAAAAATAA	CAAAGGATTT	CACACCATAG	GCAAAATCAA	420
	CCAGTCTTTT	AACTTAAATA	ATTCTCCACA	GTAAATAATA	CATATATGTA	CATATATATT	480
	AAAAGCAATT	AAATTAGACC	TTTTAAAAAT	GCACAGCACA	GCCTGGAAAA	ATATTGCTT	540
	AGCATGTTCT	TACGTATAGC	AACTATTGCT	GTGATGTTTT	TCCCTTTTGG	AATGTAAAGG	600
15	AGTCCCTCTT	CAAAAAAGAG	ATCAATTCAT	TCATCAATTA	AGAATACACC	TTTCTGTAA	660
	TTTTTGGACT	GAAGCAATTT	ATTAAAGCTC	AAATTAATA	CAGGGATGAT	GCAACTGAAA	720
	ATATCCAGGT	GACCTTTCAT	AAACCTAAGC	AGCTCAGATA	CATCAATATT	TCTCTTCATA	780
	CTTGTTGGCA	ATAAAACCTT	TAAACACTTG	GCACACAGCA	TAAGTAATCT	ATAAAACAA	840
	TTTAGAGGCA	TTAAAAAAT	CTGCACATAA	GACCCATGAC	TTTAAACACAT	GATAAATACT	900
20	GTGATGTGG	AAGGGTCATT	GAAGAATAAC	AAATAAATAC	CATGAATTGT	TAATACATCA	960
	TTGCAGAGTA	GAAAGTAACA	AGGTGCACAT	AAATATTTTT	AAATGCAATT	CTTTCAGCCA	1020
	CAGTCAGTTT	TTTTATATCA	CTCTCGCCAA	AACTTTGAGC	ATTTTCACAG	GATTAAAGTT	1080
	CAGAGACAAT	AAAAAATACA	AGTCTTTCAT	AGTAACATGT	TCTCTCTCTC	TGCTCTGGG	1140
	TTTTATTTC	CCCTCACTTA	AGTCAACATT	TCAAGTTTTT	CTCCTGGCTC	AGAATCAAAA	1200
25	TTTATTTTCA	AGTGCCCTTT	CTGATTTGTC	TGAATGAATA	TTCCATCTCT	CATGCTACCG	1260
	ATCCGCT						

Seq ID NO: B28 DNA sequence
Nucleic Acid Accession #: NM_002581.2
Coding sequence: 368..5251

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	CAGATAAAGG	AGCGGGGAGA	GAAATTAATT	GCCAAACCAG	AGGAGTTGGG	CTGTATTTTT	180
	CAAGAGTGGG	GAGAGTGGAG	CACACACCTT	GAGGAGGAAA	GCGAGAAAGA	AAAGAAAAAA	240
	GCAAGTGAAG	GGGGGCTCGC	CCAAGAAAGG	TGAAGAACGC	AAGAAAGTCG	AGGCGCCGAG	300
	GCTCCCAAAG	CTGGCAGCTC	CGGGTGGCGG	TGCAGGGGCG	AAGGGGGGGG	CGGGGGGAAC	360
40	GTGCGCATG	CGGCTCTGGA	GTGGGTGCTG	GCACCTGGGG	CTGCTGAGCG	CCGCGCTGGG	420
	CTGCGGGCTG	GCCGAGCGTC	CCCGCCGGGC	CCGAGAGAGC	CCGCGGGCCG	GCCGACCCCC	480
	GCGCCGCCGC	GCCGCCGCCG	CCACCTGCGC	CACCCGCGGC	CCGCGGCCGC	CGCGCCTCGC	540
	CGCGCGCGCC	GCCGCCGCCG	GGCGTGGCTG	GGAAGCCGTG	CGCGTCCCCC	GGCGGCGGCA	600
	GCAGCGGGAG	GCGAGGGGCG	CCACCGAGGA	GCCGAGCCCG	CCGAGCCGGG	CGCTCTATTT	660
45	CAGCGGGCGA	GGCGAGCAGC	TGCGAGTCCT	CCGGGCCGAC	CTCGAGCTGC	CCCGGGACGC	720
	GTTCACGCTG	CAAGTGTGCG	TGCGAGCGGA	GGGGGGCCAG	AGGTCTCCCG	CAGTGATCAC	780
	AGGGCTGTAT	GACAAATGTT	CTTATATCTC	ACGTGACCGA	GGATGGGTG	TGGGCATTCA	840
	CACCATCAGT	GACCAAGACA	ACAAAGACCC	ACGCTACTTT	TTCTCTTTGA	AGACAGACCG	900
	AGCCCCGCAA	GTGACCACCA	TCAATGCCCA	CCGCAGCTAC	CTCCCAGGCC	AGTGGGTATA	960
50	CCTAGCTGCC	ACCTATGATG	GGCAGTTCAT	GAAGCTCTAT	GTGAATGGTG	CCCAGGTGGC	1020
	CACCTCTGGG	GAACAAGTGG	GTGGCATAAT	CAGCCCACTG	ACCCAGAAAT	GCAAAAGTGT	1080
	CATGTTAGGG	GGCAGTGCCT	TGAATCACAA	CTACCGGGGC	TACATCGAGC	ACTTCAGTCT	1140
	GTGGAAGGTG	GCCAGGACTC	AGCGGGAGAT	ACTGTCTGAC	ATGGAACCC	ATGGCGCCCA	1200
	CACCTGCTCT	CCTCAGCTCC	TCCCTCAGGA	GAACCTGGGAC	AATGTGAAGC	ATGCCCTGGT	1260
55	CCCCATGAAG	GATGGGACCA	GCCCCAAAGT	GGAATTCAGC	AATGCCCAAG	GCTTCTGCT	1320
	GGACACGAGT	CTGGAGCCTC	CTCTGTGCGG	ACAGACATTG	TGTGACAAAC	CAGAGGTCAT	1380
	TGCCAGCTAC	AATCAGCTCT	CAAGTTTCCG	CCAGCCCAAG	GTGGTGCCTG	ACCGCTGGT	1440
	CAACCTCTAT	GAAGATGATC	ATAAGAACCC	GACGGTGACG	CGCGAGCAGG	TGGACTTCCA	1500
	GCACCATCAG	CTGGCTGAGG	CCTTCAAGCA	ATACAACATC	TCCTGGGAGC	TGGACGTGCT	1560
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	GGATTGCGCG	CACCTGCGCC	ACCCTGCCTT	CGTGAAGAAG	CAGCACACAC	GGGTGTGTGA	1740
	CATGGACTGC	AACTATGAAC	GGTTCACCTT	TGATGGTGGA	GAGTGTGTGT	ACCCTGAAAT	1800
	CACCAATGTC	ACTCAGACTT	GCTTTGACCC	CGACTCTCCA	CACAGAGCCT	ACTTGGATGT	1860
65	TAATGAGCTG	AAGAACATTC	TTAAATTGGA	TGGATCAACA	CATCTCAATA	TTTTCTTTGC	1920
	AAAATCTCTA	GAGGAGGAGT	TGGCAGGAGT	AGCAACTTGG	CCATGGGACA	AGGAGGCCCT	1980
	GATGCACTTA	GGTGGCATTG	TCTTGAACCC	ATCTTCTAT	GGCATGCTGT	GGCACACCCA	2040
	CACCATGATC	CATGAGATTG	GTCAACAGCT	GGGCTCTAT	CACGTCTTCC	GAGGCATCTC	2100
	AGAAATCCAG	TCCTGCAGCT	ACCCCTGCAT	GGAGACAGAG	CCCTCTCTCG	AGACTGGAGA	2160
70	CCTCTGCAAT	GATACCAACC	CAGCCCCTAA	ACACAAGTCC	TGTGGTGACC	CAGGGCCAGG	2220
	AAATGACACC	TGTGGCTTTC	ATAGCTTCTT	CAACACTCCT	TACAACAAC	TCATGAGCTA	2280
	TGCAGATGAC	GACTGTACGG	ACTCCTTCAC	GCCCAATCAA	GTGCGCCAGAA	TGCATGTTA	2340
	CCTGGACCTG	GTCTACACAG	GCTGGCAGCC	CTCCAGGAAA	CCAGCGCTGT	TTGCCCTCGC	2400
	CCCCAAGTT	CTGGGCCACA	CAACGGACTC	TGTGACACTG	GAGTGGTTCC	CACCTATAGA	2460
75	TGGCCATTTC	TTTGAAAGAG	AATTGGGATC	AGCATGTGAT	CTTTGCGCTG	AAGGGAGAA	2520
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	ACTGACCATC	AGACTCTGGG	ACGTGGGCGA	GGAGGTGTAT	GGCATCCAAA	TCTACACGCT	2940
	GGATGAGCAC	CTGGAGATCG	ATGCTGCCAT	GTGACCTCC	ACTGCAGACA	CCCCACTCTG	3000
	TCTACAGTGT	AAGCCCCCTGA	AGTATAAGGT	GGTCCGGGAC	CCTCTCTCC	AGATGGATGT	3060
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Seq ID NO: B29 Protein sequence
Protein Accession #: NP_002572.1

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LQVWLRAEGG QRSAPVITGL YDKCSYISRD RGWVVGIIHTI SDQDNKDPY FFSLKTRDR 180
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Seq ID NO: B30 DNA sequence
Nucleic Acid Accession #: NM_032808.1
Coding sequence: 61..1008

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Seq ID NO: B31 Protein sequence
 Protein Accession #: NP_116197.1

1 11 21 31 41 51
 MLHELLRLQE IQLVGGQLAV VEPYAFRGLN YLRVLNVSGN QLTLEELVF HSVGNLETLI 60
 LDSNPLACDC RLWVFRRRW RLNFNRQOPT CATPEFVQVK EFKDFPDVLL PNYFTCRRAR 120
 IRDRKAQQVF VDEGHTVQFV CRADGDPPEA ILWLSPRKHL VSAKSNGLRT VFPDGTLEVR 180
 YAQVDNGTY LCIAANAGBN DSMPAHLHVR SYSPDWP HQP NKTFAFISNQ PGEGEANSTR 240
 ATVPFPFDIK TLIIATTMGF ISFLGVVLF C LVLFLWSRG KGNTKHNIEI EYVPRKSDAG 300
 ISSADAPRK NMKMI

Seq ID NO: B32 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 CAGCACATAC AAGAAACATA CAGTGTACCT CAAAAGGGGC CCTTGAAATG TCATCAAAGG 60
 GTAATAACCT AGTGAGTGAG TTGTGATGTC ATCTGGAACA TAGGAAATGG GGCTCTTAGC 120
 GTATTTCGTA CGAAGGAAGC CAGGCTGGTC CTGGCAGGAA GTAATGATA ATCTTTGGGA 180
 AACCAGGACC CTGCCTCCCA GCCCAGAGGT GGAGGAGGGC GGTCAAGGTG GGGCTACAG 240
 TGGCAGACGA CTGACAAAGG TAGAGGAAA TGTAAATAGCA CATCTACGCT GCAGTCTGGT 300
 GAAAGTGGCC GGGGTGGTCC TTGGAACAA GTTGGGCTGT TCTTGGCAGG AATTAGTGAC 360
 AGCCTTTCG TCACGGGCGG GGACGCTTG ATTTAAAAA AATAAATAA TAAACGTCT 420
 GGGTATAGAA A

Seq ID NO: B33 DNA sequence
 Nucleic Acid Accession #: NM_006174.1
 Coding sequence: 71..1408

1 11 21 31 41 51
 GAAAGGCTAT CGGTAACAAC TGACCTGCCA CAAAGTTAGA AGAAAGGATT GATTCAAGAA 60
 AGACTATAAT ATGGATTAG AGCTCGACGA GTATTATAAC AAGACACTTG CCACAGAGAA 120
 TAATACTGCT GCCACTCGGA ATTCTGATTT CCCAGTCTGG GATGACTATA AAAGCAGTGT 180
 AGATGACTTA CAGTATTTTC TGATTGGGCT CTATACATTT GTAAGTCTTC TTGGCTTTAT 240
 GGGGAATCTA CTTATTTTAA TGGCTCTCAT GAAAAAGCGT AATCAGAAGA CTACGGTAAA 300
 CTTCTCATATA GGCATCTGG CCTTTCTGA TATCTTGGTT GTGCTGTTTT GCTCACCTTT 360
 CACACTGACG TCTGTCTTGC TGGATCAGTG GATGTTTGGC AAAGTCATGT GCCATATTAT 420
 GCCTTTTCTT CAATGTGTGT CAGTTTGGT TTCAACTTTA ATTTTAATAT CAATTGCCAT 480
 TGTCAAGTAT CATATGATAA AACATCCCAT ATCTAATAAT TTAACAGCAA ACCATGGCTA 540
 CTTTCTGATA GCTACTGTCT GGACACTAGG TTTTGCCATC TGTCTCTCCC TTCCAGTGTT 600
 TCACAGTCTT GTGGAACCTT AAGAAACATT TGGTTCAGCA TTGCTGAGCA GCAGGTATTT 660
 ATGTGTTGAG TCATGGCCAT CTGATTGATA CAGAATTGCC TTTACTATCT CTTTATTGCT 720
 AGTTCAGTAT ATTCTGCCCC TAGTTTGTCT TACTGTAAGT CATACAAGTG TCTGCAGAAG 780
 TATAAGCTGT GGAATTGTCC ACAAGAAAA CAGACTTGAA GAAAATGAGA TGATCAACTT 840
 AACTCTTCAT CCATCCAAAA AGAGTGGGCC TCAGGTGAAA CTCTCTGGCA GCCATAAATG 900
 GAGTTATTCA TTCATCAAAA AACACAGAAG AAGATATAGC AAGAAGACAG CATGTGTGTT 960
 ACCGTCTCCA GAAAGACCTT CTCAAGAGAA CCACTCCAGA ATACTTCCAG AAAACTTTGG 1020
 CTCTGTAAAG AGTCAGTCTT CTTTCATCCAG TAAGTTCATA CCAGGGGTCC CCACTTGCTT 1080
 TGAGATAAAA CCTGAAGAAA ATTCAAGTGT TCATGAATTG AGAGTAAAC GTTCTGTTAC 1140

AAGAATAAAA AAGAGATCTC GAAGTGTITT CTACAGACTG ACCATACTGA TATTAGTATT 1200
 TGCTGTAGT TGGATGCCAC TACACCTTTT CCATGTGGTA ACTGATTTTA ATGACAATCT 1260
 TATTTCAAAT AGGCATTTCA AGTTGGTGTA TTGCATTTGT CATTTGTTGG GCATGATGTC 1320
 CTGTTGTCTT AATCCAATTC TATATGGGTT TCTTAATAAT GGGATTAAAG CTGATTTAGT 1380
 GTCCCTTATA CACTGTCTTC ATATGTAATA ATTCTCACTG TTT

Seq ID NO: B34 Protein sequence
 Protein Accession #: NP_006165.1

1 11 21 31 41 51
 MDLEDEYYN KTLATENNTA ATRNSDFPVV DDYKSSVDDL QYFLIGLYTF VSLLGFMGNL 60
 LILMALMKKR NQKTTVNFLI GNLAFSIDL VLFCSPTFLT SVLLDQWMFG KVMCHIMPFL 120
 QCVSVLVSTL ILISIAIVRY HMIKHPISSN LTANHGYFLI ATVWTLGFAI CSPLPVFHSI 180
 VELQETFGSA LLSRYLCVE SWPDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240
 GLSNKENRLE ENEMINLT LH PSKSGPQVK LSGSHKWSYS FIKHRRRYS KKTACVLPA 300
 ERPSQENHSR ILPENFGSVR SQLSSSSKFI PGVPTCFEIK PEENSVDVHEL RVKRSVTRIK 360
 KRRSRVFYRL TILILVFAVS WMPLHLFHV TDFNDNLISN RHFKLVYCIC HLLGMMSCCL 420
 NPILYGLFNN GIKADLVSLI HCLHM

Seq ID NO: B35 DNA sequence
 Nucleic Acid Accession #: NM_014279.1
 Coding sequence: 286..1689

1 11 21 31 41 51
 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
 CCTGCCACGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
 CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGTCTGA TCCAGGCGTG 180
 GGGACACAGG CCAGGCGCGG CCGCGCGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
 TCCGCGTCCA CGCAGCGCGC GCGCGGCCAG CACCCAGGCG CCTGCGTCC AGGTCGTGG 300
 AGGTGGCAGC GAGACATGCA CCCGCGCGG AAGCTCCTCA GCCTCCTCTT CCTCATCTCT 360
 ATGGGCACTG AACTCACTCA AGTGCTGCCC ACCAACCCTG AGGAGAGCTG GCAGGTGTAC 420
 AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTCCGCC ACAGCAGACC 480
 ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
 ATGTCTCAAT CCATAGAGGT CTTGGACAGG CCGAGCCAGA GAGACTTGCA GTACGTGGAG 600
 AAGATGGAGA ACCAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660
 AAGCAACACC TGGCCAGGCA GTTTAAGGCG ATAAAGCGA AAATGGATGA ACTTAGGCCT 720
 TTGATACCTG TGTGGAAGA GTACAAGGCC GATGCCAAT TGGTATTGCA GTTTAAGAG 780
 GAGGTCCAGA ATCTGACGTC AGTGCTTAAC GAGCTGCAAG AGGAAATTGG CGCCTATGAC 840
 TACGATGAAC TTCAGAGCAG AGTGTCCTAT CTTGAAGAAA GGCTCCGTGC ATGCATGCAA 900
 AAACTAGCTT GCGGGAAGTT GACGGGCATC AGTGACCCCG TGACTGTCAA GACCTCCGGC 960
 TCGAGGTTCT GATCCTGGAT GACAGACCTT CTCGCCCTCG AAGGCGATAA CCGGCTGTGG 1020
 TACATGGAGC GCTATCACAA CAACCGCTTC GTACGTGAGT ACAAGTCCAT GGTGACTTTC 1080
 ATGAACACGG ACAATTTTCA CTCCCACCGT CTCCCACACC CTGCTCGGG CACGGGGCAG 1140
 GTGGTCTACA ACGGTTCTAT CTACTTCAAC AAGTTCCAGA GCCACATCAT CATCAGGTTT 1200
 GACCTGAAGA CAGAGACCAT CCTCAAGACC CGCAGCCTGG ACTATGCCGG TTACAACAAC 1260
 ATGTACCACT ACGCTGGGG TGGCCACTCG GACATCGACC TCATGGTGA CGAGAGCGGG 1320
 CTGTGGGCGG GTGACGCCAC CAACCAAGAC GCTGGCAACA TCGTGGTCAG TAGGCTGGAC 1380
 CCGGTGTCCC TGCAGACCTT GCAGACCTGG AACACGAGCT ACCCCAAGCG CAGCGCCGGG 1440
 GAGGCCTTCA TCATCTGCGG CACGCTGTAC GTCAACCAAC GCTACTCAGG GGGTACCAAG 1500
 GTCCACTATG CATACACAGC CAATGCCTCC ACCTATGAAT ACATCGACAT CCCATTCCAG 1560
 AACAAATACT CCCACATCTC CATGCTGGAC TACAACCCCA AGGACCGGGC CCGTATGTC 1620
 TGGAAACAAC GCCACAGAT CCTCTACAAC GTGACCTCTT TCCACGTCAT CCGCTCCGAC 1680
 GAGTTGTAGC TCCTCTCTCC TGGAGGCCAA GGGCCACAGT CCTCACCAACA AAGGGAATCC 1740
 TGTGAAACTG CTGCCAAAAA GATACCAATA AACTAACA TAACGATCTT GAAAAATCAT 1800
 CAGCAGTGCG GATTCTGACA TCGAGGGATG GCATTACCTC CGTGTCTTCT CCTTTGAGC 1860
 CGGCGGGGCA CAGACCTCGG AAGAAACTCC CGTATTGCA GCTGGAACTG CAGCCCAAGG 1920
 CGCCCCGGTT TTCTTCCCGC CCTGTCTCCT CTCTGGTCAA ACAACATACT AAAGAGGCGA 1980
 GGCAATGACT GTTGGCCAGT TCTCACCGGG GAAAAACCA CTGTTAGGAT GGCATGAACA 2040
 TTTCTTAGA TCGTGGTCAG CTCGAGGAA TGTGGCGTCC AGGCTCTTTG AGAGCCATGG 2100
 GCTGCACCCG GCCGTAGGCT AGTGTAATCT GCATCCCAT GCACTGCCGT TCTTGTACTG 2160
 TGTGTCTGTC TCTTAGATTA ACGTGCTGA GGCTCCACAT AGCTCCTGGA CCTGTGTCTA 2220
 GTACATACTG AAGCGATGGT CAGAGTGTGT AGAGTGAAGT TGCTGTGCCC ACATTGTTT 2280
 AACTCGCGTA CCCCGTAGAT ACATTGTGCA ACGTCTCTCT GTTATTCCCT TGAGGTGGTA 2340
 ACTTCGTATG TTAGGTTTAT GCGATGATTG TTGTAATGCA AATGCCGTAG TTTGGATTAA 2400
 TAAGTGGATG GTTTTTGTTT CTAATAAGAA AAAAAAATC AGTGTTCACC CTTATAGAGA 2460
 CATAGTCAAG TTCATGTTGA TAATAATCAA AGGAATTACT CTCTCTTGT TAAATTAGCT 2520
 AAATCATGTA ACCGCAGATA GGAAGGGCTC ACCTGGGGAA ACTCTGGTTT CCGATGGGAC 2580
 AGGAAAGTCA TACGGGCAAC AGTATGCGGA AAGTACGTTT TTTTAAGTAA AAAACAAAGG 2640
 CAAACTTTGT ACTATCCAGT TATCTAAGGA ACAATAAAAA CATTAGGAGA AAAAAAAGG 2700
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: B36 Protein sequence
 Protein Accession #: NP_055094.1

1 11 21 31 41 51
 MPGRWRWQD MHPARKLLSL LFLILMGTEL TVLPNTPEE SWQVYSSAQD SEGRICITVV 60
 APQQTMCSDR ARTKQLRQLL EKVQNMSSQI EVLDRRTORD LQYVEKMEQK MKGLESKFQK 120
 VEESHKQHLA RQFKAIKAKM DELRLPIPLV EBYKADAKLV LQFKEVQNL TSVLNLQEE 180
 IGAYDYDELQ SRVNLLEERL RACMQKLACG KLTGISDPVT VKTSGSRFGS WMTDPLAPEG 240
 DNRVWYMDGY HNNRFVREYK SMVDFMNTDN FTSHRLPHEW SGTGQVYVNG SIYFNKFQSH 300
 IIRFDLKT E TILKTRSLDY AGYNNMYHYA WGGHSDIDL M VDESLWAVY ATNQAGNIV 360

VSRLDPVSLQ TLQTWNTSYP KRSAGEAFII CGTLYVTNGY SGGTKVHYAY QTNASTYEI 420
DIPFQNKYSH ISMLDYNPKD RALYAWNNGH QILYNVTLPF VIRSDEL

Seq ID NO: B37 DNA sequence
Nucleic Acid Accession #: NM_006334.1
Coding sequence: 286..693

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1      11      21      31      41      51
|      |      |      |      |      |
10 GCGCGGGGGA GCCATTAGGA GGCGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
   CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
   CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGTCTGA TCCAGGCGTG 180
   GGGACACGAG CCAGGCGCGG CCGCCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
   TCCGCGTCCA CGCAGCCGCC GGCCGGCCAG CACCCAGGGC CTGTCATGCC AGGTCTGTTG 300
15 AGGTGGCAGC GAGACATGCA CCCGGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG 360
   ATGGGCACTG AACTCACTCA AGTGCTGCCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420
   AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTCCGCCC ACAGCAGACC 480
   ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
   ATGTCTCAAT CCATAGAGGT CTTGGACAGG CGGACCAGAG GAGACTTGCA GTACGTGGAG 600
20 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660
   AAGCAACACC TGGCCAGGCA GTTTAAGGGC TAACTTAAAA GAGTTTTCCT AATGCTGCAG 720
   TGACTGAAGA AGCAGTCCAC TCCCATGTAA CCATGAAAGA GAGCCAGAGA GCTTTTTCGA 780
   CCATGCAATT TTAATATTAT TTTCCAATAC TTAGCACCAT TTCACTAAGG AACCTTGAAT 840
   ACAACCAAGG TCCTCCTTTG CATGCGACTG TAGCTGCATT TCATGAATAG TTTGAACCTT 900
25 TGTCATATGCA TTTTGTGAAA AAGAAAGAAA AAAAAAATT CGTGTATGTG ACTCAAAGCA 960
   TGTAACCTTA AGATGTTGCA TTCTAAACTG ACAATAAAGA CCTTTCCTCC

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Seq ID NO: B38 Protein sequence
Protein Accession #: NP_006325.1

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1      11      21      31      41      51
|      |      |      |      |      |
30 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQVLPTNPEE SWQVYSSAQD SEGRICITVV 60
   APQQTMCSSD ARTKQLRQLL EKQVNMSQSI EVLDRRTQRD LQYVEKMENQ MKGLESKFKQ 120
35 VEESHKQHLA RQPKG

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Seq ID NO: B39 DNA sequence
Nucleic Acid Accession #: NM_058199.1
Coding sequence: 286..795

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1      11      21      31      41      51
|      |      |      |      |      |
45 GCGCGGGGGA GCCATTAGGA GGCGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
   CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
   CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGTCTGA TCCAGGCGTG 180
   GGGACACGAG CCAGGCGCGG CCGCCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
   TCCGCGTCCA CGCAGCCGCC GGCCGGCCAG CACCCAGGGC CTGTCATGCC AGGTCTGTTG 300
   AGGTGGCAGC GAGACATGCA CCCGGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG 360
   ATGGGCACTG AACTCACTCA AAATAAAAGA GAAAACAAAG CAGAGAAGAT GGGAGGGCCA 420
50 GAGAGCGAGA GGAAGACCA AGGAGAGAAG ACACTGAACG AGCTTCCCTT GTTTTGCCTG 480
   GAAGCCACG CTGGCTCCCT GGCTCTGCCG AGGATGTGCA GTCCAAATCC CAATCCAGCA 540
   GTGGGGTTAT GTGCTCCCGC TTACCTCTAG AGCCCTTCTC CTGGTGCTGC CCAGACGATC 600
   AGCCAGTCCC TCCTGGAGAG GTTCTGCATG GCCTCTAGGA GAGAAGTTTT CTGGGCCCCA 660
   GGAAGGCCTG GTGGAGGGTG GTGGTTGTGC ACTGTTGCTG GACAGATGCA TTCATTCTATG 720
55 TGCACACACA CACACACACA TGCACACACA GGGGAGCAGA TACCTGAGA GAAGAGCCAA 780
   CCAGTCCCTG ATTATGGGCA AGCTGCCCCA CAAAGGGCTA TGCCTGTGTC TTATTGAGAC 840
   ACCTTGCCAA AGAGATGGCT GATTCTGGGT GGTCTCTGGC ATGGCCGCAC CCAAGGGCCC 900
   TCCAAGCCTT AATGGCACCC TGAAGCCTCC ATGCCCAGGC CAAAAGATGC TTTTCTCTCC 960
60 TAAAAAATAA AAAAAAATAA

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Seq ID NO: B40 Protein sequence
Protein Accession #: NP_478106.1

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1      11      21      31      41      51
|      |      |      |      |      |
65 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQNKRENKAE KMGGPESERK TTGEKTLNEL 60
   PLFCLEAHAG SLALPRMCSP NPNPAVGLCR PAYPQSPSPG AAQTISQSLI ERFCMASRRE 120
   VFLAPGRPGG GWWLCTVAGQ MHSFMTCTH THAHTGBQIP AEKSQPGPD

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Seq ID NO: B41 DNA sequence
Nucleic Acid Accession #: AY038071.1
Coding sequence: 1..1686

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1      11      21      31      41      51
|      |      |      |      |      |
75 ATGAGCAATC AGTACCAGGA GGAGGGCTGC TCCGAGAGGC CCGAGTGCAA AAGTAAATCT 60
   CCAACTTTGC TCTCCTCCTA CTGCATCGAC AGCATCCTGG GCCGAGGAG CCCGTGCAAA 120
   ATGCGGTTGC TGGGAGCGCG GCAGAGCTTG CCTGCTCCGC TGACCAGCCG CGCCGACCCG 180
   GAAAAGGCCG TGCAAGGCTC CCCTAAGAGC AGCAGCGCCC CGTTCGAGGC CGAGCTGCAC 240
80 CTGCCGCCCA AGCTGCGCGC CCTGTACGGC CCGGGCGGGG GCCGCTCCTT TCAGGGTGCG 300
   GCAGCGCGCG CGGCGCGCGG GCGGCGCGCG GCGGCAGCGG CCGCCACGGC CACGGCGGGT 360
   CCACGCGGGG AGGCCCTCTC GCGGCCACCG CCAACCGCGC GGGCCGGGGA ACGGCCGGAC 420
   GCGCGAGGGG CCGCGCGCGC AGCGCGCGCC GCGGCGCGCG CGGCTGGGA CACGCTCAAG 480
   ATCAGCCAGG CGCCGAGGT GAGCATCAGC CGCAGCAAGT CGTACCGCGA GAACGGGGCG 540

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5
 10
 15
 20

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CCCTTCGTGC CGCCGCCGCC CGCGCTGGAC GAGCTGGGCG GCCCGGGGGG CGTCACGCAC 600
CCGGAGGAGC GCCTCGGCGT GGCCGGCGGC CCGGGCAGCG CCCCGGCTGC GGGTGGTGGC 660
ACCGGCACCG AGGACGACGA GGAGGAGCTG CTGGAGGACG AAGAAAGATGA GGACGAGGAA 720
GAGGAACATGC TGGAGGACGA CGAGGAGGAG CTGCTGGAGG ACGACGCCCG CGCGCTGCTC 780
AAGGAGCCCC GGCGCTGTCC TGTGGCCGCC ACTGGCGCCG TGGCCGCAGC AGCTGCCGCT 840
GCAGTGGCCA CAGAGGGCGG GGAGCTGTCA CCCAAGGAGG AGCTGCTGCT GCACCCGGAA 900
GACGCTGAGG GCAAGGACGG CGAGGACAGC GTGTGCCTCT CTGCGGGCAG CGACTCGGAG 960
GAGGGGCTGC TGAACGCAAA ACAGAGGCGC TACCGCACCA CGTTCAACAG CTACCAGCTG 1020
GAGGAACATGC AGCGGGCCTT CCAGAAGACG CACTACCCGG ACGTCTTAC CAGGGAGGAA 1080
CTGGCCATGA GGCTGGACTT GACCAGGGCC CGAGTCCAGG TCTGGTTCCA GAACCGTCGG 1140
GCCAAGTGGC GCAAGCGGGA GAAGGCAGGC GCGCAGACCC ACCCCCTGG GCTGCCCTTC 1200
CCGGGGCCGC TCTCCGCCAC CCACCCGCTC AGCCCTTACC TGGACGCCAG CCCCTTCCTT 1260
CCGCACCACC CGGCGCTCGA CTCGCTTGG ACTGCGCTG CCGCCGCCGC CGCCGCCGCC 1320
TTCCGAGGCC TACCTCGCC TCCGGGCTCG GCCAGCCTGC CGCCAGCGG GCGCGCGCTG 1380
GGCCTGAGCA CTTTCTCGG AGCGGCAGTG TTCCGACACC CAGCTTTCAT CAGCCCGGCA 1440
TTCCGCAGGC TTTTTCAC AATGGCCCC CTGACACAGC CGTCGACCGC GGCCGCGCTC 1500
CTGAGACAGC CCACACCCGC CGTGGAGGGC GCAGTGGCAT CGGGCGCCTT GGCCGACCCG 1560
GCCACGGCGG CCGCAGACAG ACGCGCCTCT AGCATAGCCG CGCTGAGGCT CAAGGCCAAG 1620
GAGCACGCGG CGCAGCTCAC GCAGCTCAAC ATCTGCCCG GCACACGAC GGGCAAGGAG 1680
GTGTGC
  
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Seq ID NO: B42 Protein sequence
 Protein Accession #: AAK93901.1

25
 30
 35

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1 11 21 31 41 51
| | | | |
MSNQYQEEGC SERPECKSKS PTLSSYCID SILGRRSPCK MRLLGAAQSL PAPLTSRADP 60
EKAVQGSFKS SSAPFPAELH LPFKLRRLYG PGGGRLLQGA AAAAAAAAAA AAAAAATATAG 120
PRGEAPFPFP PTARPGERPD GAGAAAAAAA AAAAAMDTLK ISQAPQVSIS RSKSYRENGA 180
PFVPPPALD ELGGPGGVTH PEERLGVAGG PGSAPAAGGG TGTEDDEEEL LEDEDEDEDE 240
EELLEDEEEE LLEDDARALL KEPRRCPVAA TGAVAAAAAA AVATEGGELS PKELELLHPE 300
DAEGKDGEDS VCLISAGSDSE EGLLKRKQRR YRTTFTSYQL EELERAFQKT HYPDVFTREE 360
LAMRLDLTEA RVQVWFQNRK AKWRKREKAG AQTHPPGLPF PGPLSATHPL SPYLDASFPF 420
PHHPALDSAW TAAAAAASAAA FPLPPPPGS ASLPPSGAPL GLSTFLGA AV FRHPAFISPA 480
FGRLFSTMAP LTSASTAAAL LRQPTPAVEG AVASGALADP ATAAADRRAS SIAALRLKAK 540
EHAAQLTQLN ILPGTSTGKE VC
  
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Seq ID NO: B43 DNA sequence
 Nucleic Acid Accession #: CAT cluster

40
 45
 50
 55

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1 11 21 31 41 51
| | | | |
CGCTGCCCC CCCGTTGCTT CTCTCTCTTC CCTTCTGCCT GCGTGCCTGC CCGTCTTTGG 60
TTCCGCCGGT TCCGTGCGCC CTCTCTGGGC TTCCGGCTCA CCCCTCCGCT GGTGTGCTGCT 120
CTGCTCTCCT CCGCTCTCAT GCCCTTTTCA GCTCCTACTC TGGTGTGCTC CCCCTCCCTC 180
GCTCGTTTCT CTTGTTCTCT TCCTTCCCGG TTCTGTGTTCT GCTTCTTCTG GTTCCCTCTC 240
GTCGTGTGTT GTGGGTCGTC CTCTGCGTCC TGCGTCTTTC TCTTGCGTTT CCGCGCGCTT 300
CCTGTTTTGG TCCCTCTGGT TCTCGCGCGG TTCTGTGTGC GCGGGCGGCC CCGTCTTTTC 360
TTGGTGCTTT GCTCCTGCTC TCTGTCTGGT GTTCTCCGCC GTCTGTGTCT TTCTCTCTTT 420
ATCTTCTGTT TCTCTTTTTT CTGTTTCTT CTGTTTTTTT TTTGTCTTTG TTTTCTCTTA 480
GCTGAGGTTG GGGAGAGATA ACGCTGTAAA CTTTATTATT TCAGGAAATC TGGAAACCTA 540
CAGTCTCCAT GCCTGCTCAG CCAAGAAGGA GCTCACTGTG GGCACCAGAG ACAGGGACCC 600
AATGTGGAGA CCTGTGAGCC TGTGTCCGCG CCGTGAACCT CAAGCAGAGG GCAGGCTTCC 660
TGAGCATTGA AGAGTAATTA TGGGAGAACA AAACAGAAAC TGAAGAATA TGCAAGGTGT 720
CTTTCTTGA TGTATTCCA TGATAGATAG TAGGGGCAGG AGTGAGAGAG GCTGACTAGG 780
TCTGGACATG TCCCTGTGGA GAGTCAGGGT GTGATTCGGA GAGGCGCATG AGAAGGAAGG 840
TGGATTTTAA GGCTGGAAT CTGAGGGTCA GTGTCCAAG TCACCTCAGAG ACAGAATCAC 900
AGCATAGCCC TTGCTGATGG CAA
  
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Seq ID NO: B44 DNA sequence
 Nucleic Acid Accession #: NM_014421.1
 Coding sequence: 718..1497

65
 70
 75
 80

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1 11 21 31 41 51
| | | | |
CCACGCGTCC GCGGGAGGCC CGCGCGAGC GTAGCGCAAG TCCGCTCCCT AGGCATCGCT 60
GCGCTGGCAG CGATTGCTG TCTCTGTGA GTACGGGAC AACGCTTCGG GGCAACTGTG 120
AGTGCGCGTG TGGGGACCT CGATTCTCT CAGATCTCGA GGATTGCTC CGGGGACGTC 180
TCTGATCCCC TACTATAAGC GCCTGCTAAC TTGAAAAAGG AGCACTGTGT CCTGCAAGT 240
TTGACACATA AAGGATAGGA AAAGAGAGGA GAGAAAAAGCA ACTGAGTTGA AGGAGAAGGA 300
GCTGATGCGG GCTTCTGAT CAATTAAGAG GAGAGTTAAA CCGCGGAGAT CCCGGCGGGA 360
CCAAGGAGGT GCGGGGCAAG AAGGAACGGA AGCGGTGCGA TCCACAGGGC TGGGTTTTCT 420
TGACACCTGG GTACACGCTC CTGCGGAGA AAGCGCTCG CATTGTGATT CTTCAGTTA 480
TTGCAAGAAT TCCGTGCTGT GTGGAGAAGC GGGTCTCGCT TGGGTTCCGC TAATTCTGT 540
CCTGAGGCGT GAGACTGAGT TCATAGGGTC CTGGGTCCCC GAACCAAGGA GGGTTGAGGG 600
AACACAATCT GCAAGCCCC GCGACCCAAG TGAGGGGCC CGTGTGGGG TCTTCCCTCC 660
CTTTGCATTC CCACCCCTCC GGGCTTTGGG TCTTCTGGG GACCCCTCG CCGGGAGATG 720
CGCGGCTTGA TCGGAGCAA GGATTCGTCC TGCTGCTGCT TCCTACTGCG CGCGGTGCTG 780
ATGGTGGAGA GCTACAGAT CGGCAGTTCG CGGGCCAAAC TCAACTCCAT CAAGTCTCT 840
CTGGGCGGGG AGACGCTCG TCAGGCCGCC AATCGATCTG CCGGCATGTA CCAAGGACTG 900
GCATTCGCGG GCAGTAAGAA GGGCAAAAC CTGGGGCAGG CTAACCTTG TAGCAGTGAT 960
AAGGAGTGTG AAGTTGGGAG GTATTGCCAC AGTCCCCACC AAGGATCATC GGCCTGCATG 1020
GTGTGTCGGA GAAAAAGAA GCGCTGCCAC CGAGATGGCA TGTGCTGCC CAGTACCCGC 1080
TGCAATAATG GCATCTGTAT CCCAGTTACT GAAAGCATCT TAACCCCTCA CATCCCGGCT 1140
  
```

CTGGATGGTA CTCGGCACAG AGATCGAAAC CACGGTCATT ACTCAAACCA TGACTTGGGA 1200
 TGGCAGAATC TAGGAAGACC ACACACTAAG ATGTCACATA TAAAAGGGCA TGAAGGAGAC 1260
 CCTGCGCTAC GATCATCAGA CTGCATTGAA GGGTTTTGCT GTGCTCGTCA TTTCTGGACC 1320
 AAAATCTGCA AACCACTGCT CCATCAGGGG GAAGTCTGTA CCAAACAACG CAAGAAGGGT 1380
 5 TCTCATGGGC TGGAAATTTT CCAGCGTTGC GACTGTGCGA AGGCCTGTCT TTGCAAAGTA 1440
 TGGAAAGATG CCACCTACTC CTCCAAAGCC AGACTCCATG TGTGTCAGAA AATTGTATCA 1500
 CCATTGAGGA ACATCATCAA TTGCAGACTG TGAAGTTGTG TATTTAATGC ATTATAGCAT 1560
 10 GGTGGAATAA AAGGTTTCAGA TGCAGAAGAA TGGCTAAAAT AAGAAACGTG ATAAGAATAT 1620
 AGATGATCAC AAAAAGGGAG AAAGAAAACA TGAAGTGAAT AGATTAGAAT GGGTGACAAA 1680
 TGCAGTGCGC CCAGTGTTC CATTATGCAA CTGTCTATG TAAATAATGT ACACATTGT 1740
 GGAAAATGCT ATTATTAAGA GAACAAGCAC ACAGTGGAAA TTACTGATGA GTAGCATGTG 1800
 ACTTTCCAAAG AGTTTAGGTT GTGCTGGAGG AGAGGTTTCC TTCAGATTGC TGATTGCTTA 1860
 TACAAATAAC CTACATGCCA GATTTCTATT CAACGTTAGA GTTTAACAAA ATACTCCTAG 1920
 15 AATAACTTGT TATACAATAG GTTCTAAAAA TAAAATTGCT AAACAAGAAA TGAAAACATG 1980
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Seq ID NO: B45 Protein sequence
 Protein Accession #: NP_055236.1

1 11 21 31 41 51
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 RCNNGICIPV TESILTPHIP ALDGRHRDR NHGHYSNHD L GWQNLGRPHT KMSHIKGHEG 180
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Seq ID NO: 46 DNA sequence
 Nucleic Acid Accession #: NM_019885.1
 Coding sequence: 1..1539

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 65 CGCGACAAGA GCTGCAAGCT GCCATCCCC AAGGGATCCA TGGGCTTCCC GCTCATCGGA 180
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 70 AAGCGCAAGG TCTTCTCCAA GATCTTCAGC CACGAGGCC TGGAGAGTTA CCTGCCCAAG 480
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 CACAGTCGTT TTAATATTGA AAAAGCACTT GTGTGTTTT TTTTGATATG AAACCTGGTAC 4380
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Seq ID NO: B47 Protein sequence
Protein Accession #: NP_063938.1

1 11 21 31 41 51
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 60 ETCHWLLQGS GFQSSRRREKY GNVFKTHLLG RPLIRVTGAE NVRKILMGEH HLVSTEWPRS 120
 TRMLLGPNTV SNSIGDIHRN KRKVFSPKIFS HEALESYLPK IQLVIQDTRL AWSSHPAIN 180
 VYQEAQKLTF RMAIRVLLGF SIPEEDLGHF FEVYQQFVDN VFSLPVDLPF SGYRRGIQAR 240
 QILQKGLEKA IREKLQCTQG KDYLDALELL IESSKEHGKE MTMQELKDG T LELIFAAYAT 300
 65 TASASTSLIM QLLKHPTVLE KLRDELRAHG ILHSGGCPCE GTLRDLTSLG LRYLDCVIKE 360
 VMRLFTPISG GYRTVLQTFE LDGFQIPKGV SVMYSIRDTH DTAPVFKDVN VFDPPDRFSQA 420
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Seq ID NO: B48 DNA sequence
Nucleic Acid Accession #: AB040527.1; AL136582.1
Coding sequence: 94..2319

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 80 GGGTCAGGC CTTCGCATCT TATCGAATGA GCCCTGGGAA CTGGAAAAAC CTGTGCTGGC 300
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 CGCTGCCCGT ACCGCCCTCA GTCAGGTGGT CGCTAGCCAC CGGGTGGCCA CGCCGCAAGT 480
 CTGAGGAGAG GATACCCAGC CCACGACCTA CGCCGCGGAG GCTCAGGGGC CCACCCCTGA 540
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TTACATTAAA GTTGCAAAAT TAAA

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Seq ID NO: B49 Protein sequence
Protein Accession #: BAB33378.1; CAB66517.1

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1 11 21 31 41 51
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APEAPATSAQ SQTGSPAQEA ATEGPSSACA FSQAPCAREV DANRPSTAFI QNDVDFDTQ 240
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Seq ID NO: B50 DNA sequence
Nucleic Acid Accession #: XM_084965.1
Coding sequence: 356..2014

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Seq ID NO: B51 Protein sequence
 Protein Accession #: XP_084965.1

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 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGGLILPGSL TASLECVKEE 240
 TPRAAREPEE PSQDAPRDPF GCGDIADQE EEAGPSCDKH VPGPGKPLS KKNPGVVAYQ 300
 GGGEEMASDP EVDDTYLQEF WDMLSQTEEQ GPPEQEGAAG VAAALETKVV PETPKDTRCV 360
 EAAKDASSVK RRRLLNRPIE PPKPEEPKHP EKEQEGVFN SDEGYWDSST GPPEEDSSSS 420
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Seq ID NO: B52 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..2016

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 GGGAAGATTA ATAAAGCTGC CTTCAAATTA TTCAAGAAGA GGAATTCGGG TGGCACCATG 240
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 CCCCCAGAG CCGCAGGGCC CGGCGGGGCC TCCCTCGCCA GCAGCTCGGT GGCCAAGTCG 480
 CACAGCTTCT TCTCGTGCT GAAGAAGAAC GGGCGCTCGG AAAACGGCAA GGGAGAGCCT 540
 GTGGAGCCGA CCAAGGCGCG CGGCAACAA AAGCGGGGGC TCGGGGGGCT GTTCAGCGGC 600
 ATGCGCTGGC ACAGGAAGA CAAGCGGGCC AAGCGGAGG CCGCGGAGG GCGCGCGCCC 660
 GGGGGCGGCT TGATCCTACC CGGCTCGCTC ACCGCCAGCC TGGAGTGCCT CAAGGAGGAG 720
 ACGCCCAGAG CCGCGCGCGA GCGGAGGAG CCCAGCCAGG ACGCCCGCG AGACCCAGCA 780
 GGTGAGCCCG CAGGGGGAGA GGAGGTGCCC GCCCCGCGG ACCGCGCCCC AGCGCGGAGC 840
 TGCCGAGAGG CAGAGGGCCT CGCGCACCCC GCGCACACCG GCGCCCGGG AGAGGACGCC 900
 GCGGGGCATC GGGCGGCCGA GCGGGGGCCC GGGGAGGTCC GCACGGCAGA GGACGCTTCC 960
 AGGACGGGG CCGTTCCTCGT AAAGACGGTC CCCCTTGTCT ACTCGAAGG CCGCAGCGGC 1020
 CGGGCGCCCG CCGCCCCAGA CCCTGCCTCT GTCGATCCAC CCTCAGACCC GTCGGCAGAT 1080
 CGTATTTGTT TGATGTTTTC TGACGTGACT TCACTGAAAA GCTTTGACTC TCTTACAGGC 1140
 TGTGGAGATA TTATTGAGA CCAAGAGGAA GAGGCAGGTC CCAGCTGTGA CAAGCATGTC 1200
 CCGGGGCCAG GCAAGCCGGC TCTGTCTAAA ATGAACCCCG CGCTGGTGGC CTACCAAGGA 1260
 GCGGGGAAG AGATGGCCAG CCGGACGAG GTGGACGACA CCTATCTACA GGAGTTCTGG 1320
 GACATGCTCT CCCAGACCGA GGAGCAGGGA CCCGAGCCCC AGGAGGGCGC GGTAAAGGTG 1380
 GCAGCTGCGC TGGAAACCAA GGTGTGCCCC GAGACCCCA AAGACACCAG GTGTGTGGAA 1440
 GCGGCCAAGG ACGCTCTCT GGTCAAGCGC AGGAGGCTCA ACCGATTCCT CATCGAGCCC 1500
 CATCTAAGG AGGAGCCCAA GCACCCGGAG AAGGAGCAGC AGGAAGGCGT CCCCAACAGC 1560
 GACGAGGGCT ACTGGGACTC CACCACGCCA GGCCAGAGG AAGACAGCTC GAGCAGCGGG 1620
 AAGAGGGCGG GCATCCCGCG GATAGCTAC AGCGGGGACG CGCTCTATGA TCTCTATGCT 1680
 GACCCGACG GAAGTCCAGC AACCTTCTCT GGAGGGAAGG ACAACGAGGA GACGTCTCTC 1740
 CTGTCCCGGT TAAAGCCCGT ATCTCCAGGC ACCATCACCT GTCCACTGCG AACACCAGGC 1800
 AGCTTGCTGA AGGACTCTAA GATCCCTATT AGCATCAAGC ACCTGACCAA CCTTCCATCT 1860
 AGCATCCCG TGGTGACCA GCAACCTTCC AGGAGTGAGA TGCCCAAGAA AAAAAATCCG 1920
 GTTTCCAAAG TGCTGGTCCG CAGAGTCAGC AACCGGGGCT TGGCTGGGAC CACCATCAGA 1980
 GCAACGGCCT GCCACGACAG TGCCAAAAAG TTGTGA

Seq ID NO: B53 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 METSRSRGGG GAVSERGGAG ASVGVCRRKA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60
 GKINKAAPFL FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120
 EEPRGGGDSG GGGGGRPNFG PPRAAGPGGG SLASSSVAKS HSFFSLKKN GRSENGKGE 180
 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGGLILPGSL TASLECVKEE 240
 TPRAAREPEE PSQDAPRDPF GEPAGGEEVP APADRAPARS CREAEGLAHP GDTGARGEDA 300

AGHRRRAEPGP GEVTRTAEDAS RTGAVPVKTV PLVDSEGGSG RAPAAPDPAS VDPPSDPSAD 360
 RICLMFSDVT SLKSFDSLTV CGDIIADQEE EAGPSCDKHV PGPCKPALSK KNPVVVAYQG 420
 GGEEMASPE VDDTYLQEFW DMLSQTTEEQ PEPQEGAANKV AAALETKVVP ETPKDRTRCVE 480
 AAKDASSVKR RRLNRIPIEP HPKEEPKHPK KEQQEGVPSN DEGYWDSTTP GPEDSSSSSG 540
 5 KAGIIPRDSY SGDRLVDLYA DPGSPATLP GGDNEETSS LSRLKPVSPG TITCPLRTPG 600
 SLLKDSKIPI SIKHLTNLPS SHPVVHQQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR 660
 ATACHDSAKK L

Seq ID NO: B54 DNA sequence
 Nucleic Acid Accession #: NM_014138.1
 Coding sequence: 60..854

1 11 21 31 41 51
 15 CTGCAGAGAC TTCCCAGGAA GTTCCAGCGC CCTCTCAGCC TTCTGACTCA GAACAGCCGA 60
 TGATGGGCCT CAGTAACCTG AGCCCCGGTC CTGGCCCCAG CCAGGCCGTG CCTCTCCAG 120
 AGGGGCTGCT CCGCCAGCGG TACAGAGAGG AGAAGACCCT GGAAGAGCGG CGGTGGGAGA 180
 GGCTGGAGTT CCTTCAGAGG AAGAAAGCAT TCCTGCGGCA TGTGAGGAGG AGACACCGCG 240
 20 ATCACAATGGC CCCTATGCT GTTGGGAGGG AAGCCAGAAT CTCCCCATTA GGTGACAGAA 300
 GTGAGAATCG ATTCCGATGT GAATGTCGAT ACTGCCAGAG CCACAGGCCG AATCTTTCTG 360
 GGATCCCTGG GGAGAGTAAC AGGGCCCCAC ATCCCTCCTC CTGGGAGACG CTGGTGACAG 420
 GCCTCAGTGG CTTGACTCTC AGCCTAGGCA CCAACCAGCC CGGCCCTCTG CCTGAAGCGG 480
 CACTCCAGCC ACAGGAGACA GAGGAGAAGC GCCAGCGAGA GAGGCAGCAG GAGAGCAAAA 540
 25 TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTG CACCCCCATG 600
 GGATGGAGAC CCGAAGGGAC TCAGACGGAG CCGCCGTGTT GGCAGCGCCT GGGTGTGGGC 660
 CCATTTTGGG GACCAACAG CAAGCTGTGG TCGGATGAGT GCCAGGACCT GTGTACCGGG 720
 ACACGTGGGA GTCTCTCCAG CATGATGCTT GACTGACCCG AGGAAGGTCC TCATGTTTCG 780
 TGCCTGTGAT TCTCGGATGG CTGTGAGGCA TTCCTTGGCA AGGGACGCTG CGTACCAGCG 840
 30 GTCCTCACCG CATCTCACAT GGCTCCTGTG ATGCATGTTG TCGCTTTCCC ACCCGGGATC 900
 TCCATCTCTC TTCCTTCTCT GCTGTCACTA AGAGATCACA TGCTGTGTGA GTGTGAATGC 960
 CTTGTGCGTG TCCTGTGCTT TTGCACCAAT GAGTTGACTG CCTCTGAGAA GCAGCACTAG 1020
 GCCTGTTGAA ATGCAATGTG CTGCCCTGAG ATCCAGTTTC AAGAATGGGC AGGTAAACGC 1080
 AGTTTGGGAA AGGAATGTGG AATGAGAACT TGGTGGTTCA CCGCTGTACT ATTTGTGTAA 1140
 35 ATGTTTACGT ATGTGATAAG CTACATGTAT GTAAATGTTG CAATACCCCT AACAGTCGAG 1200
 TAGTAGTCTC CCTTACAGGA ATTTTGTGACG GGGTTCCTCA TCATCAATAC CAAATAAATA 1260
 TATGTAGGAA TGGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1320
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 1380
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

Seq ID NO: B55 Protein sequence
 Protein Accession #: NP_054857.1

1 11 21 31 41 51
 45 MMGLSNLSPG PGPSQAVPLP EGLLRQRYRE EKTLEERRWE RLEFLQRKKA FLRHVRRRHR 60
 DHMAPYAVGR EARISPLGDR SQNRFRCECR YCQSHRPNLS GIPGESNRAP HPSSWETLVQ 120
 GLSGLTSLSG TNQPGPLPEA ALQPQETEEK RQRERQESK IMFQRLKQW LEEN

Seq ID NO: B56 DNA sequence
 Nucleic Acid Accession #: NM_000025.1
 Coding sequence: 198..1424

1 11 21 31 41 51
 55 GCTACTCCTC CCCAAGAGC GGTGGCACCG AGGGAGTTGG GGTGGGGGGA GGCTGAGCGC 60
 TCTGGCTGGG ACAGCTAGAG AAGATGGCCC AGGCTGGGGA AGTCGCTCTC ATGCCTTGCT 120
 GTCCCCCTCC CTGAGCCAGG TGATTTGGGA GACCCCTCTC TTCCTTCTTT CCTTACCGCC 180
 CCACGCGCGA CCGCGGGATG GCTCCGTGGC CTCACGAGAA CAGCTCTCTT GCCCATGGC 240
 CGGACCTCCC CACCCTGGCG CCCAATACCG CCAACACCAG TGGGCTGCCA GGGGTTCCGT 300
 60 GGGAGGCGGC CCTAGCCGGG GCCCTGCTGG CGCTGGCGGT GCTGGCCACC GTGGAGGCA 360
 ACCTGCTGGT CATCGTGGCC ATCGCCTGGA CTCGAGACT CCAGACCATG ACCAACGTGT 420
 TCGTGAATTC GCTGGCCGCA GCCGACCTGG TGATGGGACT CCTGGTGGTG CCGCGGCGCG 480
 CCACCTTGGC GCTGACTGGC CACTGGCCGT TGGGCGCCAC TGGCTGCGAG CTGTGGACCT 540
 CGGTGGACGT GCTGTGTGTG ACCGCCAGCA TCGAAACCCT GTGCGCCTG GCCGTGGACC 600
 65 GCTACCTGGC TGTGACCAAC CCGCTGCGTT ACGGCGCACT GGTCAACAAG CGTTCGCCCC 660
 GGACAGCTGT GGTCTCTGTG TGGGTCTGTG CGGCGCGGT GTGCTTTGCG CCAATCATGA 720
 GCCAGTGGTG GCGGTAGGG GCGGACGCG AGGCGCAGCG CTGCCACTCC AACCCGCGCT 780
 GCTGTGCTCT CGCCTCCAAC ATGCCCTACG TGCTGCTGTC CTCCTCGGTC TCCTTCTACC 840
 70 TTCCTCTTCT CGTGATGCTC TTCGTCTAGC CGCGGTTTTT CGTGGTGGCT ACGGCCAGC 900
 TCGCTTGTCT GCGCGGGGAG CTGGGCGGCT TTCGCCCCGA GGAGTCTCCG CCGGCGCGCT 960
 CGCGCTCTCT GCGCCCGGCC CCGGTGGGGA CGTGCCTCC GCCCGAAGGG GTGCCCGCCT 1020
 GCGGCGGCGC GCCCGCGCGC CTCCTGCCTC TCCGGGAACA CCGGCGCCTG TGACCTTGG 1080
 GTCTCATCAT GGGCACCTTC ACTCTCTGCT GGTGGCCCTT CTTTCTGGCC AACGTGCTGC 1140
 75 GCGCCCTGGG GGGCCCCCTC CTAGTCCCAG GCGCGGCTTT CTTGCCCCGT AACTGGCTAG 1200
 GTTATGCCAA TTCTGCCCTC AACCCGCTCA TCTACTGCGC CAGCCCGGAC TTTCGACGCG 1260
 CCTTCCGCGC TCTTCTGTGC CGCTGCGGCC GTGCTGCTGC TCCGGAGCCC TGCGCGCGCG 1320
 CCGCGCCGCG CCTCTTCCCC TCGGGCGGTC CTGCGGCCCG GAGCAGCCCA GCGCAGCCCA 1380
 80 GGCTTTGCCA ACGGCTCGAC GGGGCTTCTT GGGGAGTTTC TTAGGCTTGA AGGACAAGAA 1440
 GCAACCAACT TGTGTATCAG AACCTGTGGA AACCTCTGCT CCTCTGTTCA GAATGAGTCC 1500
 CATGGGATTC CCGGCTGTG AACTCTACCT CTCCAGAAC TGACGACTGG GCCATGTGAC 1560
 CCAAGGAGGG ATCCTTACCA AGTGGGTTTT CACCATCCTC TTGCTCTCTG TCTGAGAGAT 1620
 GTTTTCTAAA CCGGCGCTT GAACCTCACT CCTCCCTCAG TGGTAGTGTG CAGGTGCGCT 1680
 GGAGCAGCAG GCTGGCTTTG GTAGGGGAC CATCACCCG GCTTGCCTGT GCAGTCAGTG 1740
 AGTGCTTAGG GCAAGAGAG CTCCCTGCTT TCATTCCTT CTGCCACCCA AACCTGATG 1800

5 AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGGT AGAAAAGACC 1860
 AAGATTTGGG GTTTTATCTC TGGTTCCCTT ATTACTGCTC TCAAGCAGTG GCCTCTCTCA 1920
 CTTTAGCCAT GGAATGGCTC CGATCTACCT CACAGCAGTG TCAGAAGGAC TTCGCCAGGG 1980
 TTTTGGGAGC TCCAGGGTTC ATAAGAAGGT GAACCATTAG AACAGATCCC TTCTTTTCTT 2040
 TTTGCAATCA GATAAATAAA TATCACTGAA TGCAGTTCAT CCTCGGCCCA CTTTCCCTCC 2100
 GTTTGTTTTT TTTTCATAAT CCACTTACTC CTTTCCCTTC TACTCTGCGC TGGCTTTTGA 2160
 CAGAGGCAGT AAATTAGGCC TAATCCTCAC TCTTTTCTTC CTAATCTTCA TCAACAAAAA 2220
 AATGAAAAGT CTGCTGGGAC GAAGGGGAGT GAGCTTGAGC CTTTGATATC TTGCTCCCCC 2280
 10 ACCCTTCCCTG AAATCTCTGA AATCCAGTTG CCATTGAGTA GCAAAGCCAC GCTCCCCACA 2340
 GGACTTGGAC AGAGGGCCCA CAGGGGGATG GGCTGGCTGT GGCCAGGTTT AGGGCAGGGG 2400
 GCATTGTGCC CCTCCATGCT ATAATCCAGT GGTGCCCTTAC ATGGTGTGTG TGTGTGTGTG 2460
 TGCCTGTGTG TGTGTGTGTG TGTGTCTGGA GGCACAGGCA CAAAGCATTG CTTGGGTGG 2520
 TCAATGTCT TGTGTCTATA ATATATTCTG ATGTTTCCCA GCCTTCCAC AACCTCTACC 2580
 15 TTCCCACTCA CTTTCCCCAG CTACAAAAAT CTGTATTATC CTCTTAAAGT AAAACTGGAG 2640
 TTAC

Seq ID NO: B57 Protein sequence
 Protein Accession #: NP_000016.1

20 1 11 21 31 41 51
 MAPWPHENSS LAPWPDLPPL APNTANTSGI PGVPWEAALA GALLALAVLA TVGNNLLVIV 60
 AIAWTPRLQT MTNVFVTSIA AADLVMLLV VPPAATLALT GHWPLGATGC ELWTSVDVLC 120
 25 VTASITLCA LAVDRYLAVT NPLRYGALVT KRCARTAVVL VVVVSAAVSF APIMSQWVRV 180
 GADAEQRCH SNPRCCAFAS NMPYVLLSSS VSFYLLPLVM LFVYARVFFV ATRQLRLRLG 240
 ELGRFPPEES PAPRSRLAP APVGTCAPE GVPACGRRPA RLLPLREHRA LCTLGLIMGT 300
 FTLCWLPPFL ANVLRALGGP SLVPGPAFLA LNWLYANSA FNPLYCRSF DFRSAFRRL 360
 CRCGRRLPE PCAARPALE PSGVPAARSS PAQPRLCQRL DGASWGV

30 Seq ID NO: B58 DNA sequence
 Nucleic Acid Accession #: NM_032553.1
 Coding sequence: 37..1038

35 1 11 21 31 41 51
 CACCATTAGG CAAAGATAGT TTCTCTAGAG AGAATCATGC CTGCTAATTA CACGTGTACC 60
 AGGCCAGATG GAGACAATAC AGATTTTCGA TACTTTATTT ATGCAGTGAC ATACACTGTC 120
 ATTCTTGTGC CAGGTCTCAT AGGGAATATA TTAGCCCTGT GGGTATTCTA TGGTTATATG 180
 40 AAAGAAACAA AACGAGCTGT GATATTTATG ATAACTTAG CCATTGCTGA CTACTACAA 240
 GTTCTTTCTT TGCCACTGAG GATCTTCTAC TACTTGAATC ATGACTGGCC ATTTGGGCCT 300
 GGTCTCTGCA TGTCTGTTT CTACCTGAAG TATGTCAACA TGTATGCAAG CATCTACTTC 360
 TTGGTCTGCA TCAGTGTGCG ACGATTTTGG TTTCTCATGT ACCCCTTTCG CTTCATGAC 420
 TGCAACAGCA AATATGACCT GTACATCAGC ATTGCTGGCT GGCTGATCAT CTGCCTTGCC 480
 45 TGTGTACTCT TTCCACTCCT CAGAACCAGT GATGATACCT CTGGCAATAG GACCAAATGC 540
 TTTGTGGATC TTCTTACCAG GAATGTCAAC CTGGCCAGT CCGTGTGTAT GATGACCATT 600
 GGCAGTTTGA TTGGGTTTGT AACTCCGCTT CTGATTGTCC TATATTGTAC CTGGAAGACG 660
 GTTTTATCAC TGCAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC 720
 TTGAAGATGA TTCTAACCTG TGCAGGGGTA TTCTTAATTT GCTTTGCACC TTATCATTTT 780
 50 AGTTTTCTTT TAGATTTCTT GGTGAAGTCC AATGAAATTA AAAGCTGCCT AGCCAGAAGG 840
 GTGATTCTAA TATTCTATTC TGTGGCATTG TGTCTTGCTA GTCTGAATTC ATGTCTTGAC 900
 CCAGTCATAT ACTACTTTTC CACTAATGAG TTCCGAAGAC GGCTTTCAAG ACAAGATTG 960
 CATGACAGCA TCCAATCCCA TGCAAAATCC TTTGTGAGTA ACCATACAGC TTCCACCATG 1020
 ACACCTGAAT TATCTAAAAA CAAAAAACA AACTGAATGT GACCTGAAAT GCAAGTACAT 1080
 CAGAACATAT CTGCAATACC CAAGCCACAG GGAAGAACTT GCAAAACAAC ACAGCTTTTC 1140
 55 AGTTCGTCTC TATCTTACTG CTATGGGGAA TTCCTTCTT CAAAGCAGGA CCTATTTGGA 1200
 GCATTACGAT CCACGATTAT TGATGTTGAC ATGTCCATGT AGTAATTTTT CTTCAGT

60 Seq ID NO: B59 Protein sequence
 Protein Accession #: NP_115942.1

65 1 11 21 31 41 51
 MPANYTCTRP DGDNTDFRYF IYAVTYTVIL VPGLIGNILA LWVFYGYMKE TKRAVIFMIN 60
 LAIADLLQVL SLPLRIFYYL NHDWPFPGPL CMFCFYLYV NMYASIVFLV CISVRRFWFL 120
 MYPPRFHDCQ QKYDLYISIA GWLIICLACV LFPLLRSTDD TSGNRTKCFV DLPTNRNVLN 180
 QSVVMMTIGE LIGFVTPLLI VLYCTWKTIV SLQDKYPMAQ DLGEKQKALK MILTCAGVFL 240
 ICFAPYHFSF PLDFLVKSNE IKSCLARRVI LIFHSVALCL ASLNSCLDPV IYFSTNEFR 300
 RRLSRQDLHD SIQLHAKSFV SNHTASTMTF ELC

70 Seq ID NO: B60 DNA sequence
 Nucleic Acid Accession #: CAT cluster

75 1 11 21 31 41 51
 GATTCGGATT TTAATCCGAC TCACTATAGG GAATTTTGGC CCTCGAGGCC AAGAATTCGG 60
 CCGAGGGT AGACATTTAA CTTGAGTCTT TTCATATCAC GGTATGCTTT TATTTTACCC 120
 TCATATATAA TTAATTTTCA TCTGGGCATA TATTTCCAGA TTAGAAATCA TTTCTTTTCA 180
 TACATTTTAA GGAATTTATA CATTTGCATC TGAAATTTGA TTCATTATCT TCTAGAAACC 240
 80 AAGAGTGGAC TTGGTATCCG TCTGATTATA TTTTCTTTGT TGGTAAAGAG CCTCTTTTTC 300
 CCCTTTTAT TTTCACTCTC TCTTCTCTA GTGTTTATAA TCTTATTTT ATGAATGTAG 360
 TCTAATTATT TAGAACACTG TCTCCAGTA TGTGTTTATT TGGGTTGTG TTTTGAACAT 420
 TGCTCCAGG TCGAGTTTAA TGTGTGTTA TGTTCCTAT TTGAGGTGG ACACTTAGAA 480
 AATTTTCTCA ATTCGAAAAC TATTTTCTCT CAGCACTCAG AAATTTTAT CAAAGATTAT 540
 TTCCACGATT ATTTCTGTCT CTGGTTTTTC CGTGTCTTA ACCTAGAATT CAATTGTTA 600

ATGTTAGACC TTACACATCT TCAATGTATC ATATATATTT CACTCATATT ATTTATTGTC 660
 ATATCTTTTG GACTATTGTG TGAAAGCAAT AAATGTATAT TACTTTAAAA AAAAAAATAA 720
 AAAACTHCAAT TTTCAAATTT AATACACACA AATTGTGCAT ACCCACACAC ATATACCACA 780
 GATATATTCA TTTTCAGGAT TTCTTTAAAG GTTATTTTAA AAATAATCAT ATTCTTATTT 840
 TGTGAACGTG GGGATTCTCT GAAACTTTT GAAAACTCTC ATTAGTCTGT GTTTGTGTGG 900
 TTTCTTTAAA TTATCTCTTC CTTCAGAATT ACTTTTGTGT TTTGAATTG AGTCTTTGCC 960
 ATTCATAAGG CGGGCTTTCC TTGAATACCA GATAACTCTG AGTTTCTGT TCATATTTAA 1020
 GAATAAATAA CTAATTTGA AAAAAAATAA AAAAA

Seq ID NO: B61 DNA sequence
 Nucleic Acid Accession #: NM_014522.1
 Coding sequence: 846..3911

15 1 11 21 31 41 51
 CTGGTGGTCC AGTACCTCCA AAGATATGGA ATACACTCCT GAAATATCCT GAAAACTTTT 60
 TTTTTCAGCA ATCCTTTAAT AAGCAGTTAT GTCAATCTGA AAGTTGCTTA CTGTACTCTT 120
 ATATTAATAG CTATTCCTGT TTTCTTATC CAAAGAAAAA TCCTCTAATC CCCTTTTCAC 180
 ATGATAGTTG TTACCATGTT TAGGCATTAG TCACATCAAC CCCTCTCCTC TCCCAAACTT 240
 CTCTCTTCA AATCAAACCT TATTAGTCCC TCCTTTTATA TGATTCTCTG CCTCGTTTTA 300
 TCCAGATCAA TTTTTCCTCA CTTTGATGCC CAGAGCTGAA GAAATGGACT ACTGTATAAA 360
 TTATTCATTG CCAAGAGAAT AATTGCATT TAAACCCATA TTATAACAAA GAATAATGAT 420
 TATATTTTGT GATTGTGAAC AAATACCCCT TATTTCCCTT TAACATTGA ATTAAATATT 480
 TTAATTTTGT GTATCTCTTT TAACATCTTT GGTATATTAA AGTATTATCT TTTATATATT 540
 TATCAATGGT GGACACTTTT ATAGGTACTC TGTGTCAATT TTGATACGT AGGTATCTTA 600
 TTTCAATTAT CTTTATCTTT AATGTACGAA TTCATAATAT TTGATTGAGA ACAAAATTAT 660
 CACTAATTAA CAGAGTGTCA ATTATGCTAA CATCTCATT ACTGATTTTA ATTTAAACA 720
 GTTTTGTGTA ACATGCAATG TTAGGGTTGG CTTCTTAATA ATTTCTCTCT CCTCTCTCT 780
 CTCTCTCTCT CTTTGGTCCA GTGTGTGCG GGTAAATACA ACAAACTGTA ACAAGTGTAC 840
 CTGGTATGGA CTTGTGTGCC GGGACGTACA TTTTCGCGGT CCTGCTAGCA TGCGTGGTGT 900
 TCCACTCTGG CGCCAGGAG AAAAACTACA CCATCCGAGA AGAAATGCCA GAAAACGTCC 960
 TGATAGGCGA CTTGTGTAAG GACCTTAAC TGTGCTGAT TCCAAACAAG TCCTTGACAA 1020
 CTGCTATGCA GTTCAAGCTA GTGTACAAGA CCGGAGATGT GCCACTGATT CGAATTGAAG 1080
 AGGATACCTG TGAGATCTTC ACTACTGGCG CTCGCATTGA TCGTGAGAAA TTATGTGCTG 1140
 GTATCCCAAG GGATGAGCAT TGCTTTTATG AAGTGGAGGT TGCCATTTTG CCGATGAAA 1200
 TATTAGACT GGTTAAGATA CGTTTCTGTA TAGAAGATAT AAATGATAAT GCACCATTGT 1260
 TCCAGCAAC AGTTATCAAC ATATCAATTC CAGAGAACTC GCCTATAAAC TCTAAATATA 1320
 CTCTCCAGC GGCTGTTGAT CCTGACGTAG GAATAAACGG AGTTCAAAC TACGAACATA 1380
 TTAAGAGTCA AAACATTTT GGCCTCGATG TCATTGAAAC ACCAGAAGGA GACAAGATGC 1440
 CACAACGTAT TGTTCAAAAG GAGTTAGATA GGGAAGAGAA GGATACCTAC GTGATGAAAG 1500
 TTAAGGTGTA AGATGGTGGC TTCTCTCAA GATCCAGTAC TGCTATTTTG CAAGTGAGTG 1560
 TTAAGGTGTA AGATGGTGGC TTCTCTCAA GATCCAGTAC TGCTATTTTG CAAGTGAGTG 1620
 TTAAGGTGTA AGATGGTGGC TTCTCTCAA GATCCAGTAC TGCTATTTTG CAAGTGAGTG 1680
 CAGAAAATGC TCCTGTAGGC ACTTCAGTGA CACAGCTCCA TGCCACAGAT GCTGACATAG 1740
 GTGAAAATGC CAAGATCCAC TTCTCTTTCA GCAATCTAGT CTCCAACATT GCCAGGAGAT 1800
 TATTTCACTT CAATGCCACC ACTGGACTTA TCACAATCAA AGAACCCTG GATAGGGAAG 1860
 AAACACCAA CCACAGTTA CTGGTTTGG CAAGTATGAG TGGATGATG CCAGCAAGAG 1920
 CAATGGTGCT GGTAAATGTT ACAGATGTCA ATGATAATGT CCCATCCAT GACATAAGAT 1980
 ACATCGTCAA TCCTGTCAAT GACACAGTTG TTCTTTCAGA AAATATTCCA CTCAACACCA 2040
 AAATGCTCT CATAACTGTG ACGGATAAGG ATCGGACCA TAATGGCAGG GTGACATGCT 2100
 TCACAGATCA TGAATCCCTT TTCAGATTAA GGCCAGTATT CAGTAATCAG TTCTCTCTGG 2160
 AGACTGCAGC ATATCTTGAC TATGAGTCCA CAAAAGAATA TGCCATTAAA TTAAGTGGCTG 2220
 CAGATGCTGG CAAACCTCCT TTGAATCAGT CAGCAATGCT CTTATCAAAA GTGAAAGATG 2280
 AAAATGACAA TGTCTCAGTT TTCACCCAGT CTTTCGTAA TGTGTTCTAT CTGAGAAATA 2340
 ACTCTCTCTG CATCCAGTTG AGGAAAGTAA GTGCAATGGA TGCAGACAGT GGGCCTAATG 2400
 CTAAGATCAA TTACTGTCTA GGCCTGATG CTCACCTGA ATTCAAGCTG GATTGTCTGA 2460
 CAGGCATGCT GACTGTAGTG AAGAACTAG ATAGAGAAAA AGAGGATAAA TATTTATTCA 2520
 CAATCTCTGG AAAAGATAAC GGGGTACCAC CCTTAACCAG CAATGTCAAC GTCTTTGTAA 2580
 GCATTATTGA TCAGAAATGAC AATAGCCAG TTTTCACTCA CAATGAATAC AACTTCTATG 2640
 TCCAGAAAA CCTTCCAGG CATGGTACAG TAGGACTAAT CACTGTAACT GATCCTGATT 2700
 ATGGAGACAA TTTGTCAGTT ACGCTCTCCA TTTTAGATGA GAATGATGAC TTCACCATG 2760
 ATTACAAAC TGGTGTATC CGACCAATA TTTCAATTGA TAGAGAAAA CAAGAATCTT 2820
 ACACCTTTCTA TGTAAAGGCT GAGGATGGTG GTAGAGTATC ACGTTCTTCA AGTGCCAAAG 2880
 TAACCATAAA TGTTGTTGAT GTCAATGACA ACAAAACAGT TTTCAATTGTC CCTCCTTCCA 2940
 ACTGTTCTTA TGAATTGGTT CTACCGTCCA CTAATCCAGG CACAGTGGTC TTTCAAGTAA 3000
 TTGCTGTTGA CAATGACATG GGCATGAATG CAGAGGTTCTG TTACAGCATT GTAGGAGGAA 3060
 ACACAAGAGA TCTGTTTGA ATCGACCAAG AAACAGGCAA CATAACATTG ATGGAGAAAT 3120
 GTGATGTTAC AGACCTTGGT TTACACAGAG TGTGTTGCAA AGCTAATGAC TTAGGACAGC 3180
 CTGATCTCT CTTCAGTGTG GTAATTGTCA ATCTGTTCTG GAATGAGTCTG GTGACCAATG 3240
 CTACACTGAT TAATGAACTG GTGCGCAAAA GCACGTGAAGC ACCAGTGACC CCAATACTG 3300
 AGATAGCTGA TGTATCTTCA CCAACTAGTG ACTATGTCAA GATCCTGTTT GCAGCTGTTG 3360
 CTGGCACCAT AACTGTCGTT GTAGTTATTT TCATCACTGC TGTAGTAAAG TGTGCGCCAG 3420
 CACCACACCT TAAGGCTGCT CAGAAAAACA AGCAGAAATC TGAATGGGCT ACCCCAAACC 3480
 CAGAAAAAGC GCAGATGATA ATGATGAAGA AAAAGAAAA GAAGAAGAAG CATTCCCCCTA 3540
 AGAATCTGCT GCTTAATTTT GTCATATTG AAGAAACTAA GGCAGATGAT GTTGACAGTG 3600
 ATGGAACAG AGTCACACTA GACCTTCTTA TTGATCTAGA AGAGCAACA ATGGGAAAGT 3660
 ACAATTGGGT AACTACACCT ACTACTTTCA AGCCGACAG CCCTGATTG GCCGACACT 3720
 ACAATCTGC CTCTCCACAG CCGCTCTCC AAATTCAGCC TGAACCTCCC CTGAATTCGA 3780
 AGCACCACAT CATCAAGAA CTGCTCTCG ATAACACCTT TGTGGCCTGT GACTCTATCT 3840
 CCAAGTGTTC CTCAAGCAGT TCAGATCCCT ACAGCGTTTC TGACTGTGGC TATCCAGTGA 3900
 CGACCTTCGA GGTACCTGTG TCCGTACACA CCAGACCGGT AGGTATCCAA GTTCTAACA 3960
 CAACTTTCTA ACTATTTTTT TATTATTATT TTCAGTTGAT GTAGAATTT ACAAAATCTA 4020
 TTGACTTCAA AGAGGGATCA AAACAATCAT ATTCTACAGA TGTACCCAAT AGATATATGG 4080
 ATTCAATTAA GTTTGTGAGA AGATGAGAAC AAAATAACTA CTGATTTAGG AAAATGGAT 4140
 GCAGAATAAT AATTATAGTA GGGGCAATTT TGTCTGTAGA TGGCAGTATG ACAATCTTG

CTAGAGAATA TATTGAAAAA AACTTCAACA CAAAGGGTTG TAGCACTGTC CTCAGTACCA 4200
 TTGTGTGCAT GAGGATCAGA ATAGTCTGGG CTAGATACAT CACATTAAAG CTTTTCAGAA 4260
 TCTGATAAAT AGCTCTAAAT ACTAATGATA TTGACAAGCC TAGCTTCACT TGGGAAAATC 4320
 TGTGGCTGTT CACAGAAATT CAGCACCAAG TTATTCCCC CATACTCTAC CAGGCTTCA 4380
 GGTCTCATA AAGAAAAGTG TCGTTTTT CAG ATTAGGAAC CAAAATTATT TTGGTGATC 4440
 AAATCTACAG TCACACAATA TAACAAGAA GGGATTAGAA AAATGAAAGC CTAATCATTC 4500
 TCATCTTTAA GCCAGAGAAT GAAATATATA TGAGGTCTCT GGATAGCTAT TTAATATTTT 4560
 GCATATTTTAT GCAAGGTATT TTGAGCCCTT CAGAAGACAT TCT

Seq ID NO: B62 Protein sequence
 Protein Accession #: NP_055337.1

1 11 21 31 41 51
 15 MDLLSGTYIF AVLLACVVFH SGAQEKNYTI REEMPENVLI GDLLKDLNLS LIPNKSLLTA 60
 MQFKLVYKTG DVPLIRIEED TGEIFTTGAR IDREKLCAGI PRDEHCFYEV EVAILPDEIF 120
 RLVKIRFLIE DINDNAPLEFP ATVINISIEP NSAINSKYTL PAAVDPDVGI NGVQNYELIK 180
 SQNIFGLDVI ETPEGDKMPQ LIVQKELDRE EKDTYVMKVK VEDGGFPQRS STAILQVSVT 240
 20 DTNDNHPVFK ETEIEVSIPE NAPVGTSTVQ LHATDADIGE NAKIHFSFSN LVSNIARRLF 300
 HLNATTGLIT IKEPLDREET PNHKLVLVAS DGGLMPARAM VLVNVDVDND NVPSIDIRYI 360
 VNPVNDTVVL SENIPLNTKI ALITVTDKDA DHNGRVTCTF DHEIFPRLRP VFSNQFLLT 420
 AAYLDYESTK EYAIKLLAAD AGKPLPNQSA MLFIKVDEN DNAPVFTQSF VTVSIPENNS 480
 PGIQLTKVSA MDADSGFNK INYLLGPDAP PEFSLDCRTG MLTVVKKLD R EKDYLFTI 540
 25 LAKDNGVPPL TSNVTVFVSI IDQNDNSPVF THNEYNFYVP ENLPRHGTVG LITVTDPDYD 600
 DNSAVTSLIL DENDDFTIDS QTGVIRPNIS PDREKQESYT FYVKAEDGGR VSRSSSAKVT 660
 INVVDVNDNK PVFIIVPPSN SYELVLPSTN PGTVVQVIA VDNDTGMNAE VRYISIVGGNT 720
 RDLFAIDQET GNITLMEKCD VTDLGLHRLV VKANDLGQPD SLFVSVIVNL FVNESVTNAT 780
 LINELVKRSK EAPVTPNTEI ADVSPTSDY VKILVAAVAG TITVVVVIPI TAVVRCRQAP 840
 30 HLKAAQKNQK NSEWATPNPE NRQIMMKKK KKKKKHSPKN LLLNFVTIEE TKADDVSDG 900
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Seq ID NO: B63 DNA sequence
 Nucleic Acid Accession #: XM_059180.2
 Coding sequence: 276..3740

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 GCCGCTAGC GAGCCTGCGC GTCGACCCCA GCCAGCGCAG CGACGGGGCG CTGCGTGGCC 180
 CAGGCGCACA CGGAAGTGCG CTTCTCTGAA GTAGCTTTGG AAAGTAGAGA AGAAAATCCA 240
 45 GTTGTCTTCT TGGAGAACAC TGGACAGCTG AATAAATGCA GTATCTAAAT ATAAAAGAGG 300
 ACTGCAATGC CATGGCTTTC TGTGCTAAAA TGAGGAGCTC CAAGAAGACT GAGGTGAACC 360
 TGGAGGCCCC TGAGCCAGGG GTGGAAGTGA TCTTCTATCT GTCGGACAGG GAGCCCTTCC 420
 GGTGGGCGAG TGCAGATGAC ACAGCAGAGG AACTGTGCAT CAGGGCTGCA CAGGCATGCC 480
 GTATCTCTCC TCTTTGTGAC AACCTCTTTG CCTGTATGA CGAAGAACACC AAGCTCTGGT 540
 50 ATGCTCCAAA TCGCACCATC ACCGTTGATG ACAAGATGTC CCTCCGGCTC CACTACCGGA 600
 TGAGGTTCTA TTTACCAAT TGGCATGGAA CCAACGACAA TGAGCAGTCA GTGTGGCGTC 660
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 60 CCATGTTACT GATTTCAATG GAAAATGAGA TGAATTGGTT TCATTCGAAT GACGGTGGAA 1200
 ACCTTCTCTA CTACGAAGTG ATGGTGACTG GGAATCTTGG AATCCAGTGG AGGCATAAAC 1260
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 TCCCTGAAAT CACTCACATT GTAATAAAGG AGTCTGTGGT CAGCATTAAAC AAGCAGGACA 1440
 65 ACAAGAAAAT GGAAGTGAAG CTCTCTTCCC ACGAGGAGGC CTTGTCTCTT GTGTCCCTGG 1500
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 70 AGGGTGCCCA GAAGCAGTTC AAGAACTTTC AGATCGAGGT GCAGAAGGGC CGTACAGTC 1800
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 75 TTGGGAGAGG CACGAGAACA CACATCTATT CTGGGACCTT GATGGATTAC AAGGATGACG 2100
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 ACATCGTGTG CCTCTATGCG GTCTGTGTCC GCGACGTGGA GAATATCATG GTGGAAGAGT 2280
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 80 CATGGAATTT CAAAGTTGCC AAACAGCTGG CAGTGGCCCT GAGCTACTTG GAGGATAAAG 2400
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 ATGGCGAGAT CCCCTTGAAA GACAAGACGC TGATTGAGAA AGAGAGATT TATGAAAGCC 2700

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GGTGCAGGCC AGTGACACCA TCATGTAAGG AGCTGGCTGA CCTCATGACC CGCTGCATGA 2760
ACTATGACCC CAATCAGAGG CCTTCTTCC GAGCCATCAT GAGAGACATT AATAAGCTTG 2820
AAGAGCAGAA TCCAGATATT GTTTCAGAAA AAAAACCAGC AACTGAAGTG GACCCACAC 2880
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TTGAGCTCTG CAGGTATGAC CCGAAGGGG ACAATACAGG GGAGCAGGTG GCTGTTAAAT 3000
CTCTGAAGCC TGAGAGTGGG GGTAAACCACA TAGCTGATCT GAAAAAGGAA ATCGAGATCT 3060
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TCCTTGTGTA GAGTGAACAC CAAGTAAAA TTGGAGACTT CGGTTTAACC AAAGCAATTG 3360
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TGGTCTTACA TGGGGGGATA GCTGTGGAAT AGATAATTG CTGCATGTTA ATTTCTCAAGA 4440
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GATCCCTGTT TTTACCATCA ATCATCACCC TGTGGTGCAC CACTTGAAAG ACCCGGCTAG 4740
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AGCCTACATC ACCAAGGCT CTGTGTCAA CCTGTGGCCA CTCTATATGC ACTTTGTTTA 5040
CTCTTTATAC AAATAAATAT ACTAAAGACT TT

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Seq ID NO: B64 Protein sequence

Protein Accession #: A39577

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1 11 21 31 41 51
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DNEQSVWRHS PKKQKNGYEK KKIIPDATPLL DASSLEYLFA QQGYDLVKCL APIRDPKTEQ 180
DGHDIENECL GMAVLAISHY AMMKMQLPPE LPKDISYKRY IPETLNKSIR QRNLTRMRI 240
NNVFKDFLKE FNNKTTCDSS VSTHDLKVKY LATLETTLKH YGAEIFETSM LLISSENMEN 300
WFHSNDGGNV LYIEVMVTGN LGIQWRHKPN VVSVEKEKNK LKRKKLENKD KKDEEKNKIR 360
EENNNFSFPF EITHIVIKES VVSINKQDNK KMEKLSSHE EALSFSVSLVD GYFRLTADAH 420
HYLCTDVAPP LIVHNQNGC HGPICTEYAI NKLRQEGSEE GMYVLRWST DFDNIMLMTVT 480
CFEKSEQVQG AQKQFNFIQI EVQKGRYSLH GSDRSFSLG DLMSHLKKQI LRTDNISFML 540
KRCCQPKPRE ISNLLVATKK AQEWQPVYPM SLSFDRILK KDLVQGEHLG RGTRTHIYSG 600
TLMDDYKDEG TSEKKIKVI LKVLDPShRD ISLAFEEAAS MMRQVSHKHI VYLGVVCVRD 660
VENIMVEEFV EGGPLDLFMH RKSDVLTTPW KFKVAKQLAS ALSYLEDKDL VHGNVCTKNL 720
LLAREGIDSE CGPFIKLSDP GIPITVLSRQ ECIERIPWIA PECVEDSKNL SVAADKWSFG 780
TTLWEICYNG EIPLKDKTLI EKERFYESRC RPTVPSCKEL ADLMTRCMNY DPNQRPFRA 840
IMRDINKLEE QNPDIYSRKK NQPTVEDPTH FEKRFLKRIR DLGEGHFGKV ELCRYDPEDN 900
TGEQVAVKSL KPESGGNHIA DLKKEIILR NLYHENIVKY KGICTEDGGN GIKLIMEFLP 960
SGSLKEYLPK NKNKINKLQQ LKYAVQICKG MDYLGSRYV HRDLAARNVL VESEHQVKIG 1020
DFGLTKAIET DKEYYTVKDD RDSPVFWYAP ECLMQSKFYI ASDVWSFGVT LHELLTYCDS 1080
DSSPMALFLK MIGPTHGQMT VTRLVNTLKE GKRLPCPPNC PDEVYQLMRK CWFEPQSNRT 1140
SFQNLIEGFE ALLK

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Seq ID NO: B65 DNA sequence

Nucleic Acid Accession #: NM_004867.1

Coding sequence: 140..931

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CGCAGCCCGA AGATTCACTA TGGTGAAAAT CGCCTTCAAT ACCCCTACCG CCGTGCAAAA 180
GGAGGAGGCG CGGCAAGACG TGGAGGCCCT CCTGAGCCGC ACGGTCAAGG CTCAGATACT 240
GACCGGCAAG GAGCTCCGAG TTGCCACCCA GGA AAAAGAG GGCCTCTCTG GGAGATGTAT 300
GCTTACTCTC TTAGGCCTTT CATTCTCTT GGCAGGACTT ATTGTTGGTG GAGCCTGCAT 360
TTACAAGTAC TTCATGCCCA AGAGCACCAT TTACCGTGGG GAGATGTGCT TTTTGTATTC 420
TGAGGATCCT GCAAAATCCC TTCGTGGAGG AGAGCCTAAC TTCCTGCCTG TGACTGAGGA 480
GGCTGACATT GCTGAGGATG ACAACATTGC AATCATTTGAT GTGCCTGTCC CCAGTTTCTC 540
TGATAGTGAC CCTGCAGCAA TTATTCATGA CTTTGAAAAG GGAATGACTG CTTACCTGGA 600
CTTGTGCTG GGAACATCT ATCTGATGCC CCTCAATACT TCTATTGTTA TGCCTCCAAA 660

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AACTCTGGTA GAGCTCTTTG GCAACTGGC GAGTGGCAGA TATCTGCCTC AACTTATGT 720
 GGTTCGAGAA GACCTAGTTG CTGTGGAGGA AATTCGTGAT GTTAGTAACC TTGGCATCTT 780
 TATTACCAA CTTTGCATA ACAGAAAGTC CTTCCGCCTT CGTCGCAGAG ACCTCTTGCT 840
 GGGTTTCAAC AAACGTGCCA TTGATAAATG CTGGAAGATT AGACACTTCC CCAACGAATT 900
 TATTGTTGAG ACCAAGATCT GTCAAGAGTA AGAGGCAACA GATAGAGTGT CCTTGGTAAT 960
 AAGAAGTCAG AGATTTACAA TATGACTTTA ACATTAAGGT TTATGGGATA CTCAAGATAT 1020
 TTACTCATGC ATTTACTCTA TTGCTTATGC CGTAAAAAAA AAAAAAAAAA AAAAAAAAAA 1080
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Seq ID NO: B66 Protein sequence
 Protein Accession #: NP_004858.1

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MVKIAFNTPT AVQKEEARQD VEALLSRTVR TQILTGKELR VATQEKEGSS GRCLMTLLGL 60
 SFILAGLIVG GACIYKYFMP KSTIYRGEMC FFDSEDPANS LRGGEPNPLP VTEADIRE 120
 DNIAIDIVFV PSFSDSDPAA IHDPEKGMT AYLDLLLGNC YLMPINTSIV MPPKNLVLELF 180
 GKLAGSRVLP QTYVUREDLV AVEEIRDVS N LGIFYQLCN NRKSFRLRRR DLLLGFNKRA 240
 IDKCKIRHF PNEFIVETKI CQE

Seq ID NO: B67 DNA sequence
 Nucleic Acid Accession #: XM_083862.1
 Coding sequence: 121..813

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ACGCGGGAGG TCTGAGCTGT GGGCTGAGGC AGCGCAGCCG CTGCGCCAGG GTGCGCGATG 60
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 ATGGGACAGC AAATTTCCGA TCAGACACAG TTGGTTATTA ACAAGTTACC AGAAAAAGTA 180
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Seq ID NO: B68 Protein sequence
 Protein Accession #: XP_083862.1

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MGQQISDQIQ LVINKLPKPV AKHVLVRES GSLTYEEFLG RVAELNDVTA KVASGQEKHL 60
 LFEVQPGSDS SAFKVVVVR VCTKINKSSG IVEASRIMNL YQFIQLYKDI TSQAAGVLAQ 120
 SSTSEEPDEN SSVVTSQAS LWMGRVKQLT DEBECCICMD GRADLILPCA HSFQCKCIDK 180
 WSDRRHNCPI CRLQMTGANE SWVSDAPTE DDMANYILNM ADEAGQPHRP

Seq ID NO: B69 DNA sequence
 Nucleic Acid Accession #: NM_002975.1
 Coding sequence: 180..1151

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Seq ID NO: B70 Protein sequence
Protein Accession #: NP_002966.1

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MQAAWLLGAL VVPQLLGFGH GARGAEREWE GSWGGAQEEE REREALMLKH LQEALGLPAG    60
RGDENPAGTV EGKEDWEMEE DQEEEEEEEA TPTPSSGSPS SPTPEDIVTY ILGRLAGLDA    120
10     LRLGHLVRLH ALDTRVVELT QGLRQLRNAA GDTRDAVQAL QEAQGRAERE HGRLEGCLKG    180
      LRLGHKCFLL SRDFEAQAAA QARCTARGGS LAQPADRQQM EALTRYLRAA LAPYNWPVWL    240
      GVHRRRAEGL YLPENGQRVS FFAWHRSRPR ELGAQPSASP HPLSPDQPNG GTLENCVAQA    300
      SDDGSWWDHD CQRRLYVCE FPF

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Seq ID NO: B71 DNA sequence
Nucleic Acid Accession #: BC000839.1

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15     1      11      21      31      41      51
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CTGGCCAGGG CGACTGGCGG ATAAGGTCTT GTGCGTGGCC TCGAGGCTTA AAAGTAGCAG    60
20     TGGGGCTTTG TGAAGGACAA AATGGCGATG GCGGGCCGTG TAGGTCCCCC TTCCTATGAT    120
      GAGGACCTTT TCACAGACCT GTACTGAGCT CCGTGAGGAT AAGTAACTCT GAGGAGATGG    180
      GCCCTGCAAG CCTCCTTCTT AGCCGTCTGT TCAGAAAATA GCGTTTTCGA AATGCCCTGA    240
      GTTGACCTAA TGTCTTATTG GGCTCCTGTC TGCAGGATT TACGCGCAGT TGAACCGGAA    300
      GAGAGCTCTG TTGTTGCAAT GTTCAGCCCA CAAGAGCTTA CTGGTGAAGG AATGGGACAA    360
25     GACCCATCTT TATGCAAAAG CAGCGTTACA GTAATGTTC AGCATCTCAT AATCTATCCT    420
      GGGGAATTCA GCTGCTCCCC AGGGTGAATA CAGGTATTCC TGATGACAGT CTGCCTCTAT    480
      CTTACAGAGC AGCTTGTTCG TATATACCAT TGAAAAGCCT TCAGAGCTGA GAGGTACTAC    540
      TAACCAATAA CCTGCTTGGC TCAAAAGGCC AGCACCTTCT CTCTAAAGCC CAAGAGGAGT    600
      TTGAGGAAAA CTAGGTGTCT GTGTTCACTC CAGGCTGAAG TTACAGGTCT GAGCAAAATA    660
30     GGTGTATAAA AAATGGAATC TGTCTTGGAG GACATCAGAA GGTGAATTTT CCAAGTTCTT    720
      GGCAACCTTA GCTGTTGAAA AGCTTTCCTG GTTTGGGGGG TATTTGAGAT GTACCTTAAA    780
      GTGTTAGCAG ATACAGATTA AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGGTTTGCT    840
      GTGTATCACA TTCTCTGAT TATCACCCTC CTCTCTGCAA CATTATTTAT CTGGAATCTA    900
      CCTGCCCTTT TGTGTTTTAG ATACAAGGGC TTGGTTTTGT TACCCAGGCT GGTTCACAGG    960
35     CCATAGCTTT AAGAGATCCT CTCACCACAG ATTTCCAAAG TGCTGGGATT GCAGGTGTGA    1020
      TTCATGGCAC CCAGACTTTG CTGCTTTTCT TACATGATCC AGGCCACAGAA CCCAACTCA    1080
      GGCACGTGAT AGATGACCAC TTTCGTAAAC TACTGACCTA GCTTGTGCCC AATTGTTGAT    1140
      TGAACCTCCC ATAACCTCAC TTGCTGTCTG TTCTCTGTA TACAGCCACC TTCTGTTCCT    1200
      GTCATGAGCC TTTAGGTCTC CATTGTCATA TTGCAAATAC TATGTTCCAT GTAGGTAGCT    1260
40     CATTGAGGGC CTTGCTCTTC ACTTCAAAAA AGGTTCCCTT GAGGACTGGC TGTCATTTTG    1320
      TGTTGCTGTG TTGGTTGTTG ATGAAAATAA TAAATGATT GATTACATAA AAAAAAAAAA    1380
      AAAAAAA

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Seq ID NO: B72 DNA sequence
Nucleic Acid Accession #: CAT cluster

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TGCTAGTAGG GCCTGGGTTA ATCGGCCGAG GGTGGCTTCG TGGTCTTTAT AGCTGTTACT    60
50     CTTTGTACTT GTCTTTTCT TTTATTTCT TTTGAGCGAT TGTGCGAACA TAGCATAGCA    120
      CGCACTATGG CAGCAGGCTC GTGCTGCTCG GCCAGGGCGA CTGGCCGATA AGGTCTTGTG    180
      CGTGGCCTCG AGGCTTAAAA CTATGATGAG GACCTTTTCA CAGACCTGTA CTGAGCTCCG    240
      GGCCGTGTAG GTCCCTCTTC GATGATGGCC CTGCAAGCCT CTTGCTTAGC CGTCTGTCTA    300
55     TGAAGATAAA TAACTCTGAG GAGATGGGCC CTGCAAGCCT CTTGCTTAGC CGTCTGTCTA    360
      GAAAATAGCG TTTTCGAAAT GCCCTGAGTT GACCTAATGT CTTATTGGGC TCCTGTCTGC    420
      AGGATTTACG CGCACGTGGG AACCGAAGAG AGCTCTGTTG TTGCAATGTT CAGCCACAAA    480
      GAGCTTACTG GTGAAGGAAT GGGACAAGAC CCACTTTTAT GCAAGCCAG CGTTACAGTA    540
      ATGTTCCAGC ATCTCATAAT CTATCCTGGG GAATTCAGT GCCTCCAGG GTGAATACAG    600
      GTATCTCTCA TGACAGCTCG CCTCTATCTT ACAGAGCAGC TTGTTGCTAT ATACCATTGA    660
60     AAAGCCTTCA GAGCTGAGAG GTACTACTAA CCAATAACCT GCTTGGCTCA AAGGGCCAGC    720
      ACCTTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAACCT GGTGCTGTG TCACTCCAG    780
      GCTGAAAGTA CAGGTCTGAG CAAATAAGGT GTATAAAAAA TGGAACTGTT CTTGGAGGAC    840
      ATCAGAAGGT GAATTTTCCA AGTTCTTGGG CAACCTAGCT GTTGAAAAGC TTTCTGGGTT    900
      TGGGGGGTAT TTCAGATGTA CCTTAAAGTG TTAGCAGACA CAGATTAAGA CACTGGGAGC    960
65     CAATGAAACA GCAGTTGAGG GTTTGCTGTG TATCACATTT CTGTATTTTA TCACCCCTTT    1020
      CCTGCAACAT TATTTATCTG GAATCTACCT GCCCTTTTGT TTTTGTAGATA CAAGGGCTTG    1080
      GTTTTGTGTT CCAGGCTGGT TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGATT    1140
      TCCAAAGTGC TGGGATTGCA GGTGTGATTC ATGGCACCCA GACTTGTCTG CCTTCTTAC    1200
70     ATGATCCAGG CCCAGAACCC AAACCTCAGC ACTGTATAGA TGACCACTTT CGTAACTAC    1260
      TGACCTAGCT TGTGTCGAAT TGTGATTGTA ACTTCCCTATA ACTCCACTTC GTGTCTGTTT    1320
      CTCTGTATAC AGCCACCTTC TGTTCCTGTC ATGAGCCTTT AGGCTCCCAT TTGCATATTG    1380
      CAAATACTAT GTTCCATGTA GGTAGCTCAT TCAGGGCCTT GCTCTTCACT TCAAAAAAGG    1440
      TTCCCTTGAG GACTGGCTGT CAATTGTGTG TGCTGTGTTG GTTGTGTATG AAAATAATAA    1500
75     AATGATTGAT TACATAAAAA AAAAAAAAAA AAAAAACAAA CACAAAAAAC    1560
      CGCCGCGCTT TTTCCCGGCG GCACAAAGTT ATAAAACGCC GTCCATC

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Seq ID NO: B73 sequence
Nucleic Acid Accession #: NM_000222.1
Coding sequence: 22..2952

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80     1      11      21      31      41      51
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GATCCCATCG CAGCTACCGC GATGAGAGGC GCTCGCGGCG CCTGGGATT TCTCTGCGTT    60
      CTGCTCTTAC TGCTTACCGT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA    120

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	CCGTCTCCAC	CATCCATCCA	TCCAGGAAAA	TCAGACTTAA	TAGTCCGCGT	GGGCGACGAG	180
	ATTAGGCTGT	TATGCCTGTA	TCCGGGCTTT	GTCAAATGGA	CTTTTGAGAT	CCTGGATGAA	240
	ACGAATGAGA	ATAAGCAGAA	TGAATGGATC	ACGGAAGG	CAGAAGCCAC	CAACACCGGC	300
5	AAATACACGT	GCACCAACAA	ACACGGCTTA	AGCAATTCCA	TTTATGTGTT	TGTTAGAGAT	360
	CCTGCCAAGC	TTTTCCCTGT	TGACCGCTCC	TTGTATGGGA	AAGAAGACAA	CGACACGCTG	420
	GTCCGCTGTC	CTCTCAGAGA	CCCAGAAAGT	ACCAATTATT	CCCTCAAGGG	GTGCCAGGGG	480
	AAGCCTCTTC	CCAAGGACTT	GAGGTTTATT	CCTGACCCCA	AGGCGGGCAT	CATGATCAAA	540
	AGTGTGAAAC	GCGCCTACCA	TCCGCTCTGT	CTGCATTGTT	CTGTGGACCA	GGAGGGCAAG	600
10	TCAGTGTCTG	CGGAAAAAAT	CATCCTGAAA	GTGAGGCCAG	CCTTCAAGGC	TGTGCCTGTT	660
	GTGTCTGTGT	CCRAAGCAAG	CTATCTTCTT	AGGGAAGGGG	AAGAATTAC	AGTGACGTGC	720
	ACAATAAAAG	ATGTGTCTAG	TTCTGTGTAC	TCAACGTGGA	AAAGAGAAAA	CAGTCAGACT	780
	AAACTACAGG	AGAAATATAA	TAGCTGGCAT	CACGGTGACT	TCAATTATGA	ACGTCAGGCA	840
	ACGTTGACTA	TCAGTTTACG	GAGAGTTAAT	GATTCTGGAG	TGTTTATGTT	TTATGCCAAT	900
15	AATACTTTTG	GATCAGCAAA	TGTCACAACA	ACCTTGGGAG	TAGTAGATAA	AGGATTCATT	960
	AATATCTTCC	CCATGATAAA	CACTACAGTA	TTTGTAAACG	ATGGAGAAAA	TGTAGATTG	1020
	ATTGTTGAAT	ATGAAGCATT	CCCCAAACCT	GAACACCAGC	AGTGGATCTA	TATGAACAGA	1080
	ACCTTCACTG	ATAAATGGGA	AGATTATCCC	AAGTCTGAGA	ATGAAAGTAA	TATCAGATAC	1140
	GTAAGTGAA	TTTATCTAAC	GAGATTAAAA	GGCACCAGAG	GAGGCACTTA	CACATTCCCTA	1200
20	GTGTCCAATT	CTGACGTCAA	TGCTGCCATA	GCATTTAATG	TTTATGTGAA	TACAAAACCA	1260
	GAAATCTCGA	CTTACGACAG	GCTCGTGAAT	GGCATGCTCC	AATGTGTGGC	AGCAGGATTC	1320
	CCAGAGCCCA	CAATAGATTG	GTATTTTTGT	CCAGGAACCTG	AGCAGAGATG	CTCTGCTTCT	1380
	GTACTGCCAG	TGGATGTGCA	GACACTAAAC	TCATCTGGGC	CACCGTTTGG	AAAGCTAGTG	1440
	GTTCAGAGTT	CTATAGATTG	TAGTGCATTG	AAGCACAATG	GCACGGTTGA	ATGTAAGGCT	1500
25	TACAACGATG	TGGGCAAGAG	TTCTGCCTAT	TTTAACTTTG	CATTTAAAGG	TAACAACAAA	1560
	GAGCAAAATC	ATCCCCACAC	CCTGTTCACT	CCTTTGCTGA	TGTTTTCGT	AATCGTAGCT	1620
	GGCATGATGT	GCATTATTGT	GATGATTCTG	ACCTACAAAT	ATTACAGAAA	ACCATGTAT	1680
	GAAGTACAGT	GGAAAGTTGT	TGAGGAGATA	AATGGAAACA	ATTATGTTTA	CATAGACCCA	1740
	ACACAACCTC	CTTATGATCA	CAAAATGGAG	TTTCCCAGAA	ACAGGCTGAG	TTTTGGGAAA	1800
30	ACCTTGGGTG	CTGGAGCTTT	CGGGAAGGTT	GTGAGGCAAA	CTGCTTATGG	CTTAATTAAG	1860
	TCAGATGGCG	CCATGACTGT	CGCTGTAAAG	ATGCTCAAGC	CGAGTGCCCA	TTTGACAGAA	1920
	CGGGAAGCCC	TCATGTCTGA	ACTCAAAGTC	CTGAGTTACC	TGTTTAATCA	CATGAATATT	1980
	GTGAATCTAC	TTGGAGCCTG	CACCATTGGA	GGGCCCACCC	TGGTCATTAC	AGAAATATTGT	2040
	TGCTATGGTG	ATCTTTTGAA	TTTTTTTGAGA	AGAAAACGTG	ATTCATTAT	TGTTTCAAAG	2100
35	CAGGAAGATC	ATGCAGAAAG	TGCACCTTAT	AAGAATCTTC	TGCATTCAAA	GGAGTCTTCC	2160
	TGCAGCGATA	GTACTAATGA	GTACATGGAC	ATGAAACCTG	GAGTTTCTTA	TGTTGTCCCA	2220
	ACCAAGGCCG	ACAAAAGGAG	ATCTGTGAGA	ATAGGCTCAT	ACATAGAAAG	AGATGTGACT	2280
	CCGCCATCA	TGGAGGATGA	CGAGTTGGCC	CTAGACTTAG	AAGACTTGCT	GAGCTTTTCT	2340
	TACCAAGTGG	CAAAAGGGCAT	GGCTTTCTCT	GCCTCCAAGA	ATTGTATTCA	CAGAGACTTG	2400
40	GCAGCCAGAA	ATATCTCTCT	TACTCATGGT	CGGATCACAA	AGATTGTGTA	TTTTGGTCTA	2460
	GCCAGAGACA	TCAAGAATGA	TTCTAATTAT	GTGGTTAAAG	GAAACGCTCG	ACTACTCTGT	2520
	AAGTGGATGG	CCCTGAAAG	CATTTTCAAC	TGTGTATACA	CGTTTGAAG	TGACGTCTGG	2580
	TCCTATGGGA	TTTTCTTTTG	GGAGCTGTTT	TCTTTAGGAA	GCAGCCCCCTA	TCCTGGAATG	2640
	CCGGTGGATT	CTAAGTTCTA	CAAGATGATC	AAGGAAGGCT	TCCGGATGCT	CAGCCCTGAA	2700
45	CACGCACCTG	CTGAAATGTA	TGACATAATG	AAGACTTGCT	GGGATGCAGA	TCCCCTAAAA	2760
	AGACCAACAT	TCAAGCAAA	TGTTTCACTA	ATTGAGAAGC	AGATTTCAGA	GAGCACCAAT	2820
	CATATTACTT	CCAACCTAGC	AAACTGCAGC	CCCAACCGAC	AGAAGCCCGT	GGTAGACCAT	2880
	TCTGTGGGGA	TCAATCTCTG	CGGCAGCACC	GCTTCTCTCT	CCGACCTCT	GCTTGTGCAC	2940
	GACGATGTCT	GAGCAGAATC	AGTGTGTTGG	TCACCCCTCC	AGGAATGATC	TCTTCTTTTG	3000
50	GCTTCCATGA	TGGTTATTTT	CTTTTCTTTC	AACTTGCATC	CAACTCCAGG	ATAGTGGGCA	3060
	CCCCATGCA	ATCTGTCTTT	TCTGAGCACA	CTTTAGTGGC	CGATGATTTT	TGTCATCAGC	3120
	CACCATCCTA	TTGCAAGAGT	TCCAACCTGA	TATATTCCCA	ATAGCAACGT	AGCTTCTACC	3180
	ATGAACAGAA	AACATTCTGA	TTTGGAAAAA	GAGAGGGAGG	TATGGACTGG	GGGCCAGAGT	3240
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55	GGTAGTAATC	ACAGTTGGCC	TTTCAAGACCA	TCCATAGTAG	TATGATGATA	CAAGATTAGA	3360
	AGCTGAAAA	CTAAGTCTCT	TATGTGAAAA	ACAGAACATC	ATTAGAACAA	AGGACAGAGT	3420
	ATGAACACCT	GGGCTTAAAG	AATCTAGTAT	TTTATGCTGG	GAATGAGACA	TAGGCCATGA	3480
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60	GCCTCCCTAG	CCAGCACTTG	TATATACGCA	TCTATAAATT	GTCCTGTGTC	ATACATTGTA	3660
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	TAGAAGTAGA	TTAAGAGCCA	TATAAGTTTG	AAGGAAACAG	TTAATACCAT	TTTTTAAGGA	3780
	AACAATATAA	CCACAAAGCA	CAGTTTGAAC	AAAATCTCCT	CTTTTAGCTG	ATGAACCTTAT	3840
	TCTGTAGATT	CTGTGGAACA	AGCCTATCAG	CTTCAGAAATG	GCATTGTACT	CAATGGATTT	3900
65	GATGCTGTTT	GACAAAGTTA	CTGATTCAC	GCATGGCTCC	CACAGGAGTG	GGAAAAACCT	3960
	GCCATCTTAG	TTTGGATTCT	TATGTAGCAG	GAAATAAAGT	ATAGGTTTAG	CCTCCTTCGC	4020
	AGGCATGTCC	TGGACACCGG	GCCAGTATCT	ATATATGTGT	ATGTACGTTT	GTATGTGTGT	4080
	AGACAAATAT	TTGGAGGGGT	ATTTTGGCCC	TGAGTCCAAG	AGGGTCTTTT	AGTACCTGAA	4140
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70	TAGCTTACCA	GAAGCTTCCA	TAGTGGTGCA	GAGGAAGTGG	AAGGCATCAG	TCCCTATGTA	4260
	TTTGCAGTTC	ACCTGCACCT	AAGGCACCTT	GTTATTTAGA	CTCATCTTAC	TGTACCTGTT	4320
	CCTTAGACCT	TCCATAATGC	TACTGTCTCA	CTGAAACATT	TAAATTTTAC	CCTTTAGACT	4380
	GTAGCCTGGA	TATTATCTCT	GTAGTTTACC	TCTTTAAAAA	CAAAACAAAA	CAAAACAAAA	4440
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	CTCGCACCTT	TCCAAGTTTA	ACAGATTTTG	GGGTTGTGTT	GTCACCCAG	AGATTGTTGT	4680
	TTGCCATACT	TGTCCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4740
	AAGTGGTTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTG	4800
80	TTGCCATAGT	TGTCCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4860
	AAGTGGTTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTG	4920
	AATGCTTTT	GATAATTCCC	AAGCCCATGA	GTCCTTGAAA	ATATTTTTTA	TATATACAGT	4980
	AACTTTATGT	GTAAATACAT	AAGCGGCGTA	AGTTTAAAGG	ATGTTGGTGT	TCCACGTGTT	5040
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Seq ID NO: B74 protein sequence
Protein Accession #: NP_000213.1

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PGFVKWTFEI LDETENKQON EWITEKAEAT NTGKYTCTNK HGLSNSIYVF VRDPAKFLV 120
DRSLYGKEDN DTLVRCPLTD PEVTNYSLKG CQKPLPKDL RFIPDPKAGI MIKSVKRAYH 180
RLCLHCSVDQ EGKSVLSEKF ILKVRPAFKA VPVVSVSKAS YLLREGEEFT VTCTIKDVSS 240
SVYSTWKREN SQTQLQEKYN SWHHGDFNYE ROATLTISSA RVNDSGVFMC YANNTFGSAN 300
VTTLLEVVDK GFINIFPMIN TTVFVNDGEN VDLIVEYEF PKPEHQQWY MNRTFTDKWE 360
DYPKSENESN IRYVSELHLT RLKGTGGTY TFLVNSNDVN AAIAFNVYVN TKPEILTYDR 420
LVNGLMLQVA AGFPEPTIDW YFCPGTEQRC SASVLPVDVQ TLNSSGPPFG KLVVQSSIDS 480
SAFKHNGTVE CKAYNDVGKT SAYFNFAFKG NNKEQIHPHT LFTPLLIGFV IVAGMMCIIV 540
15 MILTYKYLQK PMYEVQWKV BEINGNNYVY IDPTQLPYDH KWEFFRNRLS FGKTLGAGAF 600
CKVVEATAYG LIKSDAAMTV AVKMLKPSAH LTEREALMSE LKVLVSYLGNH MNIVNLLGAC 660
TIGGETLVIT EYCCYGDLLN FLRRKRDSFI CSKQEDHAEA ALYKNLLHKS ESSCSDSTNE 720
YMDMKPGVSY VVPTKADKRR SVRIGSYIER DVTPAIMEDD ELALDLEDLL SFSYQVAKGM 780
20 AFLASKNCIH RDLAARNILL THGRITKICD FGLARDIKND SNYVVKGNAR LPVKWMAPEP 840
IFNCVYTFES DVWSYGIPLW ELFSLGSSPY PGMPVDSKFY KMIKEGFRML SPEHAPAEMY 900
DIMKTCWDAD PLKRPTFKQI VQLIEKQISE STNHIYSNLA NCSPNRQKPV VDHSVRINSV 960
GSTASSQPL LVHDDV

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Seq ID NO: B75 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58..2298

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GGCCAGACTG GGAAGAAATC TGAGAAGGGA CCAGTTGTGT GGCGGAAGCG TGTAAAATCA 120
GAGTACATGC GACTGAGACA GCTCAAGAGG TTCAGACGAG CTGATGAAGT AAAGAGTATG 180
TTTAGTTCCTA ATCGTCAGAA AATTTTGGAA AGAACGGAAA TCTTAAACCA AGAATGGAAA 240
CAGCGAAGGA TGACAGCTGT GCACATCCTG ACTTCTGTGA GCTCATTCGG CGGGACTAGG 300
35 GAGTGTTCGG TGACCAAGTA CTTGGATTTT CCAACACAAG TCATCCCAT TAAAGACTCTG 360
AATGCAGTTG CTTCACTACC CATAATGTAT TCTTGGTCTC CCCTACAGCA GAATTTTATG 420
GTGGAAGATG AAATCTTTT ACATAACATT CCTTATATGG GAGATGAAGT TTTAGATCAG 480
GATGGTACTT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAAGTACA CGGGGATAGA 540
40 GAATGTGGGT TTATAAATGA TGAATTTT GTGGAGTTGG TGAATGCCCT TGGTCAATAT 600
AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAAGCAGAAA 660
GATCTGGAGG ATCACCAGAG TGATAAAGAA AGCCGCCCAC CTCGGAAT TCTCTCTGAT 720
AAAATTTTGG AGGCCATTTC CTCAATGTTT CCAGATAAGG GCACAGCAGA AGAACTAAAG 780
GAAAAATATA AAGAACTCAC CGAACAGCAG CTCCAGGCG CACTTCTCC TGAATGTACC 840
45 CCCAACATAG ATGGACCAA TGCTAAATCT GTTCAGAGAG AGCAAAGCTT ACCTCCTTT 900
CATACGCTTT TCTGTAGCGG ATGTTTTAAA TATGACTGCT TCCTACATCC TTTTCATGCA 960
ACACCCAAAC CTTATAAGCG GAAGAACACA GAAACAGCTC TAGACAACAA ACCTGTGGA 1020
CCACAGTGTT ACCAGCATTT GGAGGGAGCA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG 1080
CGGATAAAGA CCCCAACCAA ACGTCCAGGA GCGCGCAGAA GAGGACGGCT TCCCAATAAC 1140
50 AGTAGCAGGC CCAGCACCCC CACCATTAAT GTGCTGGAAT CAAAGGATAC AGACAGTGAT 1200
AGGGAAGCAG GGACTGAAAC GGGGGGAGAG AACAATGATA AAGAAGAAGA AGAGAAGAAA 1260
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CCAAATATTG AACCTCCTGA GAATGTGGAG TGGAGTGGTG CTGAAGCCTC AATGTTTGA 1380
GTCTCATTTG GCATCTACTA TGACAATTTC TGTGCCATTG CTAGGTTAAT TGGGACCAAA 1440
ACATGTAGAG AGGTGTATGA GTTTAGAGTC AAAGAATCTA GCATCATAGC TCCAGCTCCC 1500
55 GCTGAGGATG TGGTACTTCC TCCAAGGAAA AAGAAGAGGA AACACCGGTT GTGGGCTGCA 1560
CACTGCAGAA AGATACAGCT GAAAAAGGAC GGCTCCTCTA ACCATGTTTA CAATATCAA 1620
CCCTGTGATC ATCCACGGCA GCCTTGTGAC AGTTCGTGCC CTTGTGTGAT AGCACAATAA 1680
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TGCAAAGCAC AGTGCAACAC CAAGCAGTGC CCGTGCTACC TGGCTGTCCG AGAGTGTGAC 1800
60 CCTGACCTCT GTCCTACTTG TGGAGCCGCT GACCATGGG ACAGTAAAAA TGTGTCTGTC 1860
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GCAGGCTGGG GGATTTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC 1980
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65 ATGTGCAGCT TTCTGTTCAA CTTGAACAAAT GATTTGTGG TGGATGCAAC CCGCAAGGGT 2100
AACAAAATTC GTTTTGCAAA TCATTCGGTA AATCCAACT GCTATGCAAA AGTTATGATG 2160
GTTAACGGTG ATCAGAGAT AGGTATTTT GCCAAGAGAG CCATCCAGAG TGGCGAAGAG 2220
CTGTTGTGTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCGG CATCGAAAGA 2280
70 GAAATGGAAA TCCCTTGACA TCTGCTACCT CTTCCCTCTC CTCTGAAACA GCTGCCTTAG 2340
CTTCAGGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAATTCTG 2400
AATTTGCAAA GTACTGTAAG AATAATTTAT AGTAATGAGT TTAATAATCA ACTTTTATT 2460
GCCTTCTCAC CAGCTGCAAA GTGTTTGTGA CCAGTGAATT TTTGCAATAA TGCAGTATGG 2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAACCTGAA AAAAAA AAAAAA

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Seq ID NO: B76 Protein sequence
Protein Accession #: NP_004447

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80      1      11      21      31      41      51
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KQRIQPVHI LTVSVSLRGT RECSVTSDDL FPTQVIPLKT LNAVASVPIM YSWSPLQONF 120
MVEDETVLHN IPYMGDEVLD QDGTFFIEELI KNYDGKVVHD RECGFINDEI FVELVNALGO 180
YNDDDDDDDG DDPEEREKQK KDLEDHRDDK ESRPPKFPFS DKILEAISSM FPDKGTAERL 240
KEKYKELTEQ QLEFALPEEC TPNIDGPNAK SVQREQSLHS FHTLFCRRCF KYDCFLHPFH 300
ATPNTYKRKN TETALDNKPC GPQCYQHLEG AKEFAAALTA ERIKTPPKRP GGRRRGRPLN 360

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NSSRPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEEK KDETSSSSEA NSRCQTPIKM 420
 KPNIEPPENV EWSGAEASMF RVLIGTYIDN FCAIARLIGT KTCRQVYEFV VKESSIIAPA 480
 PAEDVDTPPR KKKRKHRLWA AHCRIQLKK DGSSNHVYNY QPCDHPRQPC DSSCPVCIAQ 540
 NFCEKFCQCS SECQNRFPFGC RCKAQCNTKQ CPCYLAVREC DPDLCLTCGA ADHWDSKNVS 600
 CKNCISIQRGS KKHLLAPSD VAGWGIFIKD PVQKNEFISE YCGEIIISQDE ADDRGRKVYDK 660
 YMCSEFLNLFN NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
 ELFVDYRYSQ ADALKYVGIE REMEIP

Seq ID NO: B77 DNA sequence
 Nucleic Acid Accession #: NM_007015
 Coding sequence: 1..1005

1 11 21 31 41 51
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 TGCAGCCCCC CGGCGTAGCG TACGCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC 120
 AAGGTGGGAG CCGTGGTCCCT CATTTCGGGA GCTGTGCTGC TGCTCTTTGG GCCCATCGGG 180
 GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240
 ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGAGAGACC 300
 20 TTTAAATGAG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCCTA GAATGGCATC 360
 ACAGGAATTC GTTTTGCTGG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420
 ATTCCTGAGG TGGGCGCCGT GACCAACAG AGCATCTCCT CCAACTGGA AGGCAAGATC 480
 ATGCCAGTCA AATATGAAGA AAATCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
 GACAACAGCT TCTTGAGTTC TAAGGTGTTA GAACTCTGCG GTGACCTTCC TATTTCTTGG 600
 25 CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAAGAA GAGAAGTGGT AAGAAAAATT 660
 GTTCCAACCTA CCACAAAAG ACCACACAGT GGACACGGA GCAACCCAGG CGCTGGAAGA 720
 CTGAATAATG AAACAGACC CAGTGTCAA GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780
 CCTTATCATC AGCAGGAAGG GGAAGCATG ACATTCGACC CTAGACTGGA TCACGAAGGA 840
 ATCTGTTGTA TAGAATGTAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900
 30 GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCTG CAGAGTCATC 960
 ATGCCATGTA GCTGTGGGT GGCCCGTATC TTGGGCATGG TGTGAAATCA CTTCATATAT 1020
 CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATTA AGGCAGGTTG 1080
 ATGTGTATGG GACCATAAAA TATTTTACCA CGCAGCCTGA GCGGTTATTC TTGACACTCT 1140
 35 TAACAGAAAT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAAAATGCA CTGAAAGGGT 1200
 AGTTCAAGTC TAAATGCCA TAACCCCGTT ATTTGTTATT TTTTATTTGC ATTGATTTGC 1260
 CATAAGTCTT CCCTTGCTTG CATCTTCCA AGCTATTTCG AAATAAACAC GAAAATTTAC 1320
 AGTTTGCC

Seq ID NO: B78 Protein sequence
 Protein Accession #: NP_008946

1 11 21 31 41 51
 45 MTENS DKVPI ALVGPDDVEF CSFPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60
 AFYFWKGS DS HIYNVHYTMS INGKLQDGS EIDAGNNLET FRMGSGAEEA IAVNDFQNGI 120
 TGIRFAGGEK CYIKAQVKAR IPEVGAVTKQ SISKLEGI MPVKYEENSL IAVVADQPVK 180
 DNSFLSSKVL ELCGDLPIFW LKPTYPKIQR RERREVRKIP VPTTTKRPHS GPRSNFAGR 240
 50 LNNETRPSVQ EDSQAFNPDN FYHQEGESM TFDPRLDHEG ICCIECRSY THCQKICEPL 300
 GGYYPWPYNY QGCRSACRVI MPCSWWVARI LGMV

Seq ID NO: B79 DNA sequence
 Nucleic Acid Accession #: NM_012449.1
 Coding sequence: 66..1085

1 11 21 31 41 51
 55 CCGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60
 AATTAAATGGA AAGCAGAAAA GACATCACAA ACCAAGAAGA ACTTTGGAAG ATGAAGCCTA 120
 60 GGAGAAATTT AGAAGAAGAC GATTATTGTC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180
 AAAGACCTGT GCTTTTGATC TTGCACCAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
 CAGAACTTCA GCACACACAG GAACTCTTTC CACAGTGGCA CTGCCCAATT AAAATAGCTG 300
 CTATTATAGC ATCTCTGACT TTTCTTTACA CTCTTCTGAG GGAAGTAATT CACCCTTTAG 360
 CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAAGTCTTG 420
 CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG 480
 65 TCCAACCTCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540
 TAACAAGAAA GCAGTTTGGG CTTCTCAGTT TCTTTTGTGC TGTACTGCAT GCAATTTATA 600
 GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAACTGG GCATATCAAC 660
 AGGTCCAACA AAATAAAGAA GATGCCTGGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT 720
 70 ATGTGTCTCT GGAATTGTG GGAATGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC 780
 CATCTGTGAG TGAATCTTTG ACATGGAGAG AATTTCACTA TATTCAGAGC AAGCTAGGAA 840
 TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCTGGAAT AAGTGGATAG 900
 ATATAAAACA ATTTGTATGG TATACACCTC CAACTTTTAT GATAGCTGTT TTCCTTCCAA 960
 TTGTTGTCTT GATATTTAAA AGCACTACTAT TCCTGCCATG CTTGAGGAAG AAGATACTGA 1020
 75 AGATTAGACA TGGTTGGGAA GACGTCACCA AAATTAACAA AACTGAGATA TGTTCACAGT 1080
 TGTAGAATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140
 TCAAGTTTGT ATTTGTTAAT AAAATGATTA TCAAGGAAA AAAAAAAAAA AAAAA

Seq ID NO: B80 Protein sequence
 Protein Accession #: NP_036581.1

1 11 21 31 41 51
 80 MESRKDITNQ EELWKMPPRR NLEEDDYLHK DTGETSMLKR PVLHLHLQTA HADEFDCPSE 60
 LQHTQELFPQ WHLPKIAIAI IASLTFLYTL LREVIHPLAT SHQQVYFKIP ILVINKVLEPM 120

VSITLLALVY LPGAIAIVQ LHNKTKYKFF PHWLDKWMLT RKQFGLLSFF FAVLHAIYSL 180
 SYPMRRSYRY KLLNWAYQOV QONKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240
 VSDSLTWREF HYIQSKLGIV SLLLGTHIAL IFAWNKWIDI KQFVWYTPPT FMIAVFLPIV 300
 VLIFKSILFL PCIRKKILKI RHGWEDVTKI NKTEICSQL

Seq ID NO: B81 DNA sequence
 Nucleic Acid Accession #: NM_000684
 Coding sequence: 87..1520

10 1 11 21 31 41 51
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 TGCTACCGCG GCCCGGGCTT CTGGGGTGTT CCCCAACCAC GGCCAGCCCC TGCCACACCC 60
 CCGCCCCCGG GCCTCCGCAG CTCGGCATGG GCGCGGGGGT GCTCGTCTTG GCGCCTCCG 120
 AGCCCGGTAA CCGTCTCGTCG GCGGCACCGC TCCCGACCGG CGCGGCCACC GCGCGCGGGC 180
 15 TGCTGGTGCC CGCGTCGCGG CCCGCCCTCGT TGCTGCCTCC CGCCAGCGAA AGCCCGGAGC 240
 GCCTGTCTCA GCAGTGGACA GCGGGCATGG GTCTGTCTGAT GCGGCTCATC GTGCTGCTCA 300
 TCGTGGCGGG CAATGTGCTGT GTGATCGTGG CCATCGCCAA GACGCCCGGG CTGCAGACGC 360
 TCACCAACCT CTTTCATCATG TCCCTGGCCA GCGCCGACCT GGTTCATGGGG CTGCTGGTGG 420
 TGCCGTTTCGG GGCCACCATC GTGGTGTGGG GCGGCTGGGA GTACGGCTCC TTCTTCTGCG 480
 20 AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540
 TTGCCCTGGA CCGGTACCTC GCCATCACTC CGCCCTTCCG CTACCAGAGC CTGCTGACGC 600
 GCGCGCGGGG GCGGGGCTCT GTGTGACCGG TGTGGGCCAT CTCGGCCCTG GTGTCTCTCC 660
 TGCCCATCTT CATGCATCTG TGGCGGGCGG AGAGCGACGA GGCGCGCCGC TGCTACAACG 720
 25 ACCCCAAGTG CTGCGGATTC GTCACCAACC GGGCCTACGC CATCGCCTCG TCCGTAGTCT 780
 CCTTCTACGT GCCCCTGTGC ATCATGGCCT TCGTGTACTT CCGGGTGTTC CGCGAGGCC 840
 AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCCGCTT CCTCGCGCGC CCAGCGCGGC 900
 CGCCCTCGCC CTCGCCCTCG CCCGTCCCGG CGCCCGCGCC GCGCGCCGGA CCCCGCGGCC 960
 CCGCGCGCGG CGCGGCCACC GCGCCGCTGG CCAACGGGCG TCGGGGTAAG CGCGGGCCCT 1020
 CGCGCCTCGT GCGCCTACGC GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG 1080
 30 TCTTCAAGCT CTGCTGGGCTG CCCTTCTTCC TGGCCAAAGT GGTGAAGGCC TTCCACCGCG 1140
 AGCTGGTGCC GCACGCGCTC TTCGTCTTCT TCAACTGGCT GGGCTACGCC AACTCGGCT 1200
 TCAACCCCAT CATCTACTGC CGCAGCCCCG ACTTCCGCAA GGCCTTCCAG GGAATGCTCT 1260
 GCTGCGCGCG CAGGCTGCGC CGCCGGCGCC ACGCAGACCA CGGAGACCGG CCGCGCGCCT 1320
 CGGGCTGTCT GCGCCGCGCC GGACCCCGCG CATCGCCCGG GCGCGCCTCG GACGACGACG 1380
 35 ACGACGATGT CGTCGGGGCC ACGCGCGCCG CGCGCTGCTG GAGACCCCTG GCGGCTGCA 1440
 ACGCGGGGGG GCGCGCGGAC AGCGACTCGA GCCTGACGA GCGGTGCCCG CCGGCTTCCG 1500
 CCTCGGAATC CAAGGTGTAG GCGCGCGCGC GGGCGCGCGA CTCGCGGCAC GCGTTCACG 1560
 GGGAAAGAGG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAATCGA AGCCCAACAAT 1620
 40 CCGCTGCTGA ATCATCCGAG GCAAAGAGAA AAGCCACGGA CCGTTGCACA AAAAGGAAAG 1680
 TTTGGGAAGG GATGGGAGAG TGGCTTGCTG ATGTTCTTTC TTG

Seq ID NO: B82 Protein sequence
 Protein Accession #: NP_000675.1

45 1 11 21 31 41 51
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 MGAGVLVLGA SEPNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQWTAG 60
 MGLLMALIVL LIVAGNVLVI VAIKTPRLQ TLNLFIMSL ASADLVMGLL VVPFGATIVV 120
 50 WGRWEYGSFF CEIWTSDVVL CVTASITELC VIALDRYLAI TSPFRYQSLT TRARARGLVC 180
 TVWALSALVS FLPILMHWR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM 240
 AFVYLRVFRE AQKQVKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RPAATAATAP 300
 LANGRAGKRR PSRLVALREG KALKTLGIIM GVFTLCWLPF FLANVVKAFH RELVDPDLFV 360
 FFWNLGYANS AFNPILYCRS PDFRKAPOGL LCCARRAARR RHATHGDRPR ASGCLARPGP 420
 55 PPSFGAASDD DDDDVVGATP PARLLEPWAG CNGGAADSD SSDLDEPCRPG FASESKV

Seq ID NO: B83 DNA sequence
 Nucleic Acid Accession #: NM_000729.2
 Coding sequence: 2..421

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 65 GACGCAGCGG GTGCCTCCCG CAGATCCCGC GGGCTCCGGG CTGCAGCGGG CAGAGGAGGC 180
 GCCCCGTAGG CAGCTGAGGG TATCGCAGAG AACGGATGGC GAGTCCCGAG CGCACCTGGG 240
 CGCCCTGCTG GCAAGATACA TCCAGCAGGC CCGGAAAGCT CCTTCTGGAC GAATGTCCAT 300
 CGTTAAGAAC CTGCAGAACC TGGACCCAG CCACAGGATA AGTGACCGGG ACTACATGGG 360
 CTGATGAGAT TTTGGCCGTC GCAGTGCCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420
 70 GCCGCCATCA GCCCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAAT AAGACAACAA 480
 TCACACTCAT AACTCATTGT CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540
 TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACACGCT CACAGAGAGT 600
 TGTGCAAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT 660
 TATGCTATTA AAGTGATTTC ATTCTGCC

Seq ID NO: B84 Protein sequence
 Protein Accession #: NP_000720.1

80 1 11 21 31 41 51
 | | | | | |
 MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEEAP RQLRVSQRT DGESEHLGA 60
 LLARYIQQAR KAPSGRMSIV KNLQNLDPH RISDRDYMGW MDFGRSAEBE YEYPS

TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis

5	<u>A1 DNA SEQUENCE</u>	
	Gene name:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Unigene number:	Hs.154210
	Probeset Accession #:	M31210
10	Nucleic Acid Accession #:	M31210
	Coding sequence:	251-1396
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60	<u>A2 Protein sequence:</u>	
	Gene name:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Unigene number:	Hs.154210
	Probeset Accession #:	M31210
65	Protein Accession #:	AAA52336
	Signal sequence:	none found
	Transmembrane domains:	50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301
	Cellular Localization:	plasma membrane
70	1 11 21 31 41 51 MGPTSVPLVK AHRSSVSDYV NYDIIVRHYN YTGKLNISAD KENSIKLTSV VFILICCFII 60 LENIFVLLTI WKTKKPHRPM YFIGNLALS DLLAGVAYTA NLLLSGATTY KLTPAQWFLR 120 EGSMFVALSA SVFSLIAIAI ERYITMLKMK LHNGSNNFRL FLLISACWVI SLILGGLPIM 180 GWNCISALSS CSTVLPYHK HYILFCTTVF TLLLLSIVIL YCRIYSLVRT RSRRLTFRKN 240 ISKASRSSEN VALLKTVIIV LSVFIACWAP LFILLLLDVG CKVKTCIDILF RAEYFLVLAV 300 LNSGTNPPIY TLINKEMRRA FIRIMSCCK PSKGSAGKFK RPIIAGMEFS RSKSDNSSHP 360 QKDEGDNPET IMSSGNVNSS S	
80	<u>A3 DNA SEQUENCE</u>	
	Gene name:	G protein-coupled receptor 51
	Unigene number:	Hs.198612
	Probeset Accession #:	AA452928
	Nucleic Acid Accession #:	NM_004624.1

1	11	21	31	41	51	
ATGGCTTCCC	CGCGGAGGTC	CGGGCAGCCA	GGGCGGCCGC	CGCCGCGGCC	ACCGCGCGCC	60
GCGCGGCTGC	TACTGCTACT	GCTGCTGCCG	CTGCTGCTGC	CTCTGCGGCC	CGGGCGCTGG	120
GGCTGGGGCG	GGGGCGCCCC	CCGGCGCCGC	CCGACGAGCC	CGCGGCTCTC	CATCATGGGC	180
CTCATGCGCG	TGCCAACAGGA	GGTGGCCAA	GCGCAGCATCG	GGCGCGGTGT	GCTCCCCGCC	240
GTGGAACTGG	CCATCGAGCA	GATCGGCAAC	GAGTCACTCC	TGCGCCCTTA	CTTCTCGACG	300
CTGCGGCTCT	ATGACACGGA	GTCCGACAAC	GCAAAAGGGT	TGAAGAGCCT	TACGATGATC	360
ATAAAAATACG	GGCCGAACCA	CTTGATGGTG	TTTGGAGGCG	TCTGTCCATC	CGTCACTATC	420
ATCATTTGACG	AGTCCCTCCA	AAAGCTGGAAT	CTGGTGCGAGC	TTTCTTTTGC	TGCAACAACG	480
CTCTGTCTTAG	CCGATAAGAA	AAATACCCCT	TATTTCTTTC	GGACGCTCCC	ATCAGACAGT	540
GCGGTGAATC	CAGCCATTCT	GAAGTTGCTC	AAGCACTACC	AGTGAAGCG	CGTGGGCACG	600
CTGACGCAAG	ACGTTTCAGAG	GTTCCTCTGAG	GTGCGGAATG	ACCTGACTGG	AGTTCTGTAT	660
CGCGAGGACA	TTGAGATTTC	AGTACCGAG	AGCTTCTCCA	AGACTCCCTG	TCCAGTGTTC	720
AAAAAGCTGA	AGGGGAATGA	TGTGCGGATC	ATCCTTGCGC	AGTTTGACCA	GAATATGGCA	780
GCAAAAGTGT	TCTGTGTGTC	ATACGAGGAG	AACATGTATG	GTAGTAATAA	TCAGTGATATC	840
ATTCCGGGGT	GGTATCGAGC	TTCTTGGTGG	GAGCAGGTGC	ACACGGAAGC	CAACTCATCC	900
CGCTGCTCTC	GGAGAATCT	GCTTGTGCTC	ATGAGGAGGT	ACATTGGCGT	GGATTTCGAG	960
CCCTTGAGCT	CCAAGCAGAT	CAAGACCATC	TCGGAAGAGT	CTCCACAGCA	GATAGAGGAC	1020
GAGTACAACA	ACCAAGCGTC	AGGCGTGGGG	CCCAGCAAGT	TCCACGGGTA	CGCCTACGAT	1080
GGCATCTGGS	GATCTCGCCA	GACACTCGAG	AGGGCCATGG	AGACATTCGA	TGCGCAGCAG	1140
CGGCACCGAC	GGATCCGAGA	CTTCAACTAC	ACGCACAGCA	CGCTGGGCGC	GATCATCTCT	1200
AATGCCATGA	ACGAGACCAA	CTTCTCGGG	GTCACGGGTC	AAGTTTGATT	CGAAGTGGG	1260
GAGAGAAATG	GGACCATTTA	ATTATTCAA	TTTCAAGACA	CGAGGGAGGT	GAAGTGGGGA	1320
GAGTACAACG	CTGTGGCGCA	CACACTGGAG	ATCATCAATG	ACACCATCAG	GTTCGAAGGA	1380
TCCGAACACC	CAAAAGACAA	GACCATCATC	CTGAGCAGCG	TGCGGAAGAT	CTCCCTTACT	1440
CTCTACAGCA	TCTCTCTGCG	CCTCACCATC	CTCGGATGTA	TCATGGCCAG	TGCTTTTCTC	1500
TTCTTCAACA	TCAAGAACCG	GAATCAGAA	CTCATAAAGA	TGTCGAGTCC	ATACATGAAC	1560
AACTTCTTGA	TCCTTGGAAG	GATGCTCTCC	TATGCTTCCA	TTTCTCTCTT	TGGCCTTTAT	1620
GGATCTTTTG	TCTCTGAAA	GACCTTTGAA	ACACTTTGCA	CGTTCGAGAC	CTGGATTCTC	1680
ACCGTGGGCT	ACACGACCGC	TTTTGGGGCC	ATGTTTGCAA	AGACTTGAG	AGTCCACGCG	1740
ATCTTCAAAA	ATGTGAAAT	GAAGAAGAG	ATCATCAGGT	ACCGAAAAT	TGTTGTGATC	1800
GTGGGGGACA	TGCTGCTGAT	CGACCTGTGT	ATCTGTATCT	CGTGGCAGCT	GCTGGACCCC	1860
CTGCGAAGGA	CAGTGGAGAA	GTACAGCATC	GAGCCGCGAC	CAGCAGGACG	GGATATCTCC	1920
ATCGCGCCCT	TCTCTGAGCA	CTGTGAGAAC	ACCCATATGA	CCATCTGGCT	TGGCATCGTC	1980
TATGCGCTTCA	AGGGACTTCT	CATGTTGTTT	GGTTGTTTCT	TAGTCTGGGA	GACCCGCAAC	2040
GTCAGCATGCA	CCGCACTCAA	CGACAGCAAG	TACATCGGGA	TGAGTGTCTA	CAACGTGGGG	2100
ATCATGTGCA	TCATCGGGGC	CGCTGTCTCC	TTCTTGACCC	GGAGCAGACC	CAATGTGCGG	2160
TTCTGCTATG	TGGCTCTTGT	CATCATCTTC	TGCGACACCA	TCACCTCTG	CCTGGTATTC	2220
GTGCGGAAGC	TCATCACCTT	GAGAAACAAC	CCAGATCGAG	CAACCGAGAA	CAGCGGATTC	2280
CAGTTCACTC	AGAATACGTA	GAAAGAAGAT	TTCAAACGCT	CCACTTCGGT	CACCAAGTGT	2340
AACCAAGCCA	GCACATCCCC	CCTGGAGGGC	CTACAGTCAG	AAAACCATCG	CCTGCGAATG	2400
AAGATACAGC	AGCTGGTATA	AGACTTTGGA	GAGGTACACCA	TGCGAGTCGA	GGACACACCA	2460
GAAAGACAGA	CCCTACATTA	ACGAAACCA	TACCAAGAGC	TCAATGACAT	CTCAACCTG	2520
GGAAACTTCA	CTGAGAGCAC	AGATGGAGGA	AAGGCCATTT	TAAAAAATCA	CCTCGATCAA	2580
AATCCCCAGC	TACAGTGGAA	CACAACAGAG	CCCTCTCGAA	CATGCAAAAG	TCCTATAGAA	2640
GATATAAAGT	CTCAGAAACA	CATCCAGCGT	CGCGTGTCCC	TCGAGCTCCC	CATCTCCAC	2700
CCGCTTACCT	TCCCATCCAT	CGAGGGCGTG	GAGCGCAGCT	GTGTGAGCCC	CTGCGTCAGC	2760
CCCACCGCCA	GCCCCCGCCA	CAGACATGTG	CCACCTCTCT	TCCGAGTCAT	GGTCTCGGGC	2820
CTGTAA						

plasma membrane

830

A5 DNA SEQUENCE

Gene name:

ESTs

Unigene number:

Hs.293616

Probeset Accession #:

AW043782

Nucleic Acid Accession #:

none found

Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

10 1 11 21 31 41 51
 | | | | | |
 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCTGCTGG 60
 CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCC GGGAACTACT TCACCAATGA 120
 GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA 180
 GTGTGACGGG CTGCCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
 15 GTCGAAATGT GAGCCCAACCT TCTTCCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTCTG 300
 CTTCCGGTGG AGGTGCTTGG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
 AAACCCCTCTG CTTTGTCTCA CCGCCCGCTA CCACTGCAAG AACGCGCTCT GTATTGACAA 420
 GAGCTTCTAT TGCATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
 AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
 20 TTACCCAGC ATCACCATTG CCATCATCGG CAGTCCGCTC ATTTTGTGTC TGGTGGTGGC 600
 CCTGCTGGCA CTGCTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGTGGCCCGT 660
 GCACCGGCTG CAGCACCTCT TGCTGCTGTC CCGCTGCTG GTCTTGGACC ACCCCACCA 720
 CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGTC AGGCGGAGCA 780
 GAATGCGTCG GAAGTAGGCT CCCACCCCTC CTACTCCGAG GCCTTGTCTGG ACCAGAGGCC 840
 25 TGCGTGGTAT GACCTTCTCT CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900
 CGACCTGGCC CCTTACCGCT CCGGTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCGAG 960
 CAGCAGCCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020
 GGGCACTGCT GAGCCAGGCG ACTCTGAGCC CAGCCAGGCG ACTGAAGAAG TATAAGTCCC 1080
 30 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTC TAACAATTG 1140
 TGCTCATGGG AAGCTCTTTA AGCAGCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
 AACTATCTCT GCATTCCCCT CCTCCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260
 TGACATGATC TGTGTGCGT CTTTCTGTC AGGTCACTCT TCCCTTGGGA CCCGAGATCA 1320
 CACCTCATTT TTTACATTA TTCTGTTCT GTTGAGAGA CAGCATATAA AACAGTATTG 1380
 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
 35 CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500
 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAATT CCATTGAGC 1560
 ATCAAAACCT GCTTTGCACA ATCCTATTG ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620
 AAGAAACCTT TGGACGTGAG TAACACCCCT CAGCAGTCGC AACGTATT TGGTTTGTG 1680
 AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAATTG CCCAAGAATG 1740
 40 CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTAA AATAGGCAGG 1800
 GAGCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAAGCT GCCAAGACCC 1860
 TACACCTGCT CTGGCTCTAC AGCCACTTAC CTGGTTCTG GACTGTCAAC CTCACAGCTG 1920
 ACCTGCCCCG AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980
 GTATGTCCTT GTGGCCCA CAACAGCCTGT CTGTGCTATT CATGCAGCCT CAACACTGGC 2040
 45 CTCCAAAGTT CCCTTAACAC TTGCAAGATC CTTTTACCT GTGCATTGAG ACTTGAGGAC 2100
 ACTGTTTCT ATCAGAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
 CTGCACTGTG CACGCTCCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220
 GGTCAAGGTC AGGCCCTCTC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
 AGACAATTG GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTA GAAATGCATT 2340
 50 TGAACAGTGT TGTGTTTCTT TTCCCTCTA GTTAAGGGAC TATTATATG TGTATAGGAA 2400
 AGCTGTCTCT TTTTGTGTTT TTCTTTAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC 2460
 ACACCCCTGC CCCGCTGAGC CCCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
 ACATTGTGTC ATGTTGTGAC TTTGAGTTA TTATTATCA AGTTCTTGAA GGAAGCAGAA 2580
 AGAGGAGTCT CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640
 55 TTCTCTGTG CTGCTGAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACTG 2700
 AGGTGTGTTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGAA CCAGGTAGAG 2760
 CCACTCCGGG CAGCTGTGAC CCATTGAGAA CTCTTTCCG CAGCTGAAAG AATGTTTCTG 2820
 AACCTGTTT ACCTTAATTA AAACAGAGCC TGCAAGAAAG GGGGCTAAAG TGGCATTCTG 2880
 TGATCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTACAGAA 2940
 60 AAGTAGCCA CTGCTATTTT GTTTGTGTTA AAAAAAAGAA GAAAGAAAGA AAGAAAGAAA 3000
 AACGGAAAGG AACCTAGCTG CCGTATCTTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120
 CATTTCTATC CCGTGTAGCT AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTTCTTC 3180
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATCTA ATTTAATTA ATGCGCAGT 3240
 65 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAA TGGTTTATG 3300
 AGATAAGGGA TGCTACTATA TGCTTTTATA AAACAACAG GGACATTTT ATTATAGATT 3360
 TGATTTTCTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGC GGCAGGTTT 3420
 TTTTGGGGG GAGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CAGCAATAT 3480
 70 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCA 3540
 AAAATAGTCT CATCTCTTTT TTTCTCAAA GAGATCCGTG TTTTATTTA GCATTAAAT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAACTG 3720
 GAAAGGTTGT GTGTCGTTGC TTTTGTGTTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780
 75 TTATACTTTT TAATAAATTT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG WNMCTAMARM 3840
 AAMMAAAAC AWWTGTTGGG GGGCTTGGG CTGGAAGAAA GTTTTAAACA CCACTTCGGG 3900
 TGGGGCGCG GGGCCACGT AGGTACGCG ACCACGCGG CCCAAACGGG ACCCCAGAG 3960
 GAAACCTCTG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCGCCGGG 4020
 GGAACCCGCA GAGTGTGCG TAAACCACAC CCGAAGAGAG AACTCAGAG CACACAAGCG 4080
 80 GGACTCAACC AGGAGGACCC AAGGAACCC GATAGAGTAC G

A6 Protein sequence:

Gene name:

ESTs

Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MWLLGFLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60
 EKECPKAKSK CGPTFFPCAS GIHICIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNGLCIDKSF ICDGQNNQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIGSS 180
 VIFVLVVALL ALVLHHQKRK NNLMTLPVHR LQHPVLLSRL VVLDHPHCN VTYNVNNGIQ 240
 YVASQAEQNA SEVGSPPSYS EALLDQRPAN YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEEV

A7 DNA SEQUENCE

Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)

Unigene number: Hs.149609
 Probeset Accession #: X06256
 Nucleic Acid Accession #: NM_002205
 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGGGGAGCC GGAGCCAGCA GTCCCTCTC CACGCCGTGC AGCTGCGCTG GGGCCCCCGG 60
 CGCCGACCCC CGCTSSSTGCC GCTGCTGTG CTGCTSSSTGC CGCCGCCACC CAGGGTCGGG 120
 GGCTTCAACT TAGACGCGGA GGGCCACAGCA GTACTCTCGG GGGCCCCGGG CTCCTTCTTC 180
 GGATTCTCAG TGGAGTTTTA CCGGCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240
 CCCAAGGCTA ATACAGCCA GCCAGGAGTG CTGCAGGGTG GTGCTGTCTA CCTCTGTCTC 300
 TGGGGTGCCA GCGCCACACA GTGCACCCCT ATTGAATTG ACAGCAAAGG CTCTCGGCTC 360
 CTGGAGTCCT CACTGTCCAG CTCAGAGGGA GAGGAGCCTG TGGAGTACAA GTCCTTGACG 420
 TGGTTCGGGG CAACAGTTCG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC 480
 AGCTGGCGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA 540
 GATAACTTCA CCCGAATTCT GGAGTATGCA CCCTGCCGCT CAGATTTCAG CTGGGCAGCA 600
 GGACAGGGTT ACTGCCAAGG AGGCCTCAGT GCCGAGTTCA CCAAGACTGG CCGTGTGGTT 660
 TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720
 ATTGCAAGAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
 CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGTGGTAA 840
 TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGTGTGTC CCAAGGGGAA CCTCACTTAC 900
 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCGATCCC TCTACAACCT CTCAGGGGAA 960
 CAGATGGCCT CCTACTTTGG CTATGCAGTG GCCGCCACAG ACGTCAATGG GAGACGGCTG 1020
 GATGACTTGC TGGTGGGGGC ACCCCTGCTC ATGGATCGGA CCCTGACGG GCGGCTCAG 1080
 GAGGTGGGCA GGTCTACGT CTACCTGCAG CACCCAGCG GCATAGAGCC CACGCCACC 1140
 CTTACCTTCA CTGGCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTGAC CCCCTGGGG 1200
 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC 1260
 CAGCAGGGAG TAGTGTGTTG ATTCTCTGGG GGGCCAGGAG GGCTGGGCTC TAAGCCTTCC 1320
 CAGGTTCTGC AGCCCTGTG GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380
 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCTTGGT 1440
 GTGGACAAGG CTGTGGTATA CAGGGGCGGC CCATCGTGT CCGCTAGTGC CTCCTCACC 1500
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 GCCTGCATCA ACCTTAGCTT CTGCCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT 1620
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 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAATT TCGAGACAAA 1800
 CTCTCGCCGA TTCACATGCG TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1860
 CACGGCCTCA GGCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920
 ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGT 1980
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 CAGAACTTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCCTCCAGAG 2100
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2160
 TTTGCCGTGA ACCAGAGCCG CTGTCTGGTG TGTGACCTGG GCAACCCCAT GAAGCAGGA 2220
 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC 2280
 ATCCAGTTTG ACTTCCAGT CCTCAGCAAG AATCTCAACA ACTCGCAAG CGAGCTGGTT 2340
 TCCTTTCCGC TCTCCGTGGA GGCTCAGGCC CAGTCAACCC TGAACGGTGT CTCCAAGCCT 2400
 GAGGCAGTGC TATTCCAGT AAGCGACTGG CATCCCCGAG ACCAGCCTCA GAAGGAGGAG 2460
 GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCC CAGCTCCATT 2520
 AGCCAGGGTG TGCTGGAAC TGCCTGTCCC CAGGCTCTGG AAGGTCAGCA GCTCCTATAT 2580
 GTGACCAGAG TTACGGGACT CAACTGCACC ACCAATCACC CCATTAAACC AAAGGGCCTG 2640
 GAGTTGGATC CCGAGGGTTC CTGCAACCAC CAGCAAAAAC GGGAACTTCT AAGCCGACG 2700
 CTGCTTCTCT CGGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGT 2760
 TGTGAGCTCG GGGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAAGTGA TTTCCGAGTC 2820
 TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCCTGCAGTG TGAGGCTGTG 2880
 TACAAGGCC TGAAGATGCC CTACCGAATC CTGCCTCGGC AGCTGCCCA AAAAGAGCGT 2940
 CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGCGT CCCACTGTG 3000
 ATCATCATCC TAGCATCAT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060
 TACAAGCTTG GATCTCTCAA ACGTCTCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG 3120
 CTCAAGCCTC CAGCCACCTC TGATGCCTGA

A8 Protein sequence:

Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
 Unigene number: Hs.149609
 Probeset Accession #: X06256
 Protein Accession #: NP_002196
 Signal sequence: 1-42
 Transmembrane domains: 998-1020
 Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MGSRTPEPSP	HAVQLRWGPR	RRPPLPLPLL	LLLPPPPRVG	GFNLDAEAPA	VLSGPPGSFF	60
GFSVEFYRPG	TDGVSVLVGA	PKANTSQPGV	LQGGAVYLCF	WGASPTQCTP	IEFDSKGSRL	120
LESSLSSESG	EEPVEYKSLQ	WFGATVRAHG	SSILACAPLY	SWRTEKEPLS	DPVGTCTYLS	180
DNFTRILEYA	PCRSDFSWAA	QGGYCQGGFS	AEFTKTGRVV	LGGPGSYFWQ	GQILSATQEQ	240
IAESYYPEYL	INLVQGQLQT	RQASSIYDDS	YLGYSVAVGE	FSGDDTDFV	AGVPGKNLTY	300
GVYTIILNGSD	IRSLYNSFGE	QMASYFGYAV	AATDVNGDGL	DDLVLGAPLL	MDRTPDGRPQ	360
EVGRVYVYLQ	HPAGIEPTPT	LTLTGHDEFG	RFGSSLTPLG	DLDQDGYNDV	AIGAPFGGET	420
QQGVVVFVPG	GPGLGSKSPS	QVLQPLWAAS	HTPDFFGSAL	RGGRLDNGNG	YPDILVGSFG	480
VDKAVVYRGR	PIVSASASLT	IFPAMFNPEE	RSCSLEGNPV	ACINLSFCLN	ASGKHVADSI	540
GFTVELQLDW	QKQKGVVRR	LFLASRQATL	TQTLLIQNGA	REDCREMKIY	LRNESEFRDK	600
LSPIHIALNF	SLDPQAPVDS	HGLRPLALHYQ	SKSRIEDKAQ	ILLDCGEDNI	CVFDLQLEVF	660
GEQNHVYVLD	KNALNLTFFH	QNVGEGGAYE	AELRVTAPE	AEYSGLVRHP	GNFSSLSQDY	720
FAVNQSRLLV	CDLGNPMKAG	ASLWGGRLFT	VPHLRDTKKT	IQDFDQILSK	NLNNNSQSDV	780
SFRLSVEAQA	QVTLNGVSKP	EAVLFPVSDW	HPRDQPQKEE	DLGPAVHHVY	ELINQGFSSI	840
SQGVLELSCP	QALEGQQLLY	VTRVTGLNCT	TNHPINPKGL	ELDPEGLSHH	QQKREAPSR	900
SASSGPGQILK	CPAEACFRRL	CBLGPHLQHE	SQSLQLHFRV	WAKTFLQREH	QPFSLQCEAV	960
YKALKMPYRI	LPRQLPQKER	QVATAVQWTK	AEYSYGVPLW	IIILAILFLG	LLGLGLIYIL	1020
YKLGFFKRSL	PYGTAMEKAQ	LKPPATSDA				

A9 DNA SEQUENCE

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Nucleic Acid Accession #: NM_002211.1
 Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
<u>ATGAATTTAC</u>	<u>AAACCAATTTT</u>	<u>CTGGATTGGA</u>	<u>CTGATCAGTT</u>	<u>CAGTTTGCTG</u>	<u>TGTGTTTGCT</u>	60
CAAAACAGATG	AAAATAGATG	TTTAAAAGCA	AATGCCAAAT	CATGTGGAGA	ATGTATACAA	120
GCAGGGCCAA	ATTGTGGGTG	GTGCACAAAT	TCAACATTTT	TACAGGAAGG	AATGCCTACT	180
TCTGCACGAT	GTGATGATT	AGAAGCCTTA	AAAAAGAAGG	GTTGCCCTCC	AGATGACATA	240
GAAAATCCCA	GAGGCTCCAA	AGATATAAAG	AAAAATAAAA	ATGTAACCAA	CCGTAGCAAA	300
GGAACAGCAG	AGAAGCTCAA	GCCAGAGGAT	ATTACTCAGA	TCCAACCACA	GCAGTTGGTT	360
TTGCGATTAA	GATCAGGGGA	GCCACAGACA	TTTACATTAA	AATTCAAGAG	AGCTGAAGAC	420
TATCCCATTTG	ACCTTACTAA	CCTTATGGAC	CTGTCTTACT	CAATGAAAGA	CGATTGGAG	480
AATGTAATAA	GTCTTGGAAC	AGATCTGATG	AATGAAATGA	GGAGGATTAC	TTCGGACTTC	540
AGAATTGGAT	TTGGCTCATT	TGTGGAAAAG	ACTGTGATGC	CTTACATTAG	CACAACACCA	600
GCTAAGCTCA	GGAAACCTTG	CACAAGTGAA	CAGAACTGCA	CCAGCCCATT	TAGCTACAAA	660
AATGTGCTCA	GTCTTACTAA	TAAAGGAGAA	GTATTTAATG	AACCTGTTGG	AAAACAGCGC	720
ATATCTGGAA	ATTTGGATT	TCCAGAAGGT	GGTTTCGATG	CCATCATGCA	AGTTGCAGTT	780
TGTGGATCAC	TGATTGGCTG	GAGGAATGTT	ACACGGCTGC	TGGTGTTC	CACAGATGCC	840
GGGTTTCACT	TTGCTGGAGA	TGGGAAACTT	GGTGGCATTG	TTTTACCAA	TGATGGACAA	900
TGTCACCTGC	AAAATAATAT	GTACACAAATG	AGCCATTATT	ATGATTATCC	TTCTATTGCT	960
CACCTTGTCC	AGAAACTGAG	TGAAAATAAT	ATTTCAGACAA	TTTTTGCACT	TACTGAAGAA	1020
TTTCAGCCTG	TTTACAAGGA	GCTGAAAAC	TTGATCCCTA	AGTCAGCAGT	AGGAACATTA	1080
TCTGCAAAAT	CTAGCAATGT	AATTTCAGTTG	ATCATTGATG	CATACAATTC	CCTTTCCTCA	1140
GAAGTCATT	TGGAAAACGG	CAAAATTGTCA	GAAGGAGTAA	CAATAAGTTA	CAAACTTTAC	1200
TGCAAGAACG	GGGTGAATGG	AACAGGGGAA	AATGGAAGAA	AATGTTCCAA	TATTTCCATT	1260
GGAGATGAGG	TTCAATTGGA	AATTAGCATA	ACTTCAAATA	AGTGTCCAAA	AAAGGATTCT	1320
GACAGCTTTA	AAATTAGGCC	TCTGGGCTTT	ACGGAGGAAG	TAGAGGTTAT	TCTTCAGTAC	1380
ATCTGTGAAT	GTGAATGCCA	AAGCGAAGGC	ATCCCTGAAA	GTCCCAAGTG	TCATGAAGGA	1440
AATGGGACAT	TGAGTGTGTG	CGCGTGCAGG	TGCAATGAAG	GGCGTGTGG	TAGACATTGT	1500
GAATGCAGCA	CAGATGAAGT	TAACAGTGAA	GACATGGATG	CTTACTGCAG	GAAAGAAAAC	1560
AGTTCAGAAA	TCTGCAGTAA	CAATGGAGAG	TGCGTCTGCG	GACAGTGTGT	TTGTAGGAAG	1620
AGGGATAATA	CAAAATGAA	TTATTCTGGC	AAATTCTGCG	AGTGTGATAA	TTTCAACTGT	1680
GATAGATCCA	ATGGCTTAAT	TTGTGGAGGA	AATGGTGTGT	GCAAGTGTCT	TGTGTGTGAG	1740
TGCAACCCCA	ACTACACTGG	CAGTGCATGT	GACTGTTCTT	TGGATACTAG	TACTTGTGAA	1800
GCCAGCAACG	GACGACACTG	CAATGGCCGG	GGCATCTGCG	AGTGTGGTGT	CTGTAAAGTGT	1860
ACAGATCCGA	AGTTTCAAGG	GCAAAACGTGT	GAGATGTGTC	AGACCTGCCT	TGGTGTCTGT	1920
GCTGAGCATA	AAGAATGTGT	TCAGTGCAGA	GCCTTCAATA	AAGGAGAAAA	GAAAGACACA	1980
TGCACACAGG	AATGTTCCCTA	TTTTAACATT	ACCAAGGTAG	AAAGTCGGGA	CAAATTACCC	2040
CAGCCGGTCC	AACTGTATCC	TGTGTCCCAT	TGTAAGGAGA	AGGATGTTGA	CGACTGTTGG	2100
TTCTATTATTA	CGTATTTCAGT	GAATGGGAAC	AACGAGGTCA	TGGTTCATGT	TGTGGAGAAT	2160
CCAGAGTGTC	CACTGGTCC	AGACATCAT	CCAATTGTAG	CTGGTGTGTT	TGCTGGAATT	2220

GTTCTTATTG GCCTTGCAAT ACTGCTGATA TGGAAGCTTT TAATGATAAT TCATGACAGA 2280
 AGGGAGTTTG CTAATTTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAAT 2340
 CCTATTATTA AGAGTGCCCT ACAAACCTGTG GTCAATCCGA AGTATGAGGG AAAATGA

A10 Protein sequence:

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Protein Accession #: NP_002202.1
 Signal sequence: 1-21
 Transmembrane domains: 732-754
 INB domain: 34-464
 PSI domain: 26-76
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MNLQPIFWIG	LISSVCCVFA	QTDENRCLKA	NAKSCGECIQ	AGPNCGWCTN	STFLQEGMPT	60
SARCDLEAL	KKKGCPDDI	ENPRGSKDIK	KNKNVTNRSK	GTAELKLPED	ITQIQPQQLV	120
LRLRSGEPT	FTLKFKRAED	YPIDLYLMD	LSYSMKDDLE	NVKSGLTDLM	NEMRRITSDF	180
RIGFGSFVEK	TVMPYISTTP	AKLRNPCTSE	QNCTSPFSYK	NVLSLTNKGE	VFNELVGKQR	240
ISGNLDSPEG	GFDAIMQVAV	CGSLIGWRNV	TRLIVFSTDA	GFHFAGDGKL	GGIVLPNDGQ	300
CHLENNMYTM	SHYDYPSIA	HLVOKLSENN	IQTIFAVTEE	FQPVYKELKN	LIPKSAVGTL	360
SANSSNVIQL	IIDAYNSLSS	EVILENGKLS	EGVTISYKSY	CKNGVNGTGE	NGRKCSNISI	420
GDEVQFEISI	TSNKPCKKDS	DSFKIRPLGF	TEEVEVILQY	ICECECQSEG	IPESPKCHEG	480
NGTFECGACR	CNGBRVGRHC	ECSTDEVNSE	DMDAYCRKEN	SSEICSNNGE	CVCQCVCVRK	540
RDNTNEIYSG	KFCECDNFNC	DRSNGLICGG	NGVCKCRVCE	CNPNTYGSAC	DCSLDTSTCE	600
ASNQICNCR	GICECGVCKC	TDPKFQQTCC	EMCQTCGLVC	AEHKECVQCR	AFNKGEKKDT	660
CTQECYSYFNI	TKVESRDKLP	QPVQPDVPSH	CKEKDVDCCW	FYFTYSVNGN	NEVMVHVVEN	720
PECPTGPDII	PIVAGVVAGI	VLIGLALLLI	WKLMIIHDR	REFAKFEKEK	MNAKWDGTEN	780
PIYKSAVTTV	VNPKYEGK					

A11 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
ATGATTGCTT	CACAGTTTCT	CTCAGCTCTC	ACTTTGGTGC	TTCTCATTA	AGAGAGTGGA	60
GCCTGGTCTT	ACAACACCTC	CACGGAAGCT	ATGACTTATG	ATGAGGCCAG	TGCTTATTGT	120
CAGCAAAAGT	ACACACACCT	GGTTGCAATT	CAAAACAAAG	AAGAGATTGA	GTACCTAAAC	180
TCCATATTGA	GCTATTACCC	AAGTTATTAC	TGGATTGGAA	TCAGAAAAGT	CAACAATGTG	240
TGGGTCTGGG	TAGGAACCCA	GAAACCTCTG	ACAGAAGAAG	CCAAGAAGCT	GGCTCCAGGT	300
GAACCCAAAC	ATAGGCAAAA	AGATGAGGAC	TGCGTGGAGA	TCTACATCAA	GAGAGAAAAA	360
GATGTGGGCA	TGTGGAATGA	TGAGAGGTGC	AGCAAGAAGA	AGCTTGCCCT	ATGCTACACA	420
GCTGCCTGTA	CCAATACATC	CTGCAGTGGC	CACGGTGAAT	GTGTAGAGAC	CATCAATAAT	480
TACACTTGCA	AGTGTGACCC	TGGCTTCAGT	GGACTCAAGT	GTGAGCAAA	TGTGAAGTGT	540
ACAGCCCTGG	AATCCCTGGA	GCATGGAAGC	CTGGTTTGCA	GTCACCCACT	GGGAACTTC	600
AGCTACAATT	CTTCTGTCTC	TATCAGCTGT	GATAGGGGTT	ACCTGCCAAG	CAGCATGGAG	660
ACCATGCACT	GTATGTCCTC	TGGAGAATGG	AGTGTCTCTA	TTCAGCCTG	CAATGTGGTT	720
GAGTGTGATG	CTGTGACAAA	TCCAGCCAAT	GGGTTCTGTG	AATGTTTCCA	AAACCCTGGA	780
AGCTTCCCAT	GGAAACACAC	CTGTACATTT	GACTGTGAAG	AAGGATTGTA	ACTAATGGGA	840
GCCAGAGACC	TTCAGTGTAC	CTCATCTGGG	AATTGGGACA	ACGAGAAGCC	AACGTGTAAA	900
GCTGTGACAT	GCAGGCCCGT	CCGCCAGCCT	CAGAATGGCT	CTGTGAGGTG	CAGCCATTCC	960
CCTGTCTGGAG	AGTTACACCT	CAAATCATCC	TGCAACTTCA	CCTGTGAGGA	AGGCTTCATG	1020
TTGCAGGGAC	CAGCCAGGTT	TGAATGCACC	ACTCAAGGGC	AGTGGACACA	GCAAAATCCCA	1080
GTTTGTGAAG	CTTTCCAGTG	CACAGCCTTG	TCCAACCCCG	AGCGAGGCTA	CATGAATTGT	1140
CTTCCTAGTG	CTTCTGGCAG	TTTCCGTTAT	GGGTCCAGCT	GTGAGTTCTC	CTGTGAGCAG	1200
GGTTTTGTGT	TGAAGGGATC	CAAAAGGCTC	CAATGTGGCC	CCACAGGGGA	GTGGGACAAC	1260
GAGAAGCCCA	CATGTGAAGC	TGTGAGATGC	GATGCTGTCC	ACCAGCCCCC	GAAGGGTTTG	1320
GTGAGGTGTG	CTCATTCCCC	TATTGGAGAA	TTCACTTACA	AGTCTCTTTG	TGCCTTCAGC	1380
TGTGAGGAGG	GATTTGAATT	ATATGGATCA	ACTCAACTTG	AGTGACATC	TCAGGGACAA	1440
TGGACAGAAG	AGTTTCTTTC	CTGCCAAGTG	GTAAATGTGT	CAAGCCTGGC	AGTTCCGGGA	1500
AAGATCAACA	TGAGCTGCAG	TGGGGAGCCC	GTGTTTGGCA	CTGTGTGCAA	GTTCGCCTGT	1560
CCTGAAGGAT	GGACGCTCAA	TGGCTCTGCA	GCTCGGACAT	GTGGAGCCAC	AGGACACTGG	1620
TCTGGCCTGC	TACCTACCTG	TGAAGCTCCC	ACTGAGTCCA	ACATTCCCTT	GGTAGCTGGA	1680
CYTTCTGCTG	CTGGACTCTC	CCTCCTGACA	TTAGCACCAT	TTCTCCTCTG	GCTTCGGAAA	1740
TGCTTACGGA	AAGCAAAGAA	ATTGTGTTCT	GCCAGCAGCT	GCCAAAGCCT	TGAATCAGAC	1800
GGAAGCTACC	AAAAGCCTTC	TTACATCCTT	<u>TAA</u>			

A12 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Protein Accession #: NP_000441
 Signal sequence: 1-22
 Transmembrane domains: 555-573
 C-lectin domain: 23-139

Cellular Localization: plasma membrane

5 1 11 21 31 41 51
 | | | | | |
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRythLVAI QNKEEIEYLN 60
 SILSYSPSY WIGIRKYNV WVVVGTKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120
 DVGMWNDERC SKKKLALCYT AACTNTSCSG HGECEVETINN YTCKCDPGFS GLKCEQIVNC 180
 10 TALESPHEGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIACNVV 240
 ECDAVTNPAN GFVCECFQNP SFPWNTTCTF DCEEGFELMG AQLQCTSSG NWDNEKPTCK 300
 AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEFGM LQGPQAVECT TQGWTTQIP 360
 VCEAFQCTAL SNPERGYMNC LPSASGSFPRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN 420
 EKPTCEAVRC DAVHQPPKGL VRCASHPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
 15 WTEVPSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
 SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLLWLRL CLRKAKKFVP ASSCQSLESD 600
 GSYQKPSYIL

A13 DNA SEQUENCE

20 Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Nucleic Acid Accession #: NM_001508
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 | | | | | |
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
 CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCCTTA TTCTGGTGTA CCTGATCATC 120
 30 TTCGTGATGG GCCTTCTGGG GAACAGCGCC ACCATTCCGG TCACCCAGGT GCTGCAGAAG 180
 AAAGGATATC TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC 240
 TTGGTGTTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
 ACGTCCAGCT ACACCTGTGTC CTGCAAGCTG CACACTTTC TCTTCGAGGC CTGCAGCTAC 360
 GCTACGCTGC TGCACGTGCT GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTACCCCC 420
 35 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
 GTCACCTCCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTTG 540
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG 600
 CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTT 660
 CAGTCCAGCA TCTTCGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720
 40 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCCGGGGC 780
 ACCGCGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
 ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACAG 900
 ATTGGAGGA TCATGGCTGC GGCCAACCC AAGCAGGACT GGACGAGGTC CTACTTCCCG 960
 CGGTACATGA TCCTCTCCCT CTTCCTCGAG ACGTTTCTT ACCTCAGCTC GGTTCATCAAC 1020
 45 CCCTCTCTGT ACACGGTGTG CTGCGAGCAG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC 1080
 TGCCGCTGTG CGCTGCAGCA CGCCAACAC GAGAAGCGCC TGCGCGTACA TGCGCACTCC 1140
 ACCACCGACA GCGCCCGCTT TGTGCGAGCG CCGTTGCTCT TCGGCTCCCG GCGCCAGTCC 1200
 TCTGCAAGGA GAACTGAGAA GATTTCTTA AGCACTTTT AGAGCGAGGC CGAGCCCCAG 1260
 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACAGGCC 1320
 50 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

A14 Protein sequence:

55 Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Protein Accession #: NM_001508, NP_001409
 Signal sequence: none found
 Pfam domains: 7tm_1 [72-172, 224-344]
 60 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
 Cellular Localization: plasma membrane

65 1 11 21 31 41 51
 | | | | | |
 MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTQVLQK 60
 KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120
 ATLLHVLTL FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALFL LFAMGTEYFL 180
 VNVPSHRGLT CNRSSTRHHE QPETSNSMIC TNLSSRWTVF QSSIFGAFV YLVVLLSVAF 240
 70 MCWNMMQVLM KSQKGLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLLIV TLAVCWMPNQ 300
 IRRIMAAKVP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC 360
 CRLSLQHANH EKRLRVHAHS TDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEFQ 420
 SKSQSLSLES LEPNSGAKPA NSAAENGFBQ HEV

AI ProstateA15 DNA sequence

80 Gene name: CEGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Nucleic Acid Accession #: AJ400877
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	GGCGTCCGCG	CACACCTCCC	CGCGCCGCGC	CCGCCACCGC	CCGCACTCCG	CCGCTCTGCG	60
	CCGCAACCCG	TGAGCCATCC	ATGGGGGTCG	CGGGCCGCAA	CCGTCCCAGG	GGGGCTCTGG	120
5	CGGTGCTGCT	GCTGCTGCTG	CTGCTGCCGC	CACTGCTGCT	GCTGGCGGGG	GCCGTCCCAG	180
	CGGGTCCGGG	CCGTGCCGCG	GGGCCGCGAG	AGGATGTAGA	TGAGTGTGCC	CAAGGGCTAG	240
	ATGACTGCCA	TGCCGACGCC	CTGTGTCAGA	ACACACCCAC	CTCTACAAG	TGCTCTGCA	300
	AGCTGGCTA	CCAAGGGGAA	GGCAGGCAGT	GTGAGGACAT	CGATGAATGT	GGAAATGAGC	360
	TCAATGGAGG	CTGTGTCCAT	GACTGTTTGA	ATATTCCAGG	CAATTATCGT	TGCACTTGTT	420
10	TTGATGGCTT	CATGTTGGCT	CATGACGGTC	ATAATTGTCT	TGATGTGGAC	GAGTGCCTGG	480
	AGAACAATGG	CGGCTGCCAG	CATACCTGTG	TCAACGTCAT	GGGGAGCTAT	GAGTGTCTGT	540
	GCAAGGAGGG	GTTTTTCTTG	AGTGACAATC	AGCACACCTG	CATTACCCGC	TCCGAAGAGG	600
	GCCTGAGCTG	CATGAATAAG	GATCACGGCT	GTAGTCACAT	CTGCAAGGAG	GCCCCAAGGG	660
	GCAGCGTCGC	CTGTGAGTGG	AGGCCTGGTT	TTGAGCTGGC	CAAGAACCAG	AGAGACTGCA	720
15	TCTTGAACCT	TAACCATGGG	AACGGTGGGT	GCCAGCACTC	CTGTGACGAT	ACAGCCGATG	780
	GCCGAGAGTG	CAGCTGCCAT	CCACAGTACA	AGATGCACAC	AGATGGGAGG	AGTGCCTTGG	840
	AGCGAGAGGA	CAGTGTCTGT	GAGGTGACAG	AGAGCAACAC	CACATCAGTG	GTGGATGGGG	900
	ATAACCGGGT	GAAACGGCGG	CTGCTCATGG	AAACGTGTGC	TGTCAACAA	GGAGGCTGTG	960
	ACCGCACCTG	TAAGGATACT	TGCACAGGTG	TCCACTGCAG	TTGTCTCTGT	GGATTCACTC	1020
20	TCCAGTTGGA	TGGGAAGACA	TGTAAAGATA	TTGATGAGTG	CCAGACCCGC	AATGGAGGTT	1080
	GTGATCATT	CTGCAAAAAC	ATCGTGGGCA	GTTTGTAGTG	CGGCTGCAAG	AAAGGATTTA	1140
	AATTTATTAAC	AGATGAGAAG	TCTTGCCAA	ATGTGGATGA	GTGCTCTTGT	GATAGGACCT	1200
	GTGACCAACAG	CTGCATCAAC	CACCTGGCA	CATTGTCTTG	TGCTTGCAAC	CGAGGGTACA	1260
	CCCTGTATGG	CTTCAACCCAC	TGTGGAGACA	CCAATGAGTG	CAGCATCAAC	AACGGAGGCT	1320
	GTGACGAGGT	GTGTGTGAAC	ACAGTGGGCA	GCTATGAATG	CCAGTGCCAC	CCTGGGTACA	1380
25	AGTCCCACTG	GAATAAAAC	GACTGTGTGG	AAGTGAAGGG	GCTCTGCCCC	ACAAGTGTGT	1440
	CACCCCTGTG	GTCCCTGCAC	TGCGGTAAGA	GTGGTGGAGG	AGACGGGTGC	TTCTCTCAGT	1500
	GTCACTCTGG	CATTCACTCT	TCTTCAGATG	TCACCACCAT	CAGGACAAGT	GTAACCTTTA	1560
	AGCTAAATGA	AGGCAAGTGT	AGTTTGAAAA	ATGCTGAGCT	GTTTCCCGAG	GGTCTGCGAC	1620
30	CAGCACTACC	AGAGAAGCAC	AGCTCAGTAA	AAGAGAGCTT	CCGCTACGTA	AACCTTACAT	1680
	GCAGCTCTGG	CAAGCAAGTC	CCAGGAGCCC	CTGGCCGACC	AAGCACCCCT	AAGGAAATGT	1740
	TTATCACTGT	TGAGTTTGTG	CTTGAAACTA	ACCAAAAGGA	GGTGACAGCT	TCTTGTGACC	1800
	TGAGCTGCAT	CGTAAAGCGA	ACCGAGAAGC	GGCTCCGTAA	AGCCATCCGC	ACGCTCAGAA	1860
	AGGCCCTCCA	CAGGAGGACG	TTTCACTTCC	AGCTCTCAGG	CATGAACCTC	GACGTGGCTA	1920
35	AAAAGCCTCC	CAGAACATCT	GAACGCCAGG	CAGAGTCCTG	TGGAGTGGGC	CAGGGTCATG	1980
	CAGAAAACCA	ATGTGTCTGT	TGCAGGGCTG	GGACCTATTA	TGATGGAGCA	CGAGAAGCCT	2040
	GCATTTTATG	TCCAAATGGA	ACCTTCCAAA	ATGAGGAAGG	ACAAATGACT	TGTGAACCAT	2100
	GCCCAAGACC	AGGAAATCTT	GGGGCCCTGA	AGACCCACGA	AGCTTGGAA	ATGTCTGAAT	2160
	GTGGAGGTCT	GTGTCAACCT	GGTGAATATT	CTGCAGATGG	CTTTGCACCT	TGCCAGCTCT	2220
40	GTGCCCTGGG	CACGTTCCAG	CCTGAAGCTG	GTCGAACCTC	CTGCTTCCCC	TGTGGAGGAG	2280
	GCCTTGCCAC	CAAAATCATG	GGAGCTACTT	CCTTTCAGGA	CTGTGAACCC	AGAGTTCAAT	2340
	GTTTCACTGG	ACATTTCTAC	AACACCAACA	CTCACCGATG	TATTCGTTGC	CCAGTGGGAA	2400
	CATACCAGCC	TGAATTTGGA	AAAAATAATT	GTGTTTCTTG	CCCAGGAAAT	ACTACGACTG	2460
	ACTTTGATGG	CTCCACAAAC	ATAACCCAGT	GTAACCAACG	AAGATGTGGA	GGGGAGCTGG	2520
45	GAGATTTTAC	TGGGTACATT	GAATCCCAAA	ACTACCCAGG	CAATTAACCA	GGCAACACCG	2580
	AGTGTACGTG	GACCATCAAC	CCACCCCAAC	AGCGCCGATC	CCTGATCGTG	GTCCCTGAGA	2640
	TCTTCTCTGC	CATAGAGGAC	GACTGTGGGG	ACTATCTGGT	GATGCGGAAA	ACCTCTTCA	2700
	CCAATTTCTG	GACAACATAT	GAAACCTGCC	AGACCTACGA	ACGCCCCATC	GCCTTCACCT	2760
	CCAGGTCAAA	GAAGCTGTGG	ATTCAGTTCA	AGTCCAATGA	AGGGAAACAG	GCTAGAGGGT	2820
50	TCCAGGTCCC	ATACGTGACA	TATGATGAGG	ACTACCAAGG	ACTCATTGAA	GACATAGTTC	2880
	GAGATGGCAG	GCTCTATGCA	TCTGAGAACC	ATCAGGAAT	ACTTAAGGAT	AAGAACTTAA	2940
	TCAAGGCTCT	GTTTGTATGT	CTGGCCCATC	CCCAGAACTA	TTTCAAGTAC	ACAGCCGAGG	3000
	AGTCCCGAGA	GATGTTTCCA	AGATCGTTCA	TCCGATTGCT	ACGTTCCAAA	GTGTCCAGGT	3060
	TTTTGAGACC	TTACAAATGA	CTCAGCCAC	GTGCCACTCA	ATACAAATGT	TCTGCTATAG	3120
55	GGTTGGTGGG	ACAGAGCTGT	CTTCTTCTG	CATGTCAGCA	CAGTCGGGTA	TTGCTGCCTC	3180
	CCGTATCAGT	GACTCATTTG	AGTTCAATTT	TTATAGATAA	TACAGATATT	TTGGTAAATT	3240
	GAACCTGGTT	TTTCTTTCCC	AGCATCGTGG	ATGTAGACTG	AGAATGGCTT	TGAGTGGCAT	3300
	CAGCTTCTCA	CTGCTGTGGG	CGGATGTCTT	GGATAGATCA	CGGGCTGGCT	GAGCTGGACT	3360
	TTGGTCAGCG	TAGGTGAGAG	TCACTGTGCC	TTCTGGGGTC	TTACTCTCTC	TCAAGGAGTC	3420
60	TGTAGTGGAA	AGGAGGCCAC	AGAATAAGCT	GCTTATTCTG	AAACTTCAGC	TTCTCTTAGC	3480
	CGGGCCCTCT	CTAAGGGAGC	CCTCTGCACT	CGTGTGCAGG	CTCTGACCAG	GCAGAACAGG	3540
	CAAGAGGGGA	GGGAAGGAGA	CCCTTGACAG	CTCCCTCCAC	CCACCTTGAG	ACCTGGGAGG	3600
	ACTCAGTTTC	TCCACAGCCT	TCTCCAGCCT	GTGTGATACA	AGTTTGATCC	CAGGAACCTG	3660
	AGTTCTAAGC	AGTGTCTGTG	AAAAAATAAA	GCAGAAAGAA	TTAGAAATAA	ATAAAACTAA	3720
65	AGCACTTCTG	GAGACAT					
	<u>A16 Protein sequence</u>						
	Gene name: CEGP1						
	Unigene number: Hs.222399						
70	Probeset Accession #: AA256485						
	Protein Accession #: CAB92285						
	Signal sequence: 1-31						
	Transmembrane domains: none						
	PFAM domains: EGF-like_domains [49-84,132-167,177-213,286-321,407-442]						
	CUB_domain [809-918]						
75	Cellular Localization: may be secreted						

	1	11	21	31	41	51	
80	MGVAGRNRPG	AQWAVLLLLL	LLPPLLLLAG	AVPPGRGRAA	GPQEDVDECA	QLLDDCHADA	60
	LCQNTPTSYK	CSCKPGYQGE	GRQCEDIDEC	GNELNGGCVH	DCLNIPGNYR	CTCFDGFMLA	120
	HDGHNCLDLD	ECLENNGGCQ	HTCVNVMGSG	ECCKKEGFPL	SDNQHTCIHR	SEEGLSMKNK	180
	DHGCSHICKE	APRGSVACEC	RPGFELAKNQ	RDCILTCHNG	NGGCQHSCHD	TADGPECSCH	240
	PQYKMHMTDGR	SCLEREDTVL	EVTESNTTSV	VDGDKRVKRR	LLMETCAVNN	GGCDRTCKDT	300

STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK 360
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCQQVCVN 420
 TVGSYECQCH PGYKLHWNKK DCVEVKLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480
 SSDVTTTIRTS VTFKLENGKC SLKNAELFPE GLRPALPEKH SSVKESFRYV NLTCSSGKQV 540
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600
 FHLQLSGMNL DVAKKPPRTS ERQAESCQVG QGHAENQCVS CRAGTYDGA RERCILCPNG 660
 TFQNEEGQMT CEP CPRPGNS GALKTPPEAWN MSECGLCQP GEYSADGFAP CQLCALGTFQ 720
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHFY NTTTHRCIRC PVGTYYQPEFG 780
 KNKCVSCPGN TTTDFDGSIN ITQCKNRRCG GELGDFGTGI ESPNYPGNYP ANTECTWTIN 840
 PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSNSVTTY ETCQTYERPI AFTSRSKKLW 900
 IQFKSNEGNS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960
 LAHPQNYFKY TAQESREMPF RSFIRLLRSK VSRFLRPYK

A17 DNA sequence

Gene name: ESTs
 Unigene number: Hs.293102
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272
 Nucleic Acid Accession #: none found
 Coding sequence: 1-489 (entire sequence is an open-reading-frame)

1 11 21 31 41 51
 | | | | |
 CAAAAAGAAA TAGATAAAAT AAATGGAAAA TTAGAAGAGT CTCCTGATAA TGATGGTTTT 60
 CTGAAGGCTC CCTGCAGAAT GAAAGTTTCT ATTCCAACCTA AAGCCTTAGA ATTGATGGAC 120
 ATGCAAACTT TCAAAGCAGA GCCTCCCGAG AAGCCATCTG CCTTCGAGCC TGCCATTGAA 180
 ATGCAAAAGT CTGTTCCAAA TAAAGCCTTG GAATTGAAGA ATGAACAAAC ATTGAGAGCA 240
 GATCAGATGT TCCTCTCAGA ATCAAAACAA AAGAAGTTG AAGAAAATTC TTGGGATTCT 300
 GAGAGTCTCC GTGAGACTGT TTCACAGAAG GATGTGTGTG TACCCAAGGC TACACATCAA 360
 AAAGAAATGG ATAAAATAAG TGGAAAATTA GAAGATTCAA CTAGCCTATC AAAAATCTTG 420
 GATACAGTTC ATTCTTGTGA AAGAACAAGG GAACCTTCAA AAGACCCCTG TGACCCACGT 480
 TCAGGAAAA

A18 Protein sequence

Gene name: ESTs
 Unigene number: Hs.293102
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272
 Protein Accession #: none found
 Signal sequence: none
 Transmembrane domains: none
 Cellular Localization: nuclear

1 11 21 31 41 51
 | | | | |
 QKEIDKINGK LEESPDNDGF LKAPCRMKVS IPTKALELMD MQTFKAEPPE KPSAFEPAPAE 60
 MQKSVPNKAL ELKNEQTLRA DQMFPSESKQ KXVEENSWDS ESLRETVSQK DVCVPKATHQ 120
 KEMDKISGKL EDSTSLSKIL DTVHSCERTR ELQKDPDPR SGK

Breast**A19 DNA SEQUENCE**

Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ACCGGGCACC GGACGGCTCG GGTACTTTTCG TTCTTAATTA GGTATGCCC GTGTGAGCCA 60
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACCTGTGGC CTACTATCTC TTCCGTGGTG 120
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180
 AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTGTC ACCAGATGCA 300
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTCCTC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAAGT ACAGATGTCTG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAATGTG TGCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCTCTG GCCACGTGTT TACCTTGCA GTCACAGCCT GTGGTCATAG AAGGGGCTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900
 CTTCAATTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTTA TGACTTGTA CTCCCCAAGT CATGGACCAT CCAGGTGGGT 1020
 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCA 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT AGCCGGGCCA 1140
 CTCAGTTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACCTCCCC 1200
 GATGGAAAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 TCCCTGTCC TGAACACGCG GGCCGTCCCT TTGATTTCCA ACAAGATCTG CAACCCACAG 1320
 GACGTGTACG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380

GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACCAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCGGTG TCACCTCCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
 ACCCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA 1620
 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCTTG GAGCTCTGAG 1680
 TTCCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT 1740
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
 AGTGCACTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
 TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCACACC CAACTAATTT 1920
 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 CCTCAAATGA TGTGCCTGCT TCAGCCTCCC ACAGTGCTGG GATTACAGGC ATGGGCCACC 2040
 ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
 AGGGCGGCCT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160
 ACGAGATAAG CAGTTATGTG ACCTCAGCTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCAGTTC TTGATCTCTA GGGACCAGAA 2280
 CCAAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGGCCTAT TTTGATGATT TCTTTGTAGC ATTTGTGCT TGACGTATTA 2400
 TTGTCCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAAAAAA

A20 Protein sequence:

Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_SpC domain: 216-444
 Cellular Localization: not determined

1 11 21 31 41 51
 | | | | |
 MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIILI 60
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLQVF 120
 TAAAWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 VTALHHSYVY REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240
 LCGGSVITPL WIITAACHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFDPDGKVCWT SGWGATEDGA GDASPVLNHA 360
 AVPLISNKIC NHRDVGII SPSMLCAGYL TGGVDSCQGD SGGPLVCQER RLWLKLVGATS 420
 FGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

A21 DNA SEQUENCE

Gene name: ESTs; opposite strand to TRPS1
 Unigene number: none
 Probeset Accession #: AA428090
 Nucleic Acid Accession #: AA428090
 Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ATGAAGCCCA GTTTGAAACA CTGGGCTGAT ATAAAAATGT TTCTGAAAT AGACCAAAGG 60
 CAAGTTGTTG GAGAAGAAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAAAC 120
 TTTTCAGACA CAGATGATCT TATGTCCATA GTGGAGGAAT CAGACAGCTG CTACAACCGT 180
 GATTCTGTTG GGCTTCCCTG TAGAGCTGGA GACAGACTGC AACCCAGAC AAAACCCAGA 240
 GGAAAAACAA CTAACCTCAG CCATTGCCCC AATTTCCACC TTGCTAGTTA TCAGAGTTCA 300
 CTATTGTTTA AGCTCCAGGG GTCATACTAT GGCAATCTAC TGGTGGAAAT TATTCIGAGC 360
 AAGTGTTTTG TTCAGCTTGC AGTATTAAAA CAAAAAAAC ATTGCCTCCA GCTGCAAAAGC 420
 AAGGGCATTG CCATTATGAA AGCCCCCTCA AGACTCTCTG CTATTTTCAA AACATGGAAA 480
 GAAAAAGGGA AAAAAAGAAA AAAAATAATA ATTAGAAGGA TTTGTTCCCT AATTGGGGCT 540
 CCCAAAAATG AGAAATGAAG ATTGTATAAT GAGGGGAGAT ACTAATTATT TTAACCTCTC 600
 CAAGCAAATC TTCTGAAGCA ATCAATTATT TATATACTTT ATGTTCTGTC TTTTGTATAT 660
 TTTCTTCTG GTTAAAAACA TGCAGGTGAG TCTTGCCAAC GTCCTTTCCT ATCTGGATCT 720
 GTTCTGCCTC ATTTCTCTTT CAAAGTCATC TTTCAGGGAA CTGCGCTTGA TTAATTGTAT 780
 TTTAACCAAA CAAATAAGAT ATTGATATA TTAATTTAAA CTTTGTGAGA TGATTGATTA 840
 GGAATTGCAT CATGTTTACA TGAGTATACC GAATTCAAAG TTAACCTTCA TAAGCAGGAG 900
 TTTTACACA TCGTAACATA ATCATTACCC AATACTCGAC ACTCAATATT TGATACTCAA 960
 CTGAATGTTT TTGAAATAAA CACATTTTTA TGTATCTCT CTGGAGAAAG TAGTATATAT 1020
 CTTTTCACAC AAAATATATC AGTGAGAGAG TGTGTTGTTA AGAAAAAAA TCAAAGCACA 1080
 ACAAGTTGAG AGAGTCCAGG CTTTATCAAT ATAAGTAATA ATTTTGTAGA ATGGTGATT 1140
 GATTTCACCA TTTCAATTCA GCAGAGCCTG TATATATATA TATATATATA TATATATATA 1200
 TATATATATA TATATATATA TATATACAA TGATCTGTAT TTCTATTGCT TAGAAGGATG 1260
 AAAGTGAATC CATATAAACC ATACCAACGC CGTTATGTGT AACTGGTGGT AAAACTTTAT 1320
 TATTCAAGTT TAGATGTAAC AGACATCTTT GCTGCCTGAA GATGTTTTCG ATAAGAAATA 1380
 CACCAAGAAC ATGTTTGTGA GTAGAAATGA ACATGCACTA TGAAGACAAA ATAAAAATAA 1440
 ACCGAAAAAT TTCATGTGTT GTAAGAACAG AACTATTATA GCCAACATTC TAGTATTCAA 1500
 ATCAGGACTA CAAATTGAAT TCTTTTCTTT AGCAACATGA AATCATTTCA TATGAAAGAC 1560
 ATTTCTGCT GGTGAATATT GCTGTAAGTT AAATTTTACA TTGGCATTTT GAGATGTTCC 1620
 CCCCTCATGC CTCCCCCAA GTTTTCCATG TGGTTGTCAA ATAGTCCGC

A22 Protein sequence:

Gene name: ESTs; opposite strand to TRPS1
 Unigene number: none
 Probeset Accession #: AA428090
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 113-129
 Cellular Localization: not determined

10 1 11 21 31 41 51
 | | | | | |
 MKPSLKHWD IKMFSEIDQR QVVGEEIHLQ VVSVSYLVEN FSDTDDLMSI VEESDSCYNR 60
 DSVGLPGRAG DRLOPKTKPR GKTNNLSHLP NFHLASYQSS LLFKLQGSYY GNLLVEFILS 120
 KCFVQLAVLK QKKHCLQLQS KGIAIMKAPQ RLSAIFKTKW EKGKKEKKII IRRICSLIWA 180
 15 PKNEK

A23 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Nucleic Acid Accession #: AL133619
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 | | | | | |
 ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCCA GCTCGCCGAC CCCGGGCTCT 60
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCTT TGAGGCGCGA GAGCCCGCAG 120
 30 CTGAGGCAGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240
 GAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCCCTCCCA GGCACACTCA 300
 AACTGCGCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CTGGGGCTCA 360
 GGGGGAACAC AGGACGGGGA GCCCTCCAG ACTGTCTCTG CCCACCTGGC TGCCTGGGCC 420
 CCTGTATGCC AACCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGTACCTCT 480
 35 AGCGTGGGCT GGACGATGTT ATGCAGCCAA GCACAGCACG TGCTGCTCTC GGAAGCCCA 540
 GGGCCTGAGG TCATTGTCAGG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCCT 600
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CTGCCCCTGC TAGATCTTTG 660
 CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720
 ATGCTGGGGG CCGAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
 40 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTGTG TTCCTTGCCA CTGTGCAAG 840
 GCATTTCCCC ATCTCTGACG CGGCCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900
 GCTCACTTCC CATATCTTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGGA 960
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TTCCAGGGA 1020
 45 GACATGGAGA AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCAGTGAG 1080
 CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCTGCAGTGC TGGGGACGCT 1140
 GACAGGACAC GGAAGAGGCG CATGCTTTCC CTGCGGACCT GCTGTTCCAT GTGTCCCAAG 1200
 CCTCCTGCT TTCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGGCCTC TGCTCCCTTG 1260
 GGCGCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320
 50 AGGCTGAAGG AGGGCTCTCT ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTGCG 1380
 GGGGTAGCG CCGACACTGT GOGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440
 TCTGTCAAGT CCACTCTTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500
 TCCTTCAACA AGCAAGATTG AAAAGCTGAC GTCTCCCGA AGGCGGACCT GGAAGAGGAG 1560
 CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTTGGG TACAAGGGCA GGCCAGAAAG 1620
 55 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCGGGC 1680
 AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCCTGC CCCTTCCCTT GCGAAAGCCC 1740
 ACCACACTTA GGCAGTGCAG AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCCTGCAG 1800
 ACCCAAGAGC TCGGCGACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860
 CCGGAGGAAG WVEPGGTTCC CAGGGACCAA GAAGCCACGC ATTTCCCAA GGTCTCCACC 1920
 60 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CTGCCCGCA 1980
 CTGAAGCAGA CCCCAGGAA CACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040
 AAACGGCGCC TGCATCGCTC AGTGCTTGA

A24 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Protein Accession #: T43457
 Signal sequence: none found
 Transmembrane domains: 303-322
 Cellular Localization: not determined

75 1 11 21 31 41 51
 | | | | | |
 MSGAGVAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
 QQQHSEMLAK LHEEIEHLKR ENKGEFARGP RPALPPQAH S TLPLPQHRNT AINSSTRLG S 120
 GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180
 GPEVIAGRQV ATGCSPLDLP PSRAEMGRNP WDSPPARSL PQIAAVARPR ISSPMALSPH 240
 80 MLGAQGIWTH SIQGSPLPAI AATMGTKGGS RVLFPCHLSK ALPHPDGSPH PAQDPGLWSQ 300
 AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVGGP FPSRCGNSS E 360
 LFWAKCGPSR WQPCSCAGDA DRTREEAMLS LGTCCSMCPK PSCFPDGPSP NHLSRASAPL 420
 GARWVCINGV VVEPGGSPSA RLKEGSSRTH RPKGKRGRLA GGSADTVRSP ADSLSMSSFO 480
 SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGGARK 540

EKAESNAGA ACMGNSQHQG RQMAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600
 TQELRHLKSL LEGSQRPQAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA 660
 LKQTPKNNFA ERQKRLQAMQ KRRLHRSVL

A25 DNA SEQUENCE

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Nucleic Acid Accession #: NM_000949
 Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
15  GGAGGCTGAA ATCCCCAGAC GCCGGTTTTC TGGGCTGGGC TTCTGCTTA CTCACCTCCTT 60
    CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTCCACACA ATGGAGCTTC 120
    ATGTCCTCGT GCAGGAAGTA CTCATCGACT GATGTGGCAG ACTTTGCTCC CTGACAAAAC 180
    TAAAGAACTC TCCTATTTCAT GGAGGCGAAC ACTGAGGATG CTTTCACAT GAACCCCTGAA 240
    GTGAACCTTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAATGTGG 300
    CATCTGCAAC CGTTTTCACT CTGCTACTTT TTCTCAACAC CTGCCTTCTG AATGGACAGT 360
    TACCTCCTGG AAAACCTGAG ATCTTTAAAT GTCGTTCTCC CAATAAGGAA ACATTACACT 420
    GCTGGTGGAG GCCTGGGACA GATGGAGGAC TTCCTACCAA TTATTCACCTG ACTTACCACA 480
    GGGAAGGAGA GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCAACTCCT 540
    GCCACTTTGG CAAGCAGTAG ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600
    CTAACCAAGT GGAAGCAGT TTCTCGGATG AACTTTATGT GGACGTGACT TACATAGTTC 660
    AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAACA GCCAGAAGAC AGAAAACCCCT 720
    ACCGTGGATG TAAATGGTCT CCACCTACCC TGATTGACTT AAAAATCTGGT TGGTTACGCG 780
    TCCTGTATGA AATTCGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGCTG 840
    GGCAGCAAAC AGAGTTTAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG 900
    TTGCTGCAA ACCAGACCAT GGATCTGGA GTGCATGGAG TCCAGCGACC TTCATTGAGA 960
    TACCTAGTGA CTCACCATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCCTTCTG 1020
    CTGTCTCTG TTTGATTATT GTCTGGGCGG TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080
    GCATCTTTCC GCCAGTTTCT GGGCCAAAAA TAAAAGGATT TGATGCTCAT CTGTTGAGAG 1140
    AGGGCAAGTC TGAAGAACTA CTGAGTGCTT TGGGATGCCA AGACTTTCTT CCCACTTCTG 1200
    ACTATGAGGA CTGTGCTGGT GAGTATTTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA 1260
    TGTCACTCCA TTCAAAAGAA CACCCAAGTC AAGGTATGAA ACCCAATAC CTGGATCCTG 1320
    AACTGACTC AGGCCGGGGG AGCTGTGACA GCCCTTCCTT TTTGTCTGAA AAGTGTGAGG 1380
    AACCCAGGC CAATCCCTCC ACATTCTATG ATCCTGAGGT CATTGAGAAG CCAGAGAATC 1440
    CTGAAACAAC CCACACTGAG GACCCCGAGT GCATAAGCAT GGAAGGCATA ATCCCTTATT 1500
    TTCATGCTGG TGGATCCAAA TGTTCACAT GGCCTTACC ACAGCCAGC CAGCACAACC 1560
    CCAGATCCTC TTACCAAT ATTAATGATG TGTGTGAGCT GGCTGTGGGC CTTGCAGGTG 1620
    CACCGGCCAC TCTGTTGAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAAACCATTA 1680
    AGTCTAGAGA AGAGGGAAGG GCAACCCAGC AGAGGGAGGT AGAAAGCTTC CATTTCTGAGA 1740
    CTGACCAGGA TACGCCCTGG CTGCTGCCCC AGGAGAAAAC CCCCTTTGGC TCCGCTAAAC 1800
    CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAGATGG TGCAATATCA TTGCTACCAA 1860
    AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT 1920
    ATGCCAAGGT GTCCGGGGTC ATGGATAACA ACATCTGGT GTTGGTGCCA GATCCCATG 1980
    CTAAGAAAGT GGCCTGCTTT GAAGAATCAG CCAAGAGGC CCCACCATCA CTGAAACAGA 2040
    ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100
    TGGGTGGTTT GGATTACCTG GATCCCGCAT GTTTTACACA CTCCTTTCAC TGATAGCTTG 2160
    ACTAATGGAA TGATTGGTTA AAATGTGATT TTTCTTCAGG TAACACTACA GAGTACGTGA 2220
    AATGCTCAAG AAGTATGCTA GACTGACACT ACTAAAGCTC CCAGCTCCTT TCATGCTCCA 2280
    TTTTAAACCA CTGCTCTCTT TCTCCAGCAG CTGATTCCAG AACAATCAT TATGTTTCTT 2340
    AACTGTGATT TGATAGTTA CTTTTGCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400
    AAAAGCACAC TCTTAGTAGT TCCTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAAAAG 2460
    GCTTTCATGA TTTGGCATGG GACAGACGGA AATGAAATTG TCAAAATGT TTACCATAGA 2520
    AAGATGACAA AGAAAAATTG TCCACATAGG AAAATGCCAT GAAAATGTCT TTTGAAAAAC 2580
    AACTGCATAA CCTTACACT CCTCGTCCAT TTTATTAGGA TTACCCAAAT ATAACCATT 2640
    AAAAGAAAGAA TGCATTCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA 2700
    TTGCTGATAT GCAAGTAAGA AAT
  
```

A26 Protein sequence:

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Protein Accession #: NP_000940
 Signal sequence: 1-23
 Transmembrane domains: 237-253
 FN3 domains: 28-112, 127-215
 Cellular Localization: plasma membrane

```

75  1      11      21      31      41      51
    |      |      |      |      |      |
    MKENVASATV FTLLFLNLTC LLNGQLPPGK PEIFKCRSPN KETFTCWWRP GTDGLPTNY 60
    SLTYHREGET LMHECPDYIT GGPNSCHFVK QYTSMWRTYI MMVNATNMQG SSFSDELYVD 120
    VTYIVQPDPP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAAEW 180
    80  EIHFAQQTE FKILSLHPQG KYLVQVRCKP DHGYWSAWSP ATFIQIPSDF TMNDTTVWIS 240
    VAVLSAVICL IIVWAVALKG YSMVTCIFPP VPGPKIKGFD AHLEKKGSE ELLSALGCQD 300
    FPTSDEYEDL LVEYLEVDSD EDQHLMSVHS KEHPSQGMKP TYLDPDTSRG RGCDSPSLL 360
    SEKCEBPQAN PSTFYDPEVI EKPENPETH TWDPQCISME GKIPYFHAGG SKCSTWPLPQ 420
  
```

PSQHNPRSSY HNIITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQQREVE 480
 SFHSETDQDT PWLLPQEKTP FGSAPLDYV EIHKNVDGA LSLLPKQREN SGKPKPGTP 540
 ENNKEYAKVS GVMDNINILVL VDPHAKNVA CFESAKEAP PSLEQNQAEK ALANFTATSS 600
 KCRLQLGGGLD YLDPACFTHS FH

A27 DNA SEQUENCE

Gene name: Human neuro peptide Y receptor Y1 (NPYY1)
 Unigene number: Hs.169266
 Probeset Accession #: L07615
 Nucleic Acid Accession #: NM_000909.1
 Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CATTCCCACC CTTCCTTCTT TAATAAGCAG GAGCGAAAAA GACAAATTCC AAAGAGGATT 60
 GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATT CCAATATCGGG 120
 AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTAAA 180
 20 ATAATCTATA ACAACCAAC CAATCAAAAT GAATTCACAA TTTATTTCCC AGGTTGAAAA 240
 TCATTTCAGTC CACTCTAATT TCTCAGAGAA GAATGCCAG CTCTCGGCTT TTGAAAATGA 300
 TGATTGTCTC CTGCCCCTTG CCATGATATT TACCTTAGCT CTGCTTATG GAGCTGTGAT 360
 CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAC AAAAGGAGAT 420
 25 GAGAAATGTT ACCAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTTGCCAT 480
 CATGTGTCTC CCCTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC 540
 GATGTGTAAG TTGAATCCTT TTGTGCAATG TGTTCGAATC ACTGTGTCCA TTTTCTCTCT 600
 GGTTCCTCATT GCTGTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660
 TAATAGACAT GCCTTATGTG GTATTGCTGT GATTGGGTC CTGCTGTGG CTCTTCTTT 720
 30 GCCTTTCCTG ATCTACCAAG TAATGACTGA TGAGCCGTTT CAAAATGTAA CACTTGATGC 780
 GTACAAAGAC AAATACGTGT GCTTTGATCA ATTTCCATCG GACTCTCATA GGTGTCTCTA 840
 TACCACCTCT CTCTTGGTGC TGCAGTATTT TGGTCCACTT TGTTTTATAT TTATTTGCTA 900
 CTTCAAGATA TATATAGGCC TAAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA 960
 TAAGTACAGG TCCAGTGAAA CAAAAGAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020
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 GATCATGTCT ACCTGCAACC ACAATCTGTT ATTCCTGCTC TGCCACCTCA CAGCAATGAT 1140
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 40 ATTTAAAAAA ATCAACAACA ATGATGATAA TGAAAAAATC TGAAACTACT TATAGCCTAT 1380
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 45 AATATAAGA CTTTATACT GTACTTATG GAATGAATT TCTTTAAGT ATTACGATGC 1680
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 TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800
 TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860
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 50 TTTTTTCACC TTAAGGGAGG CTTTCATTTC CTCCGACTG ATTGTCACTT AAATCAAAAT 1980
 TTAAAAATGA ATAAAAAGAC ATACTTCTCA GCTGCAATA TTATGGAGAA TTGGGCACCC 2040
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 AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT 2160
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 55 TTGTCAAGCT TCTGGTCTAA TATGTACTCG AAAGACTTTC CGCTTACAAT TTGTAGAAAC 2280
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 AAACATATAT TTAAGAAACA AGACATACTT CAATGTATTA TACAGATAAA GTATTACATG 2640
 TGTTTGATTT TAAAGGGCGG GACATTTTAT TAAAAATCAAT ATTGTTTTTG CTTTCTCTGA 2700
 GGAGTCTCTT TCAGTTTCAT TTTTCTCAT CCCATGACTT CCCTCCGATG GT

A28 Protein sequence:

Gene name: Human neuro peptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds
 Unigene number: Hs.169266
 Probeset Accession #: L07615
 Protein Accession #: NP_000900.1
 Signal sequence: none found
 Pfam domains: 7tm_1 [57-91]
 Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286,
 300-322
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MNSTLFSQVE NHSVHNSFSE KNAQLLAFEN DDCHLPLAMI FTLALAYGAV IILGVSGNLA 60
 LIIILKQKE MRNVNINILV NLSFSDLLVA IMCLPFTFVY TLMDDHVVFE AMCKLNPFVQ 120
 CVSITVSIFS LVLIIVERHQ LIINPRGWRP NNRHAYVVGIA VIWVLAVASS LPFLIYQVMT 180
 DEFPQNVTLTD AYKDKYVCFD QPPSDSHRLS YTTLLLVLYQY FGPLCFIFIC YFKIYIRLKR 240
 RNNMMDKMRD NKYRSSETRK INIMLLSIVV AFVFCWLPIT IFNTVFDWNH QIIATCNHNL 300
 LFLLCHLTAM ISTCVNPIFY GFLNKNFQRD LQFFNFNCFDF RSRDDDDYETI AMSTMHTDVS 360

KTSCLKQASPV AFKKINNDD NEKI

A29 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)
 Unigene number: Hs.208229
 Probeset Accession #: AI819198
 Nucleic Acid Accession #: NM_032551.1
 Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

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GACGCCTGGC TCGTGCCTCT CTTCTTCGCG GCGCTGATGC TGTGCGCCT GGTGGGGAAC 180
TCGCTGGTCA TCTACGTCAT CTGCCGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240
ATGCCCAACC TGGCGGCCAC GGACGTGACC TTCCTCCTGT GCTGCGTCCC CTTCACGGCC 300
CTGCTGTACC CGTGCCTCCG CTGGGTGCTG GCGCACTCA TGTGCAAGTT CGTCAACTAC 360
ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420
TGGTACGTGA CGGTGTTCCC GTTGCGCGCC CTGCACCGCC GCACGCCCGC CCTGGCGCTG 480
GCTGTACAGC TCAGCATCTG GGTAGGCTCT CCGGCGGTGT CTGCGCCGGT GCTCGCCCTG 540
CACGCGCTGT CACCCGGGCC GCGCGCTTAC TGCACTGAGG CCTTCCCGAG CCGCGCCCTG 600
GAGCGCGCTT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGTGCGCGCT GCTCGCCACC 660
TGCCTGCTGT ATGCGGCCAT GCTGCGCCAC CTGGGCCGGG TCGCCGTGCG CCGCGCGCCC 720
GCCGATAGCG CCCTGACAGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGGCCAAG 780
GTCTCGCGCG TGGTGGCGCG CGTGGTCTCT CTCTTCGCGG CCTGCTGGGG CCCCATCCAG 840
CTGTTCTCTG TGCTGCAGGC GCTGGGCCCC GCGGGCTCCT GGCACCCACG CAGCTACGCC 900
GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCCTACA GCAACTCCGC GCTGAACCCG 960
CTGCTCTACG CCTTCCTGGG CTGCACTTTC CGACAGGCCT TCCGCCGCGT CTGCCCTTGC 1020
GCGCGCGGCC GCCCGCGCGC CCCCGCGCGG CCGGACCCCT CGGACCCCGC AGCCCCACAC 1080
GCGGAGCTGC ACCGCTCTGG GTCCACCCG GCCCGGCCCA GGGCGCAGAA GCCAGGGAGC 1140
AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA

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A30 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA
 Unigene number: Hs.208229
 Protein Accession #: AI819198
 Signal sequence: none found
 Pfam domains: 7tm_1 [59-323]
 Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
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SLVIYVICRH KPMRTVTNFI IANLAATDVT FLLCCVPFTA LLYPLPGWVL GDFMCKFVNY 120
IQQVSQVATC ATLTAHSVDR WYVTVPFLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180
HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240
ADSALQGGVL AERAGAVRAK VSRLVAAVVL LFAACWGPQI LFLVLQALGP AGSWHPRSYA 300
AYALKTWAHC MSYSNSALNP LLYAFLGSHF RQAFRRVCPC APRRRRRPRR PGPSDPAAPH 360
AELHRLGSHP APARAQKPGS SGLAARGLCV LGEDNAPL

```

A31 DNA SEQUENCE

Gene name: CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)
 Unigene number: Hs.252387
 Probeset Accession #: NM_014246
 Nucleic Acid Accession #: NM_014246
 Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

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GCCTTCGCCC TCCGGCCCGG CTGTACCTAC GCGGTGGGCG CCGCTTGACG GCCCGGGGCG 180
CCGCGGGAGC TGCTGGACGT GGGCCGCGAT GGGCGGCTGG CAGGACGTGC GCGCGTCTCG 240
GGCGCGGGGC GCCCGCTGCC GCTGCAAGTC CGCTTGGTGG CCGCAGTGC CCCGACGGCG 300
CTGAGCCGCC GCCTGCGGAC GCGCAGCAC CTTCGCGGCT GCGGAGCCGC TGCCCGGCTC 360
TGCGGAACCG GTGCCCGGCT CTGCGGGGCG CTCTGCTTCC CCGTCCCCGC GCGCTGCGCG 420
GCCGCGCAGC ATTCGGCGCT CGCAGTCCG ACCACCTTAC CCGCTGCGCG CTGCCCGCGC 480
CGCCCCAGGC CCGCTGTGCC CCGCGCTCCC ATCTGCGCTG CGCCGGGCGG CTCGGTCCGC 540
CTGCGTCTGC TGTGCGCCCT GCGGCGCGCG GCTGGCGCGG TCCGGGTGGG ACTGGCGCTG 600
GAGGCGGCCA CCGCGGGGAC GCCCTCCGCG TCGCCATCCC CATCGCCGCC CCGTCCGCGC 660
AACTTGCCCG AAGCCCGGGC GGGGCGCGCG CGACGGGCCG GCGGGGCGAC GAGCGGCAGA 720
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GGCACCTCA TCCTCCAGCT GCACGCGCAC TACACCATCG AGGGCGAGGA GGAGCGCGTG 840
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GCCACGGGCG CCGTGAGCAC GGACAGCGTA CTGGACCGCG AGACCAAGGA GACGACGCTC 960
CTCAGGGTGA AAGCCGTGGA CTACAGTACG CCGCCGCGCT CGGCCACCAC CTACATCACT 1020
GTCTTGGTCA AAGACACCAA CGACCACAGC CCGGTCTTCG AGCAGTCGGA GTACCGCGAG 1080
CGCTGCGGG AGAACCTGGA GGTGGGCTAC GAGGTGCTGA CCATCCGCGC CAGCGACCCG 1140

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	GACTCGCCCA	TCAACGCCAA	CTTGCGTTAC	CGCGTGTGG	GGGGCGCGTG	GGACGTCTTC	1200
	CAGCTCAACG	AGAGCTCTGG	CGTGGTGAGC	ACACGGGGCG	TGCTGGACCG	GGAGGAGGCG	1260
	GCCGAGTACC	AGCTCCTGGT	GGAGGCCAAC	GACCAGGGGC	GCAATCCGGG	CCCGCTCAGT	1320
5	GCCACGGCCA	CCGTGTACAT	CGAGGTGGAG	GACGAGAACG	ACAACCTACCC	CCAGTTTCAGC	1380
	GAGCAGAACT	ACGTGGTCCA	GGTGCCCGAG	GACGTGGGGC	TCAACACGGC	TGTGCTGCGA	1440
	GTGCAGGCCA	CGGACCGGGA	CCAGGGCCAG	AACGCGGCCA	TCACTACAG	CATCCTCAGC	1500
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	CCCTTGATT	TCGAGGATGT	CCAGAAATAC	TCGCTGAGCA	TTAAGGCCCA	GGATGGGGGC	1620
10	CGGCCCCCGC	TCATCAATTC	TTTCAGGGTG	GTGCTGTGTC	AGGTGCTGGA	TGTCAACGAC	1680
	AACGAGCCTA	TCTTTGTGAG	CAGCCCCCCTC	CAGGCCACGG	TGCTGGAGAA	TGTGCCCTTG	1740
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	CACATACGCC	TGGTGGACAC	GGCCTCCACC	TTTCTGGGGG	GCGGCAGCGC	TGGGCTTAAG	1860
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15	GTGTGTGCCG	AGCTGCACCG	CGAGGAGGTG	GAGCACTACA	GCTTCGGGGT	GGAGGCGGTG	1980
	GACCACGGCT	CGCCCCCAT	GAGCTCCTCC	ACCAGCGTGT	CCATCACGGT	GCTGGACGTG	2040
	AATGACAACG	ACCCGGTGT	CACGACGCC	ACCTACGAGC	TTGCTCTGAA	TGAGGATGCG	2100
	GCCGTGGGGA	GACGCGTCT	GACCTGCAG	GCCCGCGACC	GTGACGCCAA	CAGTGTGATT	2160
	ACCTACCAGC	TCACACGGG	CAACACCCGG	AACCGCTTG	CACCTCAGCAG	CCAGAGAGGG	2220
20	GGCGGCCCTCA	TCACCCCTGGC	GCTACCTCTG	GACTACAAGC	AGGAGCAGCA	GTACGTGCTG	2280
	GCGGTGACAG	CATCCGACGG	CACACGGTCG	CACACTGCGC	ATGTCCTAAT	CAACGTCAT	2340
	GATGCCAACA	CCACAGGCC	TGTCTTTTCA	AGCTCCCAT	ACACAGTGAG	TGTCAGTGAG	2400
	GACAGGCTGT	TGGGCACCTC	CATTGCTACC	CTCAGTGCCA	ACGATGAGGA	CACAGGAGAG	2460
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25	AGTGGCACCA	TGTACACCAT	GATGGAGCTG	GACTATGAGA	ACCAGGTCCG	CTACACGCTG	2580
	ACCATCATGG	CCCAGGACAA	CGGCATCCCG	CAGAAATCAG	ACACCAACAC	CCTAGAGATC	2640
	CTCATCCTCG	ATGCCAATGA	CAATGCACCC	CAGTTCCTGT	GGGATTTCTA	CCAGGGTTCC	2700
	ATCTTTGAGG	ATGCTCCACC	CTCGACACAG	ATCCTCCAGG	TCTCTGCCAC	GGACCCGGAC	2760
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30	TTCTACATCG	AGGCCACGCT	CGGTGTGATT	CGCACCCAGC	GCCGGCTGGA	CCGGGAGAA	2880
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	GCCTCGGTAG	AAATCCAGGT	GACCATCTTG	GACATTAATG	ACAATGCCCC	CATGTTTGTG	3000
	AAGGACGAAC	TGGAGCTGTT	TGTTGAGGAG	AACAACCCAG	TGGGGTCCGT	GGTGCCAAAG	3060
	ATTCGTGCTA	ACGACCTCTG	TGAAGGCCCT	AATGCCCAGA	TCATGTATCA	GATTGTGGAA	3120
35	GGGACATGCG	GGCATTTCTT	CCAGCTGGAC	CTGCTCAACG	GGGACCTCGG	TGCCATGGTG	3180
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	CTGCCCCGACT	TCCAGATCCT	CTTCAACAAC	TATGTACCCA	ACAAGTCCAA	CAGTTTCCCC	3360
	ACCGGCGTGA	TCGCTGTGAT	CCCGGCCCAT	GACCCGACG	TGTGAGACAG	CCTCAACTAC	3420
40	ACCTTCGTGT	AGGGCAACGA	GCTGCGCCTG	TTGCTGCTGG	ACCCCGCCAC	GGGCGAACTG	3480
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	TCTGATGGCA	TCCACAGCGT	CACGGCCTTC	TGCACCTGCG	GTGTCAACAT	CATCACGGAC	3600
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	TCCCGCTGCG	TGGCCCTCTT	CGTGGAGGGG	GTGGCCGCGG	TGCTGTCCAC	CACCAAGGAC	3720
45	GACGTCTTCG	TCTTCAACGT	CCAGAACGAC	ACCGACGTCA	GCTCCAACAT	CCTGAACGTG	3780
	ACCTTCTCGG	CGCTGTGCTC	TGGCGGCGTC	CGCGGCCAGT	TCTTCCCGTC	GGAGGACCTG	3840
	CAGGAGCAGA	TCTACCTGAA	TCGGACGCTG	CTGACCAACA	TCTCCACGCA	GCGCGTCTG	3900
	CCCTTCGACG	ACAACATCTG	CCTGCGCGAG	CCCTGCGAGA	ACTACATGAA	TGCGTGTCTC	3960
	GTTCTGCGAT	TCGACAGCTC	CGCGCCCTTC	CTCAGCTCCA	CCACCGTGCT	CTTCCGGCCC	4020
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	CGCGAGGGCG	GCTACACCTG	CGAGTGCTTC	GAGGACTTCA	CTGGAGAGCA	CTGTGAGGTG	4200
	GATGCCCGCT	CAGGCGCTG	TGCCAACGGG	GTGTGCAAGA	ACGGGGGCAC	CTGCGTGAAC	4260
	CTGCTCATCG	GCGGCTTCCA	CTGCGTGTGT	CCTCTGCGCG	AGTATGAGAG	GCCCTACTGT	4320
55	GAGGTGACCA	CCAGGAGCTT	CCCCCCCCAG	TCCTTCGTCA	CCTTCCGGGG	CCTGAGACAG	4380
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	GGTGTGAGTG	ACGGGCGGTG	GCACCTCTGT	CAGGTGCACT	ACTACAACAA	GCCCAATATT	4620
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	GCCCAGGGCA	CTCAGACCGG	CTCCAAGAAG	TCCCTGGATC	TGACCGGCCC	TCTACTCTG	4800
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	GGGAAGAACT	GTAGCAAGC	CATGCCCTCAC	CCCCAGCTCT	TCAGCGGTGA	GAGCGTCTGT	5100
	TCCTGGAGTG	ACCTGAACAT	CATCATCTCT	GTGCCCTGGT	ACCTGGGGCT	CATGTTCCGG	5160
	ACCGGGAAGG	AGGACAGCGT	TCTGATGGAG	GCCACCACTG	GTGGGCCCA	CAGCTTTCGC	5220
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	GTGGTGGTGC	GAGGCGCCTC	TGAAGACAAG	GTCTCCGTGC	GCCGTGGATT	CCGAGGCTGC	5520
75	ATGCAGGGAG	TGAGGATGGG	GGGGACGCC	ACCAACGTCG	CCACCTGAA	CATGAACAAC	5580
	GCACCTAAGG	TCAGGGTGAA	GGACGGCTGT	GATGTGGACG	ACCCCTGTAC	CTCGAGCCCC	5640
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5	CGCAATGAGA	CGCAGGTGGA	CGGCGCCAGG	GCCCTGCAGC	TGGTGAGGGC	GCTGCGCAGT	6420
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25	GGGATCAACC	AGACGGAAAA	CCCGTTTCTG	TGCACAGTGG	TTGCCATCCT	CCTCCACTAC	7620
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	AAGCACCATT	ATTATGGGAA	AAAAGGGATC	GTCTCCCTGC	TGAGGACCCG	ATTCTCTCTG	7980
	CTGCTGCTCA	TCAGCGCCAC	CTGGCTGCTG	GGGCTGCTGG	CTGTGAACCG	CGATGCACTG	8040
	AGCTTTCACT	ACCTCTTCGC	CATCTTCAGC	GGCTTACAGG	GCCCTTCGT	CCTCCTTTTC	8100
	CACGTGCTGC	TCAACACAGA	GGTCCGGAAG	CACCTGAAGG	GCGTGTCTCG	CGGGAGGAAG	8160
35	CTGCACCTGG	AGGACTCCGC	CACCACCAGG	GCCACCCTGC	TGACGCGCTC	CCTCAACTGC	8220
	AACACCACCT	TCGGTGACGG	GCCTGACATG	CTGCGCACAG	ACTTGGGCGA	GTCCACCGCC	8280
	TCGCTGGACA	GCACTGCTCAG	GGATGAAGGG	ATCCAGAAGC	TCGGCGGTGC	CTCTGGGCTG	8340
	GTGAGGGGCA	GCCACGGAGA	GCCAGACCGG	TCCCTCATGC	CCAGGAGCTG	CAAGGATCCC	8400
	CCTGGCCACG	ATTCGACTC	AGATAGCGAG	CTGTCCCTGG	ATGAGCAGAG	CAGCTCTTAC	8460
40	GCCTCCTCAG	ACTCGTCAGA	CAGCGAGGAC	GATGGGGTGG	GAGCTGAGGA	AAAATGGGAC	8520
	CCGGCCAGGG	CGCGCTCTCA	CAGCACCCCC	AAAGGGGACG	CTGTGGCCAA	CCACGTTCCG	8580
	GCCGGCTGGC	CCGACACAGG	CCTGGCTGAG	AGTGACAGTG	AGGACCCCG	CGGCAAGCCC	8640
	CGCCTGAAGG	TGGAGACCAA	GGTCAGCGTG	GAGCTGCACC	GCGAGGAGCA	GGGCAGTCA	8700
	CGTGGAGAGT	ACCCCCCGGA	CCAGGAGAGC	GGGGGCGCAG	CCAGGCTTGC	TAGCAGCCAG	8760
45	CCCCCAGAGC	AGAGGAAAGG	CATCTTGAAA	AATAAAGTCA	CCTACCCGCC	GCCGCTGACG	8820
	CTGACGGAGC	AGACGCTGAA	GGGCGGGCTC	CGGGAGAAAG	TGGCCGACTG	TGAGCAGAGC	8880
	CCCACATCCT	CGCGCACGTC	TTCCTTGGGC	TCTGGCGGCC	CCGACTGCGC	CATCACAGTC	8940
	AAGAGCCCTG	GGAGGGAGCC	GGGGCGTGAC	CACCTCAACG	GGGTGGCCAT	GAATGTGCGC	9000
	ACTGGGAGCG	CCCAGGCCGA	TGGCTCCGAC	TCTGAGAAAC	CGTGAGGCAA	GCCCGTCACC	9060
50	CCACACAGGC	TGCGGCATCA	CCCTCAGACC	TTGAGGCCCA	AGGGGCCACT	GCCCTTGAAG	9120
	TGGAGTGGGC	CCAGAGTTGT	GCGGTCCCCA	TGGTGGCAGC	CCCCGACTG	ATCATCCAGA	9180
	CACAAAGGTC	TTGGTTCTCC	CAGGAGCTCA	GGGCTGTCTA	GACCTGTGTA	CAAGTGCCAA	9240
	AGGCCACAGG	CATGAGGGAG	GCGTGGACCA	CTGGGCCAGC	ACCCTGAGT	CCTAAGACTG	9300
	CAGTCAAAGC	CAGAAGTGAG	AGGGGACCCC	AGACTGGGCG	CAGAGGCTGG	CCAGAGTTCA	9360
55	GGAAAGCCGG	GCACAGACCA	AAGACCGCGG	TCCAGCCCGG	CCCAGGCGGG	CATCTCATGG	9420
	CAGTGGGAC	CCGTGGCTGG	CAGCCCGGGC	AGTCTTTTGC	AAAGGCACCC	CTTGTCTTAA	9480
	AATCACTTCC	CTATGTGGGA	AAGGTGGAGA	TACTTTTATA	TATTTGTATG	GGACTCTGAG	9540
	GAGGTGCAAC	CTGTATATAT	ATTGCACTCG	TGCTGACTTT	GTTATCCCGA	GAGATCCATG	9600
	CAATGATCTC	TTGCTGTCTT	CTCTGTCAAG	ATTGCACAGT	TGTACTTGAA	TCTGGCATGT	9660
60	GTTGACGAAA	CTGGTGCCCC	AGCAGATCAA	AGGTGGGAAA	TACGTACGCA	GTGGGGCTAA	9720
	AACCAAGCCG	CTAGAAGCCC	TACAGCTGCC	TTCCGCCAGG	AAGTGAGGAT	GGTGTGGGCG	9780
	CTCCCGCCCG	GCCCCCTGGG	TCCCCAGTGT	TCGCTGTGTG	TGCGTTTGTG	CTCTGCTGCC	9840
	ATCTGCCCCG	GCTGTGTGAA	TTCAAGACAG	GGCAGTGACG	CAC TAGGAGG	GTGTGAGGAG	9900
	CCCTGCTGAG	GTCACTGTGG	GGCAGGTTG	CCACACGGCT	GTCATTTTTT	ACCTGGTCACT	9960
65	TCTGTGACCA	CCACCCCTC	CCCTCACC	CTCCAGGTG	GCCCCGGAGC	TGCAGGTGGG	10020
	GATGGCTTTG	TCCTTTGCTC	CTGCTCCCGG	TGGGACCTGG	GACCTTAAAG	CGTTGCAGGT	10080
	TCCTGATTTG	GACAGAGGTG	TGGGGCCTTC	CAGGCGGTTA	CATACCTCCT	GCCAAATCTC	10140
	TAACCTCTCT	AGACTGCGAG	GATCTCCAGG	CAGGGTCTCT	CCCTCTGGAG	TCTGACCAAT	10200
	TACTTCATTG	TGCTTCAAAT	GGCCAATTGT	GCAGAGGGAC	AAAGCCACAG	CCACACTCTT	10260
70	CAACGGTTAC	CAAACTGTTT	TTGGAAATTC	ACACCAAGGT	CGGGCCCACT	GCAGGACAGT	10320
	GGCACAGCGT	GGCCCCGAGG	GCTGTGGAAC	GGGTCCCGAG	ACTGTACAGC	ATGTTTGATT	10380
	TTAGCGTTTC	CTTTGTTCTT	CAAAATCAGG	GCCCCAAATA	GTGATCAGCA	CAGCTGCTTC	10440
	CAAAATAGGAG	AAACCATAAA	ATAGGATGAA	AATCAAGTAA	AATGCAAAGA	TGTCCACACT	10500
	GTTTTTAACT	TGACCTGAT	GAAAATGTGA	GCACTGTTAG	CAGATGCCCTA	TGGGAGAGGA	10560
75	AAAGCGTATC	TGAAAATGGT	CCAGGACAGG	AGGATGAAAT	GAGATCCCCAG	AGTCTCACA	10620
	CCTGAATGAA	TTATACATGT	GCCTTACCAG	GTGAGTGGTC	TTTCGAAGAT	AAAAAACTCT	10680
	AGTCCCTTTA	AACGTTTGGC	CCTGGCGTTT	CCTAAGTACG	AAAAGSTTTT	TAAGTCTTCG	10740
	AACAGTCTCC	TTTCACTGAT	TTAACAGGAT	TCTGCCCCCT	GAGGTGTAAT	TTTTTTGTTT	10800
	TATTTTCTTC	CACGTACTCC	ACAGCCAACA	TCACGAGGTG	TAATTTTAA	TTTGATCAGA	10860
80	ACTGTTACCA	AAAAACAAC	GTCAAGTTTA	TTGAGATGGG	AAAAATGTAA	ACCTATTTT	10920
	ATTACTTAAG	ACTTTATGGG	AGAGATTAGA	CACCTGGAGG	TTTTAACAGA	ACGTGTATTT	10980
	ATTAATGTTT	AAAAACTGG	AATTACAAAT	GAGAAGAGTC	TACAATAAAT	TAAGATTTT	11040
	GAATTTGTAC	TTCTGCGGTG	CTGGTTTCTC	TCCACAAACA	CCCCCGCCCC	TCCCCATGCC	11100
	CAGGGTGGCC	GTGGAAGGGA	CGGTTTACGG	ACGTGCAGCT	GAGCTGTCCG	TGTCCCATGC	11160
	TCCCTCAGCC	AGTGGAACGT	GCCGGAACCT	TTTGTCCATT	CCCTAGTAGG	CCTGCCACAG	11220

CCTAGATGGG CAGTTTTTGT CTTTCACCAA ATTTGAGGAC TTTTTTTTTT TGCCATTATT 11280
TCTTCAGTTT TCTTTTCTTG CACTGATCTT TCTCCTCTCC TTCTGTGACT CCAGTGACTC 11340
AGACGTTAGA CCTCTTGATG TTTTCCCACT GGTCCCTGAG GCTCTGTTC

A32 Protein Sequence

Gene name: CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSRI), Hs.252387
Unigene number:
Protein Accession #: NP_055061
Signal sequence: 1-20
Cadherin domains: 250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092, 1110-1199
Pfam domains: Laminin_EGF [2003-2048], 7tm_2 [2465-2708]
Latrophilin/GPS domains: 2407-2460
Transmembrane domains: 1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704
Cellular Localization: plasma membrane

1 11 21 31 41 51
MAPP PPPVLP VLLLLAAAA LPAMGLRAAA WEPRVPGGTR AFALRPGCTY AVGAACTPRA 60
PRELLDVGRD GRLAGRRRVS GAGRPLPLQV RLVARSAPTA LSRRRLRARTH LPGCGARARL 120
CGTGARLCGA LCFVPVPGCA AAQHSALAAP TTLPACRCPP RPRPRCPGRP ICLPPGGSVR 180
LRLLCALRAA AGAVRVGLAL EAATAGTPSA SPSPSPPLPP NLPEARAGPA RRARRGTSGR 240
GSLKFPMPNY QVALFENEP A GTLILQLHAH YTIEGEEERV SYMEGLFDE RSRGYFRIDS 300
ATGAVSTDSV LDRRETKETHV LRVKAVDYST PPRSATTYIT VLVDKTDNHS PVFEQSEYRE 360
RVRENLEVG Y EVLTIRASDR DSPINANLRY RVLGGAWDV FQLNESSGVVS TRAVLDREEA 420
AEYQLLVEAN DQGRNPGLS ATATVYIEVE DENDNYPQFS EQNYVVQVPE DVGLNTAVLR 480
VQATDRDQGG NAAIHYSILS GNVAGQFYLH SLSGILDVIN PLDFEDVQKY SLSIKAQDGG 540
RPPLINSSGV VSVQVLVDND NEPIFVSSPF QATVLENVPL GYPVVIQAV DADSGENARL 600
HYRLVDTAST FLGGGSAGPK NPAPTDFEFF QIHNSSGWIT VCAELDREEV EHSYFGEAV 660
DHGSPPMSSS TSVSITVLVD NDNDPVFTQP TYELRLNEDA AVGSSVLTLO ARDRDANSVI 720
TYQLTGGNTR NRRFALSSQRG GGLITLALPL DYKQEQQYVL AVTASDGT RS HTAHVLI NV T 780
DANTHRPVFQ SSHTYTVSVE DRPVGTSIAT LSANEDTGE NARITYVIQD PVPQFRIDPD 840
SGTMYTMMEL DYENQVAYTL TIMAQDNGIP QKSDTTTLEI LILDANDNAP QFLWDFYQGS 900
IFEDAPPSTS ILQVSATDRD SGPNRGLLYT FQGGDDGDGD FYIEPTSGVI RTQRRLDREN 960
VAVYNLWALA VDRGSPPTLS ASVEIQVTIL DINDNAPMFE KDELELFVEE NNPVGSVVAK 1020
IRANDPDEGP NAQIMYIVE GDMRHFQQLD LLNGDLRAMV ELDFEVRREY VLVVQATSAP 1080
LVSRATVHIL LVDQNDNPPV LPDFQILFNN YVTNKSNSPF TGVIICIPAH DPDVSDSLNY 1140
TFVQGNELRL LLLDPATGEL QLSRDLNDR PLEALMEVS VSDGIHSVTAF CTLRVTTITD 1200
DMLTNSITVR LENMSQEKFL SPLALFVEG VAAVLSTTKD DVVFVNQND TDVSSNINLV 1260
TFSALLPGGV RGQFFPSED L QEQIYLNRTL LTTISTQRVL PFDDNICLRE PCENYMKCVS 1320
VLREDSSAPF LSSTTVLFRP IHPINGLR CR CPPGFTGDYC ETEIDL CYSD PCGANGRCRS 1380
REGGYTCECF EDFTGEHCEV DARSGR CANG VCKNGGTCVN LLIGGFHCVC PPGEYERPYC 1440
EVTRTSFPFQ SFVTFRGLRQ RFHFTISLTF ATQERNGLLL YNGRFNEKHD FIALEIVDEQ 1500
VQLTFSAGET TTTVAPKVPS GVSDGRWHSV QVQYYNKPNI GHGLPLPHGPS GEKMAVTVTD 1560
DCDITMAVRF GKDIGNSYCA AQTGTGSKK SLDLTGPLLL GGVENLPEDF PVHNRQFVGC 1620
MRNLSVDGKN VDMAGFIANN GTREGCAARR NFCDGRRCQN GGTVCNRRNM YLCECPLRFG 1680
GKNCEQAMPH PQLFSGESV SVSDLNIIIS VPWYLGMLFR TRKEDSVLME ATSGGPTSFR 1740
LQILNNYLQF EVSHGSPDVE SVMLSGLRVT DGEWHLLIE LKNVKEDSEM KHLVTMTLDY 1800
GMDQNKADIG GMLPGLTVRS VVVGASEDK VSVRRGFRGC MQGVRMGGTP TNVATLNMNN 1860
ALKVRVKDGC DVDDPCTSSP CPPNSRCHDA WEDYSCVCDK GYLGINCVDA CHLNPCENMG 1920
ACVRSPGSPQ GYVCECGPSH YGPYCENKLD LPCPRGWGN PVCPCPCAV SKGFDPDCNK 1980
TNQCQCCKEN YYKLLAQDTF LPCDCFP HGS HSRTCDMATG QCACKPGVIG RQCNRCNDNF 2040
AEVTLGCEV IYNGCPKAF AGIWWPQTKF GQPAAVPCPK GSVGNAVRHC SGEKGLPE 2100
LFNCTTISFV DLRAMNEKLS RNETQVDGAR ALQLVRALRS ATQHTGTILFG NDVRTAYQLL 2160
GHVLQHSWQ QGFDLAATQD ADFHEDVIHS GSALLAPATR AAWEQIQRS GGTAQLLRL 2220
EGYFSNVARN VRRYTLRPFV IVTANMILAV DIFDKFNFTG ARVPRFDTH EEFPRELESS 2280
VSPFADFFRP PEKEGPELLR PAGRRTTPQT TRPGPGTERE APISRRRRHP DDAGQFAVAL 2340
VIYRTLQQL LPERYDPDRR SLRLPHRPII NTPMVSTLVY SEGAPLPRPL ERPVLVEFAL 2400
LEVEERTKPV CVFWNHS LAV GGTGGWSARG CELLSNRNTH VACQCSHTAS FAVLMDISRR 2460
ENGEVLP LKI VTYAAVSLSL AALLVAVLL SLVRMLRSNL HSIKHLAVA LFLSQLVFI 2520
GINQTENPFL CTVAAILLHY IYMSTFAWTL VESLHVYRML TEVRNIDTGP MRFYVVVGW 2580
IPAIVTGLAV GLDPQGYGNP DFCWLSLQDT LIWSFAGPIG AVIIINTVTS VLSAKVSCQR 2640
KHYYGKGI VSLRLTAFL LLLISATWLL GLLAVNRDAL SFHYLFAIFS GLQGPVLLF 2700
HCVLNQEV RK HLKGVLGGRK LHLDSATTR ATLLTRSLNC NTTFGDGPDM LRTDLGESTA 2760
SLDSIVRDEG IQKLGVS SGL VRGSHGEPDA SLMPRSCKDP FGHSDSDSE LSLDEQSSSY 2820
ASSHSSDSDE DGVGAEEKWD PARGAVHSTP KGDVAHVHVP AGWPDQSLAE SDSSEDPGSKP 2880
RLKVETKVS V ELHREEQGS RGEYPPDQES GGAARLASSQ PPEQRKGILK NKVTYPPPLT 2940
LTEQTLKGRL REKLADCEQS PTSSRTSSLG SGGPDCAITV KSPGREPGRD HINGVAMNVR 3000
TGSAQADGSD SEKP

A33 DNA SEQUENCE

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3
Unigene number: Hs.198252
Probeset Accession #: X95876
Nucleic Acid Accession #: X95876
Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
CCAACCACAA GCACCAAGC AGAGGGGCG GCAGCACACC ACCCAGCAGC CAGAGCACCA 60
GCCCAGCCAT GTCTCTGAG GTGAGTGACC ACCAAGTGCT AAATGACGCC GAGGTTGCCG 120

5
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 20
 25
 30
 35
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CCCTCCTGGA GAACCTTCAGC TCTTCCTATG ACTATGGAGA AAACGAGAGT GACTCGTGCT 180
GTACCTCCCC GCGCTGCCCA CAGGACTTCA GCCTGAACCT CGACCGGGCC TTCTTGCCAG 240
CCCTCTACAG CCTCCTCTTT CTGCTGGGGC TGCTGGGCAA CGGCGCGGTG GCAGCCGTGC 300
TGCTGAGCCG GCGGACAGCC CTGAGCAGCA CCGACACCTT CCTGCTCCAC CTAGCTGTAG 360
CAGACACGCT GCTGGTGCTG ACACGTCCCG TCTGGGCAGT GGACGCTGCC GTCCAGTGGG 420
TCTTTGGCTC TGGCCTCTGC AAAGTGGCAG GTGCCCTCTT CAACATCAAC TTCTACGCAG 480
GAGCCCTCCT GCTGGCCTGC ATCAGCTTTG ACCGCTACCT GAACATAGTT CATGCCACCC 540
AGCTCTACCG CCGGGGGGCC CCGGCCCGCG TGACCTCAC CTGCTGGCT GTCTGGGGG 600
TCTGCCTGCT TTTGCGCCTC CCAGACTTCA TCTTCCTGTC GGCCACCCAC GACGAGCGCC 660
TCAACGCCAC CCACTGCCAA TACAACCTCC CACAGGTGGG CCGCACGGCT CTGCGGGTGC 720
TGCAGCTGGT GGTGCGCTTT CTGCTGCCCC TGCTGGTCAT GGCCTACTGC TATGCCACA 780
TCCTGGCCGT GCTGCTGGTT TCCAGGGGCC AGCGGCGCCT GCGGGCCATG CGGCTGGTGG 840
TGGTGGTCGT GGTGGCCTTT GCCCTCTGCT GGACCCCTTA TCACCTGGTG GTGCTGGTGG 900
ACATCCTCAT GGACCTGGGC GCTTTGGCCC GCAACTGTGG CCGAGAAAGC AGGGTAGACG 960
TGGCCAAAGT GGTCACTCA GGCCTGGGCT ACATGCACTG CTGCCTCAAC CCGCTGCTCT 1020
ATGCCTTTGT AGGAGTCCCA TTCCGGGAGC GGATGTGGAT GCTGCTCTTG CGCTGGGCT 1080
GCCCAACCA GAGAGGCTC CAGAGGCAGC CATCGTCTTC CCGCCGGGAT TCATCCTGGT 1140
CTGAGACCTC AGAGGCTC TACTCGGCT TGTGAGGCCG GAATCCGGG TCCCTTTTCG 1200
CCCACAGTCT GACTTCCCCG CATTCAGGC TCCTCCCTCC CTCTGCCGGC TCTGGCTCTC 1260
CCCAATATCC TCGCTCCCGG GACTCACTGG CAGCCCCAGC ACCACCAAGT CTCCCGGAA 1320
GCCACCTCC CAGCTCTGAG GACTGCACCA TTGCTGCTCC TTAGCTGCCA AGCCCCATCC 1380
TGCGCGCCGA GGTGGCTGCC TGGAGCCCA CTGCCCTCT CATTTGAAA CTAAACTTC 1440
ATCTTCCCA AGTCGGGGA GTACAAGCA TGGCGTAGAG GGTGCTGCC CATGAAGCA 1500
CAGCCCAGGC CTCAGCTCA GCAGTGACTG TGGCCATGGT CCCCAGACC TCTATATTTG 1560
CTCTTTTATT TTTATGTCTA AAATCCTGCT TAAACTTTT CAATAAACAA BATCGTCAGG 1620
ACCAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA BHCLITERAT 1680
UREBHCBLAS TPBHCORTHO LOGUESMOUS ECXCRMYLEV SERQVLDASD FAFLEENSTS 1740
PYDYGENESD FSDSPPCPD FSLNFDRTFL PALYSLLFLL GLLGNGAVAA VLLSQRTALS 1800
STDFTLLHLA VADVLLVLT PLWAVDAVQ WVFGPGLCKV AGALFNINFY AGAFLLACIS 1860
FDRYLSIVHA TQIYRRDPRV RVALTCIVVW GLCLLFFALPD FIYLSANYDQ RLNATHCQYN 1920
FPQVGRFALR VLQLVAGFL PLVMAYCYA HILAVLLVSR QRRFRAMRL VVVVVAFAV 1980
CWTPYHLVVL VDILMDVGV LARNCGRESHV DVAKSVTSGM GYMHCCLNPL LYAFVGVKFR 2040
EQMWMLFTRL GRSDQRGPQR QPSSSRRESS WSETTEASYL GL
  
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A34 Protein sequence

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3
 Unigene number: Hs.198252
 Protein Accession #: P49682
 Signal sequence: none found
 Pfam domains: 7tm_1 [70-318]
 Transmembrane domains: 57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323
 DRY box: 148-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MVLEVS DHQV LNDAEVAALL ENFSSSYDYG ENESDSCCTS PPCPDPSLN PDRAFLPALY 60
 SLLFLLGLLG NGAVAAVLLS RRTALSSDTT FLLHLAVADT LLVLTPLWA VDAAVQWVFG 120
 SGLCKVAGAL FNINFYAGAL LLACISFDYR LNIHVATQLY RRGPPARVTL TCLAVWGLCL 180
 LFALPDFIFL SAHNDERLNA THCQYNFPQV GRTALRVLQL VAGFLLPLLV MAYCYAHILA 240
 VLLVSRGQRR LRMRRLVVVV VVAFALCWTP YHLVVLVDIL MDLGALARNC GRESRVDAK 300
 SVTSLGLVMH CCLNPLLYAF VGVKFRERMW MLLRLGLCPN QRLQRPSS SRDSSWSSET 360
 SEASYSGL

A35 DNA SEQUENCE

Gene name: Differentially expressed C016 gene (clone MGC:5257)
 Unigene number: Hs.69517
 Probeset Accession #: AA447522
 Nucleic Acid Accession #: BC001291
 Coding sequence: 44-541 (start and stop codons are underlined)

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1 11 21 31 41 51
| | | | |
GGGGGCGCCG CGCGCTGACC CTCCCTGGGC ACCGCTGGGG ACGATGGCGC TGCTCGCCTT 60
GCTGCTGGTC GTGGCCCTAC CGCGGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG 120
AGATCCAGAG GACTCCCAGC GAACGGACGA GGGTGACAAT AGAGTGTGGT GTCATGTTTG 180
TGAGAGAGAA AACACTTTTC AGTGCCAGAA CCCAAGGAGG TGCAAATGGA CAGAGCCATA 240
CTGCGTTATA GCGGCCCGGA AAATATTTCC ACGTTTTTTC ATGGTTGCGA AGCAGTGCTC 300
CGCTGGTTGT GCAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGAAGA 360
GCCCATGCCC TCCTTTTACC TCAAGTGTG TAAATTCGC TACTGCAATT TAGAGGGGCG 420
ACCTATCAAC TCATCAGTGT TCAAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG 480
GCTGTGGCTG GCCATCCTCC TGCTGCTGGC CTCCATTGCA GCCGGCCTCA GCCTGTCTTG 540
AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTTGTC 600
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ACATTCAGAG GAAGTCCAGA TCTCCTGAGT AGTGATTTTG GTGACAAGTT TTTCTCTTTG 780
AAATCAAACC TTGTAACCTA TTTATTGCTG ATGGCCATCT TTTTCTTGA CTCCCTCTG 840
CCTCTGAGGG CTTCAGTATT GATGGGGAGG GAGGCCTAAG TACCACATCAT GGAGAGTATG 900
TGCTGAGATG CTTCCGACCT TTCAGGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATTG 960
GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGCAGTGG GGCACACGTT 1020
AGGGCTGCCC CCATTCCAGT GGTGGAGGCG CTGTGGATGG CTGCITTTTC TCAACCTTTT 1080
  
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CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTG AAGAACTTA GACTTCACCC 1140
 ACCAGCTGGC ACAGGTGCAC AGATTCATAA ATTCCCACAC GTGTGTGTTT AACATCTGAA 1200
 ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260
 CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCACCC AAAAACAAAT ACAAGGGGAC 1320
 TTCAAAGTT CACGAAAAAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAA

A36 Protein sequence:

Gene name: Differentially expressed CO16 gene (clone MGC:5257)
 Unigene number: Hs.69517
 Probeset Accession #: AA447522
 Protein Accession #: AAH01291
 Signal sequence: 1-17 (first underlined sequence)
 Transmembrane domain: 146 - 162
 Cellular localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MALLALLLVV ALPRVWTDAN LTARQRDPED SQRTDEGDNR VVCHVCEREN TFECQNPRRC 60
 KWTEPYCVIA AVKIFPRFFM VAKQCSAGCA AMERPKEEEK RFLLEBPMPF FYLKCKCKIRY 120
 CNLEGGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSLSL

A37 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 | | | | |
 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG 60
 CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCC GGGAAACAACT TCACCAATGA 120
 GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCCG GCGCCTGGCA 180
 GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGTATGAG AAGGAGTGCC CCAAGGCTAA 240
 GTCGAAATGT GGCCCAACCT TCTTCCCTG TGCCAGCGCG ATCCATTGCA TCATTGGTCG 300
 CTTCGGGTGC AATGGGTTTG AGGACTGTCC CGATGCGAGC GATGAAGAGA ACTGCACAGC 360
 AAACCCCTCTG TTTGTCTCCA CCGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA 420
 GAGCTTCATC TCGCATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
 AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
 TTACCCGAGC ATCACCTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
 CCTGCTGGCA CTGGTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCCG 660
 GCACCCGGCTG CAGCACCGCT TGCTGCTGTC CCGCCTGGTG GTCCCTGGACC ACCCCACCA 720
 CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
 GAATGCGTCG GAAGTAGGCT CCCACCCCTC CTACTCCGAG GCCTTGCTGG ACCAGAGGCC 840
 TGGGTGGTAT GACCTTCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900
 CGACCTGCCC CCTTACCGCT CCGGTCCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960
 CAGCAGCCTC CTGAGCGTGG AAGACACCCG CCACAGCCCG GGGCAGCCTG GCGCCAGGGA 1020
 GGGCAGTGTG TAGCCCAAGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTG TAACAATTG 1140
 TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
 AACTATCTCT GCATTCCCTT CCTCCCCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260
 TGACATGATC TGTGTGCGT CTTTCTGTG AGGTCACTCT TCCCTTGGGA CCCGAGATCA 1320
 CACCTCATTT TTTCACATTA TTCTGTTTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380
 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
 CGCTGGACCC AATTCCTCTT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTGGGTTAG 1500
 ATGATCTAAC CAGGAGGCCA TCACCTGGATG GTCACCCCCC CAAAAAATT CCATTGAGC 1560
 ATCAAAACCT GCTTTGCACA ATCCTATTG ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620
 AAGAAACTT TGGACGTGAG TAACACCCCT CAGCAGTCGC AACGTTATTT TGGTTTGTG 1680
 AAGGACTCTG AAACCATCTA CCTGTATATA ATTCTGGCTT TAGAAATTTG CCCAAGAATG 1740
 CTCATTCTGA GAGCTTTCCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800
 GAGCCCTCC CATGAGTTTA TCCAAGTTCT CAGTCCTTAA AATGCAGGCT GCCAAGACCC 1860
 TACACCTGCC CTGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCACC CTCCAGCTG 1920
 ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAGTC TGACCTGGCT 1980
 GTATGTCCCT GTGCCCCACA CCCAGCCTGT CTTGCTCATT CATGCAGCCT CAACACTGGC 2040
 CTCCAAAGTT CCCTTAACAC TTGCAAAGTC CTTTTTACCT GTGCATTGG ACTTGAGGAC 2100
 ACTGGTTTCT ATCAGAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
 CTGCACTGTG CACGCTCCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220
 GGTGAGGTC AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
 AGACAATTG GAGCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340
 TGAAACAGTG TGTGTGTTTT TTCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA 2400
 AGCTGTCTCT TTTTTGTTT TTCTTTTAAAC AAGTCCAAA GAAAGATGCA AAAGGAGATC 2460
 ACACCTTGC CCCGCTGAGC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
 ACATTGTGTC ATTGTGCAC TTTGAGTTA TTATTTATCA AGTTCCTGAA GGAAGCAGAA 2580
 AGAGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640
 TTCTCTGTGT CAGCTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT 2700
 AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGAA CCAGGTAGAG 2760
 CCACCTCGGG CAGCTGTAC CATTTCAGAA CTTCTTTCCG CAGCTGAAGA AATGTTCACT 2820
 AACCTGTTTG ACGTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTGAG 2880
 TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAAACCA ATCCAAAGGA TGTACAGAA 2940
 AAGCTAGCCA CTGGTATTTT GTTTGTTTAA AAAAAAATAA GAAAGAAAGA AAGAAAGAAA 3000

AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120
 CATTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTTCTTC 3180
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATCTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTATG 3300
 AGATAAGGGA TGCTACTATA TGCTTTTATA AAACAAACAG GGACATTTT ATTATAGATT 3360
 TGATTTTAT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTTCCACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG 3540
 AAAATAGTCT CATCTCTTTT TTTCTCAAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720
 GAAAGGTGT GTGTCTGTGC TTTTGTGTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780
 TTATACCTT TAATAAATTT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GWMCTAMARM 3840
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCACTTCGGG 3900
 TGGGGCGGCG GGGCCACGT AGGTACGGCG ACCACGGGG CCCAACGGG ACCCCAGAAG 3960
 GAAACCTCG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCGCCGGG 4020
 GGAAACCGCA GAGTGTGCG TAAACACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
 GGACTCAACC AGGAGACCC AAGGGAACCC GATAGAGTAC G

A38 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MWLLGPLCLL LSSAAESQLL PGNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60
 EKECPKAKSK CGPTFFPCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNGLCIDKSF ICDQNNQC NSDEESCESS QEPGSGQVFW TSENQLVYYP SITYAIISS 180
 VIFVLVVALL ALVLHHRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240
 YVASQAEQNA SEVGSPPSYS EALLDQRPBW YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEFRDSEPSQ GTEEV

A39 DNA sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGCTGCTG GCTTCTTGAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
 GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CTCCCGAGG GCGAGGCAGC 120
 GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC 180
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240
 CCGCGGCGGC CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCCT 300
 CGCTGCGTC CTGGAAGTTT CCGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360
 TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCATC AGCGAGTGCA 420
 ACTCATAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
 GCTCTGGAC CTAGGGCCCG GCGTCGTGCG CTCCTGGGCG TCGCGGCGA GGGGAGTGGC 540
 CCGCGCGGAA AGCGCCGCGG GACAGTCAGT GACGAGGCCG GGGGGTCGCC GGGGCCACGA 600
 CTTCTCGAG ACCGTCTGCG GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660
 TGTGGGGCGC TCGCCGCTCG TCCGTCTCCT CATCTGGAA CGCCGCTTCG CTCCTGCAGC 720
 TGCTGCTGGC TGCGTGTGCT GCGCGGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780
 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCCAGCGC 840
 GGCAGCGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960
 CGGGCGGACA AAGACGGGGC CGGACGGCTC GGCAGGGCTT CATGCTTAG GGGTACCCAA 1020
 GGAGACGGCG AGGGTGCGCC CCCACCCGTG AGGGCTTGGC AGCGGTGCTC CCCTGAAGGC 1080
 TCCCGGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGG TGGTCCCGG TGGCAGACGC 1140
 CGCGGATTCC CATCTCTCC ACGCGGCGGC CCCTCTCCCC TGCAGCGGGC CGCCTTGCCT 1200
 ATCTACGTGC CGTTCCTCAT TGTGGGCTCC GTGTTTGTG CTTTATCAT CTTGGGGTCC 1260
 CTGGTGGCAG CCGTGTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCA GCAGAGCCGA 1320
 GCGCCAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCAAGTGC CAGCACCTCC 1380
 CGGGGGTCTG CCTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440
 GGGGCCCCGG CGCCCCCAAC AAGGTCACAG ACCAAGTGT GTTGGCCGGA AGGGACCATG 1500
 AACAAAGTGT ATGTCAACAT GCCACGAAT TTCTCTGTG TGAACITGTA GCAGGCCACC 1560
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGCAG 1620
 CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCCTGCA GCCTGGCTAC 1680
 AGCGAGATTC AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
 ACTGTATAAC CGAGAGTCAAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAAGTCC GCACATGTG GTGGTATTTA TGGCACGATT CCTTTGGATG 1860
 GCTTCATTG CCCCAGACT GTATGAAAC ATCTCCGAAT TAGCATTCTT GGATATGTTT 1920
 CATCCAGGAT ATCATTGATT TATGATGGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
 AGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTATTAT TATTTCTTTT 2100

TTGTTGTGTA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160
 TTTTITTTTT TTTTITTTAA TCAGACAGGG TCTTGTCTG TTGCCAGGC TGGAGTGCAG 2220
 TGGTGCATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCTGCCTC 2280
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTT 2340
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400
 TCTGCCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
 TGAGCCTTTT TTTTITTTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520
 ATTCTAAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATCCACA 2580
 GGCACACCTT AATTTCATG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640
 GGGCTATTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
 TTA AAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACCTA ATGAAGACAT TTCAGAACTC 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCCCTTC 2820
 TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTT 2880
 TATATTGAAA TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940
 TGGTTATGGT TTGGCGTTTC CTTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCCT 3000
 GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060
 AAAAAATTTT TTGCTTAGT TATAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
 TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAAGTAC GATTACTTT 3180
 GCAGATCATA AGGCTTTTTA TACTCTTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240
 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTTCTCCAC ACTGTTCTTG 3300
 ATTTCTCTC TCCTTCAGGC CTCACAGGC ACTGTATTCA TTGCCAATGT TCCAAATAT 3360
 CAAATTCAG TGAATTTAT TGTGTGTTCT TTACTTATAT AAAAAAGAT AACTTTAAGG 3420
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAATCGCT 3480
 GTATGGTATG GTCTTCTACA CATTATGTC TATAGATATC TATCGATCAT CTTCTATTC 3540
 TGTTCATGA CTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
 TTTTAAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
 TGAAAAAAA AAAAAAAA AAAAAAAA

A40 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular localization: not determined

1 11 21 31 41 51
 | | | | |
 MLSGFLMSPS TQHRAYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
 GEAEKGNRGE PPWIRAAQQ PRPPAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPEA 120
 SGRQPRGPSD CIPRFPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAEAGSG 180
 PRGKRRGTVS DEARGSPGFR LLGDRPALSG DALSAFVVPV CGALAARPSF HPGTPLRSCS 240
 CCWLRCWRRG RGPSEYCHG WLDAQGVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300
 ARLDQGGGCDN DRQQGAGEFG RADKDGPRRL GRASCLRGTD GDGEGAPFPV RAWQRCSPGE 360
 SPKGRQLLRA FPGLLPRARR RGFSSSPRGG PSPLQRPALP IYVPFLIVGS VFVAFIILGS 420
 LVAACCCRCI RPKQDPQQSR APGGNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS 480
 GARAPPTRSQ TNCCLPEGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGGYL HPPVVGTVQ 540
 HDSVEMTAVP PFMDLQPGY RQIQSPFPHT NSEQMYPVAV TV

A41 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
 CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTACACAG TTTCTTCCAA CTTGCGCATT 120
 GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
 ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
 ATGGTTATTC ATCACTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
 CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
 GAAACCACTG ATAAGCAATTT ATCACTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
 TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTCA 600
 GAAGAAAAAC TCTGCGACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
 TTACTATTTA GTTTTITTTA TGTGTTTGCA ATAGTCTTAT TAAAAAATAT GTTTTITTTA 720
 TCTGAAAAAA AAAAAAAA AAAAAAAA

A42 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular localization: secreted

5
1 11 21 31 41 51
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTIDKNLS PDGQYVPRIM 120
FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

A43 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Nucleic Acid Accession #: AF189723
Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

20
1 11 21 31 41 51
ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
TCTCAGTTTA AAAATCCCTT TATTATGCTG CTCTCTGGCT CTGCAGTCAT CAGTGTTTTA 240
ATGCATCAG TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300
25 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
CCAGAAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420
CCAGGTGATA CAGTTTGCTT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTC 480
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540
AAGGTGACAG CTCTCAGGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600
30 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCTT TGGAAACAGGA 660
GAAAATTCTG AATTGGGGGA GGTTTTTAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780
ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840
ATTAGTGTA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTCAAGTGT 900
35 ACGCTAGCTC TTGGTGTAT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960
ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCAG ATAAACTGAG AACACTGACG 1020
AAGAATGAAA TGACTGTATC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTACT 1080
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTTGTTGATG GTGATGTTGT TCATGGATT 1140
TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
40 AGAAACAATA CTCTAATGGG GAAGCCAAACA GAAGGGGCCCT TAATTGCTCT TGCAATGAAG 1260
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAA CTGAATACCC TTTTAGCTCT 1320
GAGCAAAAGT GGAATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
TGTTTTATGA AAGGTGCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAAG GAAGGCACGC 1500
45 ATGGGCTCAG CGGGACTCAG AGTCTTGCTT TTGGCTTCTG GTCCCTGAAC GGGACAGCTG 1560
ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
ACACACTCA TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATT 1680
GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCCAAAA CTTCCAGTCA AGTCTCAGGA 1740
GAAGAAATAG ATGCAATGGA TGTTTCAGCAG CTTTCACAAA TAGTACCAAA GGTTCAGTA 1800
50 TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860
TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCGA TTGCTCTGAA GGCTGCAGAC 1920
ATTGGAGTTG CGATGGGCCA GACTGGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
CTAGTGGATG ATGATTTTCA AACCATATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040
AATAACATTA AAAATTTTCT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTA 2100
55 ATCTCATTTG CTACATTAAT GAACCTTCTT AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160
ATCAATATTA TTATGGATGG ACCCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCATTC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTGATA 2280
CTTAAATATG TTTTATTCAT AATAATCATT GTTTGTGGGA CTTTGTGTTG CTTCTGGCGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
60 TTTTGTGACA TGTTCATATG ACTAAGTTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520
CTAGTTATTT ACTTTCCTCC GCTTCAGAA GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
65 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT GA

A44 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Protein Accession #: AAF27813
Signal sequence: none found
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
Cellular Localization: not determined

80
1 11 21 31 41 51
MIPVLTSKKA SELPVSEVAS ILQADLQNGL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI 60
SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQEYRSEK SLEELSKLVP 120
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS 180
KVTAQPAAAT NGDLASRSNI AFMGLTVRCG KAKGVVIGTG ENSEFGEVFK MMQAEAPKT 240
PLQKSMDDLK QQLSFYSFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGLPFIVTV 300

TLALGVMRMV KKRAIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360
 GVGYNQFGEV IVDGDDVVHGF YNPAVSRIVE AGCVCNDAVI RNNTLMGKPT EGALIALAMK 420
 MGLDGLQDDY IRKAIEYFSS EQKWMVAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480
 5 GQTLTLTQQQ RDVYQKEKAR MGSAGLRVLA LASGPBLGQL TFLGLVGIID PPRTGVKEAV 540
 TTLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG EEIDAMDVQQ LSQIVPKVAV 600
 FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMQGTGT DVCKEADAMI 660
 LVDDDFQTIM SAIEBGKGIY NNIKNFVRFO LSTSI AALT I SLATLMNFP NPLNAMQILW 720
 10 INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
 ELRDNVITPR DTTMTFTCFV FDFMFNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840
 LVIIYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVERSRKIQ KHVSTSSSF 900
 LEV

A45 DNA sequence

Gene name: ESTs
 15 Unigene number: Hs.157601
 Probeset Accession #: W07459
 Nucleic Acid Accession #: AC005383
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60
 25 TTTTATTTGC AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120
 CCTGGCGGTA GTTCTCCCGA CCTCAGCCGG GTCCGGTCTG GCCGCCCTCT CCCAGGAGAG 180
 ACAAAACAGGT GTCCACGCTG GCAGCCGCGC CCCGGGCGCC CCTCTGTGTA TCCCGTAGCG 240
 CCCCTGGGCC CGAGCCGCGC CCGGTCTGTG GAGTAGAGCC GCCCGGCGAC CGAGCGCTGG 300
 30 TCGCCGCTCT CCTTCCGTTA TATCAACATG CCCCTTTTCC TGTGTCTGGA GGCCGTCTGT 360
 GTTTTCTCTG TTTCCAGATG GCCCCATCTC CTCCCTCTCC AGGAAGTCCA TGTAAGCAAA 420
 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480
 ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCGGGAAAG GGAGCTTTGA AAGGTCCAAG 540
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CGAGAGGGGT CAGAGTGGGA 600
 GCATTCCAGT TCAGTTCAC TCCTCATCTG GAATTTCCCT TGGATTCTAT TTCAACCCAA 660
 35 CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
 CTGTCTCTGA AATACCTTCT GCACAGAGGG TTGCTGGAG CGAGAAATGC TTCTGTGCC 780
 CAGATCTCA TCATGTCAC TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAAG 840
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG 900
 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCACG TGCTGTTGGC TGAGCAGGTG 960
 40 GAGGATGCCA CCAACGGCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCCAGCGCC 1020
 ACGCCAGACT CGAGGGTCGA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGTTCCGG 1080
 GAGTTCGCTG GCAATGCCCC ATGCTGGAGA GGATCGCGGC GGACCTTGC GGTGCTGGCT 1140
 GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTGCG CACTGTCTAC 1200
 AGGACCACTT GCCCAGGCC CTGTGACTCG CAGCCTTGCC AGAATGGAGG CACATGTGTT 1260
 45 CCAGAAGGAC TGGACGGCTA CCAATGCCCT TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320
 TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCGACCTCC TCTTCTGCTG GGACAGCTCT 1380
 GCGGGCACCA CTCTGGACCG CTCTCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG 1440
 GCCGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500
 CTGTGTCGCG TGCCGTGTGG GGAGTACCAG GATGTGCTG ACCTGGTCTG GAGCTCGAT 1560
 50 GGCATTCCCT TCCGTGGTGG CCCCACTCTG ACGGGCAGTG CCTTGCGGCA GCGCGCAGAG 1620
 CGTGGCTTCG GGAGCGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGTTTGTG 1680
 CTCACCTAGT CACACTCCGA GGATGAGGTT GCGGGCCAG CGCTCACGCG AAGGGCGCGA 1740
 GAGCTGCTCC TGCTGGGTGT AGGCACTGAG GCCGTGCGGG CAGAGCTGGA GGAGATCACA 1800
 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATCCCT 1860
 55 GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCAGGGT GCCGACACA AGCCTTGGAC 1920
 CTGCTCTTCA TGTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980
 AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTGCGC 2040
 CTGGTGGTGT ATGGCAGCCA GGTGCACTG GCCTTCGGGC TGGACACCAA ACCCAACCGG 2100
 GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCCTACCTAG GTGGGGTGGG CTCAGCCGGC 2160
 60 ACCGCCCTGC TGCACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCCTGGT 2220
 GTCCCCAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCGGTTCTT 2280
 GCCCAGAAGC TGAGGAACCA TGGCATCTCT GTCTTGGTCG TGGGCGTGGG GCCTGTCCTA 2340
 AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC CGGGATTCCC TGATCCACGT GGCAGCTTAC 2400
 GCCGACCTGC GGTACCAACA GGACGTGCTC ATTGAGTGGC TGTGTGAGA AGCCAAGCAG 2460
 65 CCAGTCAACC TCTGCAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAA 2520
 GGGAGCTACC GCTGCAAGTG TCGGGATGCG TGGGAGGGCC CCCACTGCGA GAACCGTGAG 2580
 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATT TTAGAGACGCC CCTGAGGCAC 2640
 ATGGCTCCCG TGCAGGAGGG CAGCAGCGGT ACCCCTCCCA GCAACTACAG AGAAGGCTGT 2700
 GGCACTGAAA TGGTGCTTAC CTCTGTGAAT GTCTGTGCCC CAGGTCTCTA GAATGTCTGC 2760
 70 TTCCCGCCGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820
 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCACCCACA AACGATGTTG TTGAAAAGTT 2880
 TTGATGTGTA AGTAAATACC CACTTCTGTG ACCTGCTGTG CCTTGTGAG GCTATGTCAT 2940
 CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCTCTGAG ACTTAAATTT AGCGGCCTGA 3000
 CGTTCTCTTG CACACAATCA ATGCTGCCCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060
 75 AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAGACA 3120
 GCAGCTTTTC CACTTCCCCA GAGACATCTT GGATGCATTT GCATTGAGTC TGAAGGGGGG 3180
 CTTGAGGAC GTTTGTGACT TCTTGGCGAC TGCCCTTTGT GTGTGGAAGA GACTTGGAAA 3240
 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT 3300
 80 TGTGATGGG CCCAGTCTGT GAGGGCCACG TAAATCGTT CTGAGTCTG AGCAGTGTCC 3360
 ACCTTGAAGG TCTTTC

A45 Protein sequence

Gene name: ESTs

Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGW domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPFLDSFST QQEVKARIKR 120
MVFKGGRRET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
FAVGVRFRPW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPCPCD 300
SQPCQNGGTC VPGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVFFVRFPV RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLVGVS 480
EAVRAELEEI TGSFKHVMVY SDPQDLFNQI PELQKLCSSR QRPGRCTQAL DLVFMMLDTSA 540
SVGPENFAQM QSFVRSCALQ FEVNPDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APVLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLNRNGI 660
SVLVVGVGFPV LSEGLRLRAG PRDSLHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP 720
CMNEGSCVLO NGSYRCKCRD GWEGPHCENR EWSSSCVCSV QGWILETPLR HMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP

```

COLONA47 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTCACAG TTTCTTCCAA CCTTGCCATT 120
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
ATGGTTATTC ATCACCCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCTTAGAAT CATGTTTGTA 420
GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
TATGAGCCTC GGGATTTACC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTCAT 600
GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAA 720
TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

```

A48 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLRSGWGD DITWVQTYEE GLFYAQKSKK 60
PLMVIHHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDQYVPRIM 120
FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

```

A49 DNA SEQUENCE

Gene name: G protein-coupled receptor 56
 Unigene number: Hs.6527
 Probeset Accession #: AA478599
 Nucleic Acid Accession #: NM_005682
 Coding sequence: 163-2244 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
CGGCAGCAGG GTCTCGCTCT GTACACACAG CTGGAGTGCA GTGGTGTGAT CTTGGCTCAT 60
CGTAACCTCC ACCTCCCGGG TTCAAGTGAT TCTCATGCCT CAGCCTCCCG AGTAGCTGGG 120
ATTACAGGTG GTGACTTCCA AGAGTGACTC CGTCGGAGGA AAATGACTCC CCAGTCGCTG 180

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5	CTGCAGACGA	CACTGTTCCT	GCTGAGTCTG	CTCTTCCTGG	TCCAAGGTGC	CCACGGCAGG	240
	GGCCACAGGG	AAGACTTTTC	CTTCTGCAGC	CAGCGGAACC	AGACACACAG	GAGCAGCCTC	300
	CACTACAAAC	CCACACCAGA	CCTGCGCATC	TCCATCGAGA	ACTCCGAAGA	GGCCCTCACA	360
	GTCCATGCCC	CTTTCCTGTC	AGCCCCACCT	GCTTCCCGAT	CCTTCCCTGA	CCCCAGGGGC	420
	CTCTACCACT	CTGCTCTCTA	CTGGAACCGA	CATGCTGGGA	GATTACATCT	TCTCTATGGC	480
	AAGCGTGA	TCTTGCTGAG	TGACAAAGCC	TCTAGCCTCC	TCTGCTTCCA	GCACCCAGGAG	540
	GAGAGCCTGG	CTCAGGGCCC	CCCGCTGTTA	GCCACTTCTG	TCACCTCCTG	GTGGAGCCCT	600
	CAGAACATCA	GCCTGCCACG	TGCCGCCAGC	TTCACTTCT	CCTTCCACAG	TCCTCCCCAC	660
10	ACGGCCGCTC	ACAATGCCTC	GGTGGACATG	TGCGAGCTCA	AAAGGGACCT	CCAGCTGCTC	720
	AGCCAGTTCC	TGAAGCATCC	CCAGAAGGCC	TCAAGGAGGC	CCTCGGCTGC	CCCCGGCCAG	780
	CAGCAGTTGC	AGAGCCTGGA	GTGAAACTG	ACCTCTGTGA	GATTCATGGG	GGACATGGTG	840
	TCCTTCGAGG	AGGACCGGAT	CAACGCCACG	GTATGGAAGC	TCCAGCCAC	AGCCGGCCTC	900
	CAGGACCTGC	ACATCCACTC	CCGGCAGGAG	GAGGAGCAGA	GCGAGATCAT	GGAGTACTCG	960
15	GTGCTGCTGC	CTCGAACACT	CTTCCAGAGG	ACGAAAGGCC	GGAGCGGGGA	GGCTGAGAAG	1020
	AGACTCCTCC	TGGTGGACTT	CAGCAGCCAA	GCCCTGTTCC	AGGACAAGAA	TTCACGCCAA	1080
	GTCTTGGGTG	AGAAGGTCTT	GGGGATTGTG	GTACAGAACA	CCAAAGTAGC	CAACCTCACG	1140
	GAGCCCGTGG	TGCTCACTTT	CCAGCACCAG	CTACAGCCGA	AGAATGTGAC	TCTGCAATGT	1200
	GTGTTCTGGG	TTGAAGACCC	CACATTGAGC	AGCCCCGGGC	ATTGGAGCAG	TGCTGGGTGT	1260
20	GAGACCGTCA	GGAGAGAAAC	CCAAACATCC	TGCTTCTGCA	ACCACCTGAC	CTACTTTGCA	1320
	GTGCTGATGG	TCTCCTCGGT	GGAGGTGGAC	GCCGTGCACA	AGCACTACCT	GAGCCTCCTC	1380
	TCCTACGTGG	GCTGTGTCGT	CTCTGCCCTG	GCCTGCCTTG	TCACCATGTC	CGCCTACCTC	1440
	TGCTCCAGGG	TGCCCTGCCC	GTGCAGGAGG	AAACCTCGGG	ACTACACCAT	CAAGGTGCAC	1500
	ATGAACCTGC	TGCTGGCCGT	CTTCTGCTG	GACACGAGCT	TCTTGTCTAG	CGAGCCGGTG	1560
25	GCCTTGACAG	GCTCTGAGGC	TGGCTGCCGA	GCCAGTGCCA	TCTTCTGCA	CTTCTCCCTG	1620
	CTCACCTGCC	TTTCTGATG	GGGCTCGAG	GGGTACAACC	TCTACCGACT	CGTGGTGGAG	1680
	GTCTTTGGCA	CCTATGTCCC	TGGCTACCTA	CTCAAGCTGA	GCGCCATGGG	CTGGGGCTTC	1740
	CCCATCTTTC	TGGTGACGCT	GGTGGCCCTG	GTGGATGTGG	ACAACATATG	CCCCATCATC	1800
	TTGGCTGTGC	ATAGGACTCC	AGAGGGCGTC	ATCTACCTTT	CCATGTGCTG	GATCCGGGAC	1860
30	TCCCTGGTCA	GCTACATCAC	CAACCTGGGC	CTCTTCAGCC	TGGTGTTCCT	GTCAACATG	1920
	GCCATGCTAG	CCACCATGGT	GGTGACATC	CTGCGGCTGC	GCCCCACAC	CCAAAAGTGG	1980
	TCACATGTGC	TGACATGCT	GGGCTCAGC	CTGGTCTCTG	GCCTGCCCTG	GGCCTTGATC	2040
	TTCTTCTCCT	TTGCTTCTGG	CACCTTCCAG	CTTGTGCTCC	TCTACCTTTT	CAGCATCATC	2100
	ACCTCCTTCC	AAGGCTTCTC	CATCTTCATC	TGGTACTGGT	CCATGCGGCT	GCAGGCCCGG	2160
35	GGTGGCCCTC	CCCTCTGAA	GAGCAACTCA	GACTGCGCCA	GGCTCCCCAT	CAGCTCGGGC	2220
	AGCACCTCGT	CCAGCCGCAT	CTAGGCCTCC	AGCCCCACCTG	CCCATGTGAT	GAAGCAGAGA	2280
	TGGGCGCTCG	TGCGACACTG	CCTGTGGCCC	CCGAGCCAGG	CCGAGCCCCA	GGCCAGTCAG	2340
	CCGCAGACTT	TCGAAAGCCC	AACGACCATG	GAGAGATGGG	CCGTTGCCAT	GGTGGACGGA	2400
	CTCCCGGGGC	TGGGGCTTTT	GAATTGCCTT	TGGGGACTAC	TCGGCTCTCA	CTCAGCTCCC	2460
40	ACGGGACTCA	GAAGTGCGCC	GCCATGTGTC	CTAGGGTACT	GTCCCCACAT	CTGTCCCAAC	2520
	CCAGCTGGAG	GCTCTGGTCT	TCCTTACAAC	CCCTGGGCCC	AGCCTCATTT	CTGGGGGCCA	2580
	GGCCTTGGAT	CTTGAGGGTC	TGGCACATCC	TTAATCTCTG	GCCCTGCCTT	GGGACAGAAA	2640
	TGTGGCTCCA	GTTGCTCTGT	CTCTCGTGGT	CACCTGAGG	GCACTCTGCA	TCCTCTGTCA	2700
	TTTTAACCTC	AGGTGGCACC	CAGGGCGAAT	GGGGCCAGG	GCAGACCTTC	AGGGCCAGAG	2760
45	CCCTGGCGGA	GGAGAGGCC	TTTGCCAGGA	GCACAGCAGC	AGCTCGCCTA	CCTCTGAGCC	2820
	G						

A50 Protein sequence

50	Gene name:	G protein-coupled receptor 56
	Unigene number:	Hs.6527
	Protein Accession #:	NM_005682.1
	Signal sequence:	1-26
	GPS domain:	342-394
55	Pfam domain:	7tm_2[400-665]
	Transmembrane domains:	410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659
	Cellular Localization:	plasma membrane

60	1	11	21	31	41	51	
	MTPQSLQTT	LFLLSLLFLV	QGAHGRGHRE	DFRFSQRNQ	THRSSLHYKP	TPDLRISIEN	60
	SEEALTVHAP	FPAAPASRS	FPDPRGLYHF	CLYWNRHAGR	LHLLYGKRDF	LLSDKASSLL	120
	CFQHQQESLA	QGPPLLATSV	TSWNSPQNIS	LPSAASFTHS	FHSPHTAAH	NASVDMCELK	180
65	RDLQLLSQFL	KHPQKASRRP	SAAPASQQLQ	SLESKLTSVR	FMGDMVSFEE	DRINATVWKL	240
	QPTAGLQDLH	IHSRQEEES	EIMEYSVLLP	RTLFQRTKGR	SGEAEKRLLL	VDFSSQALFQ	300
	DKNSSQVLGE	KVLGIVVQNT	KVANLTPVTV	LTFQHQLPK	NVTLCQVFWV	EDPTLSSPGH	360
	WSSAGCETVR	RETQTSFCFN	HLTYFAVLMT	SSVEVDAVHK	HYLSLLSVVG	CVVSALACL	420
	TIAAYLCSRV	PLPCCRKPRD	YTIKVMHLL	LAVFLDTSF	LLSEPVALTG	SEAGCRASAI	480
70	FLHFSLLTCL	SWMGLGYNL	YRLVVEVFGT	YVPGYLLKLS	AMGWGFPIFL	VTLVALVDVD	540
	NYGPIILAVH	RTPEGVIYPS	MCWIRDSLVS	YITNLGLFSL	VFLFNMAMLA	TMVVQILRLR	600
	PHTQKWSHVL	TLLGLSLVLG	LPWALIFFSF	ASGTFQLVVL	YLSIITSFQ	GFLIFIWYWS	660
	MRLQARGGPS	PLKNSDCAR	LPISSGSTSS	SRI			

A51 DNA SEQUENCE

75	Gene name:	Hypothetical protein FLJ20063
	Unigene number:	Hs.5940
	Probeset Accession #:	AA053660
	Nucleic Acid Accession #:	AA053660
80	Coding sequence:	218-1360 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
CCCCCATGAC	TTTGTACAGC	TACTTCACTG	CTTCCCCCA	ATTAGTACAC	ATAGTTCTCTC	60

5	CACAATTCCT	ACACCTGCTC	CCCCCATAAT	CAGTACACAT	AGTTCCTCCA	CAATTCCTAT	120
	ACCTACTGCT	GCAGACAGTG	AGTCAACCAC	AAATGTAAAT	TCATTAGCTA	CCTCTGACAT	180
	AATCACCGCT	TCATCTCCAA	ATGATGGATT	AATCACAAATG	GTTCTCTCTG	AAACACAAAG	240
	TAACAATGAA	ATGTCCTCCA	CCACAGAAGA	CAATCAATCA	TCAGGGCCTC	CCACTGGCAC	300
	CGCTTTATTG	GAGACCAGCA	CCCTAAACAG	CACAGGTCCC	AGCAATCCTT	GCCAAGATGA	360
	TCCCTGTGCA	GATAATTCGT	TATGTGTAA	GCTGCATAAT	ACAAGTTTTT	GCCTGTGTTT	420
	AGAAGGGTAT	TACTACAACT	CTTCTACATG	TAAGAAAGGA	AAGGTATTCC	CTGGGAAGAT	480
	TTCAGTGACA	GTATCAGAAA	CATTTGACCC	AGAAGAGAAA	CATTCCATGG	CCTATCAAGA	540
10	CTTGATAGT	GAAATTACTA	GCTTGTTTAA	AGATGTATTT	GGCACATCTG	TTTATGGACA	600
	GACTGTAAAT	CTTACTGTAA	GCACATCTCT	GTCAACCAAGA	TCTGAAATGC	GTGCTGATGA	660
	CAAGTTTGTT	GATGTAACAA	TAGTAACAAT	TTTGGCAGAA	ACCACAAGTG	ACAATGAGAA	720
	GACTGTGACT	GAGAAAATTA	ATAAAGCAAT	TAGAAGTAGC	TCAAGCAACT	TTCTAAACTA	780
	TGATTTGACC	CTTCGGGTGG	ATTATTATGG	CTGTAACCAG	ACTGCGGATG	ACTGCCTCAA	840
15	TGGTTTAGCA	TGCGATTGCA	AATCTGACCT	GCAAAGGCCT	AACCCACAGA	GCCCTTTCTG	900
	CGTTGCTTCC	AGTCTCAAGT	GTCTGATGTC	CTGCAACGCA	CAGCAACAAG	AATGCTTAAT	960
	AAAGAAGAGT	GGTGGGGCCC	CTGAGTGTGC	GTGCGTGCCC	GGCTACCAGG	AAGATGCTAA	1020
	TGGGAAGTGC	CAAAAGTGTG	CATTTGGCTA	CAGTGGACTC	GACTGTAAGG	ACAAATTTCA	1080
	GCTGATCCTC	ACTATTGTGG	GCACCATCGC	TGGCATTGTC	ATTCTCAGCA	TGATAATTGC	1140
20	ATTGATTGTC	ACAGCAAGAT	CAATAACAA	AACGAAGCAT	ATTGAAGAAG	AGAACTTGAT	1200
	TGACGAAGAC	TTTCAAAATC	TAAAACCTGC	GTGACAGGC	TTCAACCAATC	TTGGAGCAGA	1260
	AGGGAGCGTC	TTTCTTAAGG	TCAGGATAAC	GGCCTCCAGA	GACAGCCAGA	TGCAAAATCC	1320
	CTATTCAAGA	CACAGCAGCA	TGCCCCGCCC	TGACTATTAG	AATCATAAGA	ATGTGGAACC	1380
	CGCCATGGCC	CCCAACCAAT	GTACAAGCTA	TTATTTAGAG	TGTTTAGAAA	GACTGATGGA	1440
25	GAAGTGAGCA	CCAGTAAAGA	TCTGGCCTCC	GGGTTTITTC	TTCCATCTGA	CATCTGCCAG	1500
	CCTCTCTGAA	TGGAAGTTGT	GAATGTTTGC	AACGAATCCA	GCTCACTTGC	TAAATAAGAA	1560
	TCTATGACAT	TAAATGTAGT	AGATGCTATT	AGCGCTTGTC	AGAGAGGTGG	TTTTCTTCAA	1620
	TCAGTACAAA	GTACTGAGAC	AATGGTTAGG	GTTGTTTTCT	TAATCTTTT	CCTGGTAGGG	1680
	CAACAAGAAC	CATTTCCAAT	CTAGAGGAAA	GCTCCCCAGC	ATTGCTTGCT	CCTGGGCAAA	1740
30	CATTGCTCTT	GAGTTAAGTG	ACCTAATTCC	CCTGGGAGAC	ATACGCATCA	ACTGTGGAGG	1800
	TCCGAGGGGA	TGAGAAGGGA	TACCCACCAT	CTTTCAGGG	TCACAAGCTC	ACTCTCTGAC	1860
	AAGTCAGAA	AGGGACACTG	CTTCTATCCC	TCCAATGGAG	AGATTCTGGC	AACCTTTGAA	1920
	CAGCCAGAG	CTTGCAACCT	AGCCTCACCC	AAGAAGACTG	GAAAGAGACA	TATCTCTCAG	1980
	CTTTTTTCAGG	AGGCGTGCCT	GGGAATCCAG	GAACCTTTTG	ATGCTAATTA	GAAGGCCTGG	2040
35	ACTAAAAATG	TCACATATGG	GGTGCACTCT	ACAGTTTTTG	AAATGCTAGG	AGGCAGAAGG	2100
	GGCAGAGAGT	AAAAAACATG	ACCTGGTAGA	AGGAAGAGAG	GCAAAGGAAA	CTGGGTGGGG	2160
	AGGATCAATT	AGAGAGGAGG	CACCTGGGAT	CCACCTTCTT	CCTTAGGTCC	CCTCCTCCAT	2220
	CAGCAAGGGA	GCACTTCTCT	AATCATGCCC	TCCCGAAGAC	TGGCTGGGAG	AAGGTTTAAA	2280
	AACAAAAAAT	CCAGGAGTAA	GAGCCTTAGG	TCAGTTTGAA	ATTGGAGACA	AACTGTCTGG	2340
40	CAAAAGGTGC	GAGAGGGAGC	TTGTGCTCAG	GAGTCCAGCC	GTCCAGCCTC	GGGGTGTAGG	2400
	TTTCTGAGGT	GTGCCATTGG	GGCCTCAGCC	TTCTCTGGTG	ACAGAGGCTC	AGCTGTGGCC	2460
	ACCAACACAC	AACACACAC	ACACAACCAC	ACACACAAAT	GGGGGCAACC	ACATCCAGTA	2520
	CAAGCTTTTA	CAAATGTTAT	TAGTGTCTT	TTTTATTCT	AATGCCTTGT	CCTCTTAAAA	2580
45	GTTATTTTAT	TTGTTATTAT	TATTTGTCT	TGACTGTTAA	TTGTGAATGG	TAATGCAATA	2640
	AAGTGCCTTT	GTTAGATGGT	GAAAAAATAA	AAAAAATAA	AAAAAATAA	A	

A52 Protein sequence:

Gene name: Hypothetical protein FLJ20063
 Unigene number: Hs.5940
 Probeset Accession #: AA053660
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 289-311
 EGF domain: 45-74
 SEA domain: 80-196
 Cellular Localization: plasma membrane

60	1	11	21	31	41	51	
	MVPSETQSN	EMSPTTEDNQ	SSGPPTGTAL	LETSTLNSTG	PSNPCQDDPC	ADNSLCVKLH	60
	NTSFCLCLEG	YYNYSSTCKK	GKVFPKGISV	TVSETFDPEE	KHSMAYQDLH	SEITSLFKDV	120
	FGTSVYQTV	ILTVSTSLSP	RSEMRADDFK	VDVTIVTILA	ETTSNDNEKT	TEKINKAIRS	180
65	SSSNFLNYDL	TLRCDYVGCN	QTADDCLNGL	ACDCKSDLQR	PNPQSPFCVA	SSLKCPDACN	240
	AQHKQCLIKK	SGGAPECAV	PGVQEDANGN	CQKCAFYGS	LDCKDKFQLI	LTIVGTIAGI	300
	VILSMIALI	VTARSNNKTK	HIEEENLIDE	DFQNLKLRST	GFTNLGAEGS	VFPKVRITAS	360
	RDSQMNPYS	RHSSMPRPDY					

A53 DNA SEQUENCE

Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80	1	11	21	31	41	51	
	ACCGGGCACC	GGACGGCTCG	GGTACTTTTC	TTCTTAATTA	GGTCATGCCC	GTGTGAGCCA	60
	GGAAAGGGCT	GTGTTTATGG	GAAGCCAGTA	ACACTGTGGC	CTACTATCTC	TTCCGTGGTG	120
	CCATCTACAT	TTTGGGACT	CGGAATTAT	GAGGTAGAGG	TGGAGGCGGA	GCCGGATGTC	180
	AGAGGTCTCT	AAATAGTCAC	CATGGGGGAA	AATGATCCGC	CTGCTGTGTA	AGCCCCCTTC	240

TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTTGC ACCAGATGCA 300
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAAGT ACAGATGTG CTATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAATATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCTCTG GCCAGCTGGT TACCTTGCA GTCACAGCCT GTGGTCATAG AAGGGGCTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900
 CTTAGTTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCAAGT CATGGACCAT CCAGTGGGT 1020
 CTAGTTTCCC TGTGGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAGAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 TCCCTGTGCC TGAACACGCG GGCCGTCCCT TTGATTTCGA ACAAGATCTG CAACCCACAGG 1320
 GACGTGTAGC GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACACG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA 1620
 TCCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT 1740
 CAAGCTGCTT TTTGTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTG CCCAGGCTGG 1800
 AGTGCACTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGOGATTCTC 1860
 TTGCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACACACC CAACTAATT 1920
 TTGTATTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 CCTCAAATGA TGTGCTCTCT TCAGCCTCCC ACAGTGTGCG GATTACAGGC ATGGGCCACC 2040
 ACGCCTAGCC TCAGCTCCTT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCTCTG 2160
 ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCATCTCTA GGGACCGAA 2280
 CCAAAACCCAC CCTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGCCCTAT TTTTATGATT TCTTGTAGC ATTTGGTGTG TGACGTATTA 2400
 TTGTCTTTG ATTCCAATA ATATGTTTCC TTCCCTCAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAAA

A54 Protein sequence:

Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_SpC domain: 216-444
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFFP IIVIGIALI 60
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVILQVF 120
 TAASWKTMCs DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 VTALHHSYVY REGCASHVYV TLQCTACGHR RGYSSRIYVG NMSLLSQWVP QASLQFQGYH 240
 LCGSVITPL WITAAHCVY DLXLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QFVCLPNSSE NFPDGKVCWT SGWGATEDGA GDASPVNLHA 360
 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSQCGD SGGPLVCQER RLWKLVGATS 420
 FGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

A55 DNA SEQUENCE

Gene name: Putative G protein-coupled receptor GPCR150
 Unigene number: Hs.97101
 Probeset Accession #: AA215333
 Nucleic Acid Accession #: NM_014373
 Coding sequence: 322-1338 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GTGGCCTCGA GGTGGTGGCA GGGCGGCCCC CTGCAGTCCG GAGACGAACG CACGAGCCGG 60
 GCCTCCGGAG GCAGGTTTCG CTGGAAGGAA CCGCTCTCGC TTCGTCTTAC ACTTGCGCAA 120
 ATGTCTCCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180
 AAATAACATA ATTGAAGGCA GTAAAGTGA AATTAATAG GAAGATCATC AGTCAAGGAA 240
 GACCACTGAG AGAGGACAGA AAATGAAGCA GTGTTTATC ATGTGTATT TTTTCAAGTCT 300
 TCTTGAAATT TAACTAAAAA TATGACTGCT CTCTCTTCAG AGAATGCTC TTTTCAAGTCT 360
 CAGTTACGTC AAACAAACCA GCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT 420
 GGGAAAAATAT TATTAATAT CTTTACACTA GGAATGAGAA GAAAAAACAC CTGTCAAAAT 480
 TTTATGGAAT ATTTTTCAT TTTTACAGCA TTCGTTGATC TTTTACTTTT GGTAAACATT 540
 TCCATTATAT TGTATTTCAG GGATTTTGTG CTTTAAAGCA TTAGGTTTCA TAAATACCAC 600
 ATCTGCCTAT TTAATCAAAAT TATTTCTTTT ACTTATGGCT TTTTGCATTA TCCAGTTTTT 660
 CTGACAGCTT GTATAGATTA TTGCTGGAAT TTCTCTAAAA CAACCAAGCT TTTTATTAAG 720
 TGTCAAAAAT TATTTTATTT CTTTACAGTA ATTTTAAATT GGATTTCAGT CCTTGCTTAT 780

GTTTTGGGAG ACCCAGCCAT CTACCAAGC CTGAAGGCAC AGAATGCTTA TTCTCGTCAC 840
 TGTCTTTCT ATGTCAGCAT TCAGAGTTAC TGGCTGTCAT TTTTCATGGT GATGATTTTA 900
 TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960
 ACTTCCTATA TGAATGAAAC TATCTTATAT TTTCTTTTTC CATCCCACTC CAGTTATACT 1020
 GTGAGATCTA AAAAATATTT CTTATCCAAG CTCATTGTCT GTTTCTCTCAG TACCTGGTTA 1080
 CCATTGTGAC TACTTCAGGT AATCATTTGT TTACTTAAAG TTCAGATTCC AGCATATATT 1140
 GAGATGAATA TTCCCTGGTT ATACTTTGTC AATAGTTTTC TCATTGCTAC AGTGTATTGG 1200
 TTTAATTGTC ACAAGCTTAA TTTAAAGAC ATTGGATTAC CTTGGATCC ATTGTCAAC 1260
 TGGAGTGCT GCTTCATCC ACTTACAATT CCTAATCTTG AGCAAATGA AAAGCCTATA 1320
 TCAATAATGA TTTGTTAATA TTATTAATTA AAAGTTACAG CTGTCATAAG ATCATAATT 1380
 TATGAACAGA AAGAACTCAG GACATATTAA AAAATAAACT GAACTAAAAC AACTTTTGCC 1440
 CCCTGACTGA TAGCATTTC AATGTGTCT TTTGAAGGCG TATACCAGTT ATTAATAGT 1500
 GTTTTATTTT AAAAACAATA TAATCCAAG AAGTTTTTAT AGTTATTTCAG GGACACTATA 1560
 TTACAATAT TACTTTGTTA TTAACACAAA AAGTGATAAG AGTTAACATT TGGCTATACT 1620
 GATGTTTGTG TTACTCAAAA AAACACTGCG ATGCAAACTG TTAGTAAAT CTGAGATTTC 1680
 ACTGACAACT TTAAGATATC AACCTAACA TTTTATTAA ATGTTCAAAT GTAAGCAAGA 1740
 AAAAAAAA

A56 Protein sequence

Gene name: Putative G protein-coupled receptor GPCR150
 Unigene number: Hs.97101
 Protein Accession #: NP_055188
 Signal sequence: none found
 Transmembrane domains: 23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MTALSSSENS FQYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRRKNT QONFMEYFCI 60
 SLAFVDLLLL VNISILYFR DFVLSIRFT KYHICLFTQI ISFTYGFHLHY PVFLTACIDY 120
 CLNFSKTKL SFKCQKLFYF FTVILIWISV LAYVLGDPAL YQSLKAQNAV SRHCPFYVSI 180
 QSYNLSFFMV MILFVAFITC WEEVTLVQA IRTSYMNET ILYPPFSSHS SYTVRSKIF 240
 LSKLIVCLFS TWLPFVLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN 300
 LKDIGLPLDP FVNWKCCFIP LTIPNLEQIE KPISIMIC

A57 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
 CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC 300
 TGTGCCAGCC GGGCCTCTCC CCGTCTCTCC TCCGGGCCCC CCGTCCCTGC CCGTGCAGTC 360
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAAGTC 480
 GCGCTCATTA AGCAGCTGTT TGAGGCCCCG GCCCTGAGCC AGCAGGACCG GGGACCTCTG 540
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CTTGGCACTC 600
 AGCCCTTCCA GGGTGGGCQC CCCATCGCAC CCACCTCTCT TGGCTGGAGA CCCCAGGCAG 660
 GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CCTGCGGCCC TTGCCAGATG GGCTCCCCAG 720
 GCCTGCCCCC GGCTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG 780
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCAG CTACTACTGG CCGCTGTCTG 840
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCG TTTCCAGCGG TGCCGCCCTG 900
 GGTCCCCTCT TCAGGGAAG GCATGCCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960
 AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080
 GTAAGCGGGG GGTGCTTGCC TGGCTGGGGA GCCCCAGGGA TAGCGGTCCG ACTTCAGGTT 1140
 CTGGCCAAGG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200
 GGCTGTCATG TGCCTCCAC AGACCTGGG GTGATGGCCT TCCCCTCTT GGCCGGGACG 1260
 TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA 1320
 GACAGCTCCC AGGCACGCTA TAGGCAAAAG CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380
 CTGGGGTCTC GCTCACCCCC CTTTGCTCTC ACGCCAGGCC TGTCCCCAGG TTTTCAAGCTG 1440
 GAGAGGCCAC CTCCTCAGC CAAGGAAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500
 GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT 1560
 GGGATACGCA CTGGTGGGGG GGCCCTGTCT AGCCCAACCT GGAGGGTCCC AGTGTCAACA 1620
 GAACACGGAG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680
 TCAGTGTGTG TGGGGCGCAG GGCTCCGAT GCGGGGTCTG TCGCTGGGGG GCGCAGGGCC 1740
 CCCGATGCGG GGTCAGTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACTTTGGT 1800
 ACATGTCTCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAATCT 1860
 CCTTCCGGAG CCGAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTTCC 1920
 TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980
 GCCCTCTTAC CCTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCTGG 2040
 ACCTCCTGGG CAGGAAAGGG TGCAGGTCTT GAGGGCTCTG GCCCCACAGC CCCAGCACCC 2100
 AGGTGGAGTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGCTCAGCA 2160
 GGCTGGGGTC TGCCACACAG GGCCTCCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCCC 2220

	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
	GGTGACTTCA	TCAGGAGACC	GCCACATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCACCTCCG	GAAAACTGC	CTTTCAGCCT	TGGTGTTCGG	TGCAAGGTGA	2400
5	AAAGAAATAG	GTCTCTCCAG	TTTACAGCTT	GAAATCAGGC	TAGTGAGTGG	CCCTGGAGAC	2460
	CACGAGGGGA	GAATTTAAAG	GCCCCGCTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCCCT	CCTGGAGCCT	GCCTAGGAC	GCTGGGCGGG	TCAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CCTGGGCTCT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAGGT	ACATACACGT	2640
	GCGTGACAC	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
10	CAGAAGTGTC	CCCAGTTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTTGTGTTG	ATCAAGTTCC	AAGGAAAAGG	AACATCTCAG	CCGGGCGTGG	TGGTTCACGC	2820
	CTGGAATCCC	AGCACTTGAG	GCCAGGAGTT	CCAGAGCAGC	CTGGGCAACG	CAGTGAGAGA	2880
	CCCCATCTCT	ACAARAAAAA	AAAAAGAAAG	AAAGAAAATG	AGAGATCCAG	GTTTAAAAAT	2940
	TCATAAACAC	CACAAGGAAA	CAATACACTA	TGAGACCCAG	CAGAAGCAAC	AGATTGACTC	3000
15	TAGACCCAGA	TACTAGAATT	ATCAGAGAGA	ATATAAAGTA	ACAGTGTTTT	ATATATCTAA	3060
	AGAAATAAAA	GAGATTCTCT	GAAACATGAA	AAAAAA			

A58 DNA sequence

Gene name:

ESTs

Unigene number:

Hs.157601

Probeset Accession #:

W07459

Nucleic Acid Accession #:

AC005383

Coding Sequence:

328-2751 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
25	GACAGTGTTC	CGCGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGCGTAGAAG	TGAAGTACTT	60
	TTTTATTTCG	AGACCTGGGC	CGATGCCGCT	TTAAAAAACG	CGAGGGGCTC	TATGCACCTC	120
	CCTGGCGGTA	GTTCCTCCGA	CCTCAGCCGG	GTCCGGTTCG	GCCGCCCTCT	CCCAGGAGAG	180
30	ACAAAACAGG	GTCCCAAGTG	GCAGCCGCGC	CCCGGGCGCC	CCTCCCTGTGA	TCCCGTAGCG	240
	CCCCCTGGCC	CGAGCCGCGC	CCGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG	300
	TCGCCGCTCT	CCTTCCGTTA	TATCAACATG	CCCCCTTTCC	TGTTGCTGGA	GGCCGCTCTGT	360
	GTTCCTCTGT	TTTCCAGAGT	GCCCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAGCAAA	420
	GAAACCATCG	GGAAGATTTT	AGCTGCCAGC	AAAATGATGT	GGTGCTCGGC	TGCAGTGGAC	480
35	ATCATGTTTC	TGTTAGATGG	GTCTAACAGC	GTCCGGAAAG	GGAGCTTTGA	AAGGTCCAAG	540
	CACTTTGCCA	TCACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600
	GCATTCAGT	TCAGTTCCAC	TCCTCATCTG	GAATTCCTCC	TGGATTCAAT	TTCAACCCAA	660
	CAGGAAGTGA	AGGCAAGAAT	CAAGAGGATG	GTTTTCAAAG	GAGGGCGCAC	GGAGACGGAA	720
	CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCCTGGAG	GCAGAAATGC	TTCTGTGCCC	780
40	CAGATCCTCA	TCATCGTCAC	TGATGGGAAG	TCCAGGGGGG	ATGTGGCACT	GCCATCCAAG	840
	CAGCTGAAGG	AAAGGGGTGT	CAGTGTGTTT	GCTGTGGGGG	TCAGGTTTCC	CAGGTGGGAG	900
	GAGCTGCATG	CAGTGGCCAG	CGAGCCTAGA	GGGCAGCACG	TGCTGTGGGC	TGAGCAGGTG	960
	GAGGATGCCA	CCAACGCCCT	CTTCAGCACC	CTCAGCAGCT	CGGCCATCTG	CTCCAGCGCC	1020
	ACGCCAGACT	GCAGGGTCTGA	GGCTCACCCC	TGTGAGCACA	GGACGCTGGA	GATGGTCCGG	1080
45	GAGTTGCTG	GCAATGCCCC	ATGCTGGAGA	GGATCGCGGC	GGACCCCTGC	GGTGCTGGCT	1140
	GCACACTGTG	CCTTCTACAG	CTGGAAGAGA	GTGTTCTTAA	CCCAACCTGC	CACCTGCTAC	1200
	AGGACCACCT	GCCCAGGCCC	CTGTGACTCG	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT	1260
	CCAGAAGGAC	TGGACGGCTA	CCAGTGCCCT	TGCCCGCTGG	CCTTTGGAGG	GGAGGCTAAC	1320
50	TGTGCCCTGA	AGCTGAGCCT	GGAAATGCAGG	GTGACCTTCC	TCTTCTGCT	GGACAGCTCT	1380
	GCGGGCACCA	CTCTGGACGG	CTTCCTGCGG	GCCAAAGTCT	TCGTGAAGCG	GTTTGTGCGG	1440
	GCCGTGCTGA	GCGAGGAGCT	TCGGGCCCGA	GTGGGTGTGG	CCACATACAG	CAGGGAGCTG	1500
	CTGGTGGCGG	TGCCTGTGGG	GGAGTACCA	GATGTGCCTG	ACCTGGTCTG	GAGCCTCGAT	1560
	GGCATTCCCT	TCCGTGGTGG	CCCCACCTTG	ACGGGCAAGT	CCTTGCAGCA	GGCGGCGAGG	1620
	CGTGGCTTCG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAGT	GGTGGTTTTC	1680
55	CTCACTGAGT	CACACTCCGA	GGATGAGGTT	GCGGGCCCGA	CGCGTCAAGC	AAGGGCGCGA	1740
	GAGCTGCTCC	TGCTGGGTGT	AGGCAGTGAG	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA	1800
	GGCAGCCCAA	AGCATGTGAT	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT	1860
	GAGCTGCAGG	GGAAGCTGTG	CAGCCGCGAG	CGGCCAGGGT	GCCGGACACA	AGCCCTGGAC	1920
	CTCGTCTTCA	TGTTGGACAC	CTCTGCCTCA	GTAGGGCCCG	AGAATTTTGC	TCAGATGCAG	1980
60	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGACGTGAC	ACAGGTGCGC	2040
	CTGGTGGTGT	ATGGCAGCCA	GGTGACAGCT	GCCTTCGGGC	TGGACACCAA	ACCCACCCGG	2100
	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	2160
	ACCGCCCTGC	TGCACATCTA	TGACAAAGTG	ATGACCGTCC	AGAGGGGTGC	CCGGCTGGGT	2220
	GTCCCAAAAG	CTGTGGTGGT	GCTCACAGGC	GGGAGAGGCG	CAGAGGATGC	AGCGTTTCCT	2280
65	GCCCAAGAGC	TGAGGAACAA	TGGCATCTCT	GTCTTGGTGC	TGGGCGTGGG	GCCTGTCCTA	2340
	AGTGAGGGTC	TGCGGAGGCT	TGCAGGTCCC	CGGATTTCCC	TGATCCACGT	GGCAGCTTAC	2400
	GCCGACCTGC	GGTACCACCA	GGACGTGCTC	ATTGAGTGGC	TGTGTGAGAG	AGCCAAGCAG	2460
	CCAGTCAACC	TCTGCAAAAC	CAGCCCGTGC	ATGAATGAGG	GCAGCTGCGT	CCTGCAGAA	2520
	GGGAGCTACC	GCTGCAAGTG	TCGGGATGGC	TGGGAGGGCC	CCCACTGCGA	GAACCGTGAG	2580
70	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	GGATGGATTG	TTGAGACGCC	CCTGAGGCAC	2640
	ATGGCTCCCG	TGCAGGAGGG	CAGCAGCCGT	ACCCCTCCCA	GCAACTACAG	AGAAGGGCTG	2700
	GGCACTGAAA	TGGTGGCTAC	CTTCTGGAAT	GTCTGTGCC	CAGGTCCTTA	GAATGTCTGC	2760
	TTCCCGCCGT	GGCCAGGACC	ACTATTCTCA	CTGAGGGAGG	AGGATGTCCC	AACTGCAGCC	2820
	ATGCTGCTTA	GAGACAAGAA	AGCAGCTGAT	GTCAACCCAA	AACGATGTTG	TTGAAAAGTT	2880
75	TTTATGTGTA	AGTAAATACC	CACCTTCTGT	ACCTGCTGTG	CCTTGTGAG	GCTATGTCAT	2940
	CTGCCACCTT	TCCTTTGAGG	ATAACAAGG	GGTCCCTGAAG	ACTTAAATTT	AGCGGCCCTGA	3000
	CGTTCCCTTG	CACACAATCA	ATGCTCGCCA	GAATGTTGTT	GACACAGTAA	TGCCCAGCAG	3060
	AGGCCCTTAC	TAGAGCATCC	TTTGGACGGC	GAAGGCCACG	GCCTTTCAAG	ATGGAAAGCA	3120
	GCAGCTTTTC	CACCTCCCCA	GAGACATTCT	GGATGCATTT	GCATTGAGTC	TGAAAAGGGGG	3180
80	CTTGAGGGAC	GTTTGTGACT	TCTTGGCGAC	TGCCTTTTGT	GTGTGGAAGA	GACTTGGAAA	3240
	GGTCTCAGAC	TGAATGTGAC	CAATTAACCA	GCTTGGTTGA	TGATGGGGGA	GGGGCTGAGT	3300
	TGTGCATGGG	CCCAGGTCTG	GAGGGCCACG	TAAATTCGTT	CTGAGTCTGT	AGCAGTGTCC	3360
	ACCTTGAAGG	TCTTTC					

A59 Protein sequence

Gene name: ESTs
 Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGW domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

1	11	21	31	41	51	
MPPFLLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSSAAV	DIMFLLDGSN	60
SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPLDSFST	QQEVKARIKR	120
MVFKGGRTET	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
FAVGVRFPWR	BELHALASEP	RQGHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCFPGPCD	300
SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLLDS	SAGTTLDGFL	360
RAKVVFVKRFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPLVWVSL	DGIPFRGGPT	420
LTGSALRQAA	ERGFSGSATRT	QQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
EAVRAELEEI	TGSPKHVMVY	SDPQDLFNQI	PELQKGLCSR	QRPGCRTQAL	DLVFMLDTSA	540
SVGPENFAQM	QSFVRSCLVQ	FEVNPDTVQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
APYLGGVGSA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVL	GGRGAEDAAV	PAQKLNRNGI	660
SVLVVGVGVP	LSEGLRRLAG	PRDSLHVA	YADLRHQDV	LIEWLCGEAK	QFVNLCKPSP	720
CMNEGSCVLQ	NGSYRCKCRD	GWEGPHCENR	EWSSCSVCVS	QGWILETPLR	HMAPVQEGSS	780
RTPPSNYREG	LGTEMVPTFW	NVCAPGP				

A60 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
ATGTTACAG	ATCCTGACAG	TGATCAACCT	CTGAACAGCC	TCGATGTCAA	ACCCCTGCGC	60
AAACCCCGTA	TCCCCATGGA	GACCTTCAGA	AAGGTGGGGA	TCCCCATCAT	CATAGCACTA	120
CTGAGCCTGG	CGAGTATCAT	CATTGTGGTT	GTCCATCATCA	AGGTGATTCT	GGATAAATAC	180
TACTTCCTCT	CGCGGCAGCC	TCTCCACTTC	ATCCCGAGGA	AGCAGCTGTG	TGACGGAGAG	240
CTGGACTGTG	CCTTGGGGGA	GGACGAGGAG	CACTGTGTCA	AGAGCTTCCC	CGAAGGGCCT	300
CGAGTGGCAG	TCCGCTCTCT	CAAGGACCGA	TCCCACTGCG	AGGTGCTGGA	CTCGGCCACA	360
GGGAACCTGG	TCTCTGCTTG	TTCGACAAC	TTCACAGAAG	CTCTCGCTGA	GACAGCCTGT	420
AGGCAGATGG	GCTACAGCAG	CAAACCCACT	TTCAGAGCTG	TGGAGATTGG	CCCAGACCAG	480
GATCTGGATG	TTGTTGAAAT	CACAGAAAAC	AGCCAGGAGC	TTCGATGCG	GAACTCAAGT	540
GGGCCCTGTC	TCTCAGGCTC	CCTGGTCTCC	CTGCACGTGC	TTGCCCTGTG	GAAAGAGCCTG	600
AAGACCCCCC	GTGTGGTGGG	TGGGGAGGAG	GCCTCTGTGG	ATTCTTGGCC	TGGCAGGTG	660
AGCATCCAGT	ACGACAAACA	GCACGTCTGT	GGAGGGAGCA	TCCTGGACCC	CCACTGGGTC	720
CTCACGGCAG	CCCACTGCTT	CAGGAAACAT	ACCGATGTGT	TCAACTGGAA	GGTGCGGGCA	780
GGCTCAGACA	AACTGGGCAT	CTTCCCATCC	CTGGCTGTGG	CCAAGATCAT	CATCATTGAA	840
TTCAACCCCA	TGTACCCCAA	AGACAATGAC	ATCGCCCTCA	TGAAGCTGCA	GTTCCCACTC	900
ACTTTCTCAG	GCACAGTCAG	GCCCATCTGT	CTGCCCTTCT	TTGATGAGGA	GCTCACTCCA	960
GCCACCCAC	TCTGGATCAT	TGGATGGGGC	TTTACGAAGC	AGAATGAGG	GAAGATGTCT	1020
GACATACTGC	TGCAGGCGTC	AGTCCAGGTC	ATTGACAGCA	CACGGTGCAA	TGCAGACGAT	1080
GCCTACCAAG	GGGAAGTCAC	CGAGAAGATG	ATGTGTGCAG	GCATCCCGGA	AGGGGGTGTG	1140
GACACCTGCC	AGGGTGACAG	TGGTGGGCCC	CTGATGTACC	AATCTGACCA	GTCGCATGTG	1200
GTGGGCATCG	TTAGCTGGGG	CTATGGCTGC	GGGGGCCCGA	GCACCCAGG	AGTATACACC	1260
AAGGTCTCAG	CCTATCTCAA	CTGGATCTAC	AATGTCTGGA	AGGCTGAGCT	<u>GTAA</u>	

A61 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_SPC domain: 204-429
 Cellular Localization: plasma membrane/ER

1	11	21	31	41	51	
MLQDPDSQDP	LNSLDVKPLR	KPRIPMETFR	KVGIPPIIAL	LSLASIIIVV	VLIKVILDKY	60
YFLCGQPLHF	IPRKQLCDGE	LDCPLGEDEE	HCVKSFPEGP	AVAVRLSKDR	STLQVLDSAT	120
GNWFSACFDN	FTEALAEATC	RQMGYSSKPT	FRAVEIGPDQ	DLDVVEITEN	SQELMRNNS	180
GPCLSGSLVS	LHCLACGKSL	KTPRVVGEE	ASVDSWPWQV	SIQYDKQHVC	GGSIILDPHW	240
LTAACHFRKH	TDVFNWKVRA	GSDKLGSPFS	LAVAKIIIE	FNPMPKDN	IALLMKLQFPL	300
TFSGTVRPIK	LPFFDEELTP	ATPLWIIIGW	FTKQNGGKMS	DILLQASVQV	IDSTRCNADD	360
AYQGEVTEKM	MCAGIPEGGV	DTQGDGSGGP	LMYQSDQWHV	VGIVSWGVC	GGPSTPGVYT	420
KVSAYLNWIY	NVWKAEAL					

A62 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Nucleic Acid Accession #: none found
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
CCAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
CTGAGATCCT TGCAGTAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180
AGACCCAGCT GTGCTCCTGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTAATTTCAGG 240
AAGCTGAGGA ACTGGTCTGA TGCCGAGCTC GAGTGTCACT CTACGGAAA CGGAGCCAC 300
CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
CAGAGAAGCC AGCCGATATG GATTGGCCTG CACGACCCAC AGAAGAGGCA GCAGTGGCAG 420
TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480
AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTAA CTGGAGCAG CAACGAATGC 540
AACAGCGCC AACCTTCCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600
AACTCCTGCA CCAGCCCGCT CCTCTTCCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660
TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTAA 720
GGCTTAGAGA CAGAACTTT AGCATTGGGC CCAGTAGTGG CTCTAGCTC TAAATGTTG 780
CCCGCCATC CCTTCCACA GTATCCTTCT TCCCTCCTCC CCTGTCTCTG GCTGTCTCGA 840
GCAGTCTAGA AGAGTGCAATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAAT 900
AAAGATTGTA AGACAGAAGG AAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
ACACCTTCT CCCTCTCTC CATTTGCTGC ACCCCACCCC AGCCACTCAA CTCCTGCTTG 1020
TTTTCTCTT GGCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA 1080
TACATTCCTT TAATAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA

```

A63 Protein sequence:

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Protein Accession #: none found
 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWFYHKSX CYGYFRKLRLN WSDAELEQCS 60
YNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLYRSWSG 120
KSMGGNKHCA EMSNNNFLT WSSNECNKRQ HFLCKYRP

```

A64 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

```

1      11      21      31      41      51
|      |      |      |      |      |
GCGGAACACC GGGCCGCGGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
TCCCTCGTGG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGTGGCTG CAGTGGCGCG 120
CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
AGACAGGCTG GTTGTGTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660
TCATCGTGAC CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCGAGGGA 720
GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC AAGAAGCCAA 840
AGGACCCACA CGACCTCATG TTCACAATC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
CCAGTGGCCT GGACCGGGA AAAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
ACAAATGCTC CATGTTTGAC CCCAGAGAGT ACGAGGCCCA TGTGCTGAG AATGCAGTGG 1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGAGCG CCCCAACTCA CCAGCGTGGC 1140
GTGCCACCTA CCTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
CTGAGAGCAA CCAGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGGG GCCAAAAACC 1260
AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACCT 1320
CCACAGCCAC CATAGTGCTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCCAC 1380
CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACACTG GGAGCCTGTG TGTGCTTACA 1440
CTGCAAGAAG CCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCTGT AGAGACCCAG 1500

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CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
 ATGGAAGCCC TCCCACACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC 1740
 ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCACAC CTCCCCTTTC CAGGCCAGC 1800
 TCACAGATGA CTACAGATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG 1920
 ACCATGGCAA CAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
 ATGTGCGAAG CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGT TGTGAGAAAG AAGCGGAAGA 2100
 TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGCTTC TACTATGGCG 2160
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
 AGGCCAGGCC GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
 AGGCGGGTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TTCGACTATG 2400
 AGGGCAGCGG CTCCGACGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGGTGGCGG GGAGGAGCAG TAGCGGCCCT GCCTGCAGGG TGSGGGACCA AACGTCAGCG 2580
 CACAGAGCAT CTCGAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640
 GGAAGTGGCC GTAGCAACTT GGCAGAGACA GGCATAGAGT CTGACGTTAG AGTGGTGTCT 2700
 TCCTTAGCCT TTCAGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760
 CACTTGGGCC AGGTTTGCCCT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAATA 2820
 TGCTCAACCC TGTGCTCTGG GCCTGGGCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940
 TCAAAACGTT AGAGAAAGTT CTTCAAAGT GCAGCCAGCA GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCATT CTGGTTTCCA GACCCCAATG CCTCCATTG GGATGGATCT CTGCGTTTTT 3060
 ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CCTGTTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAAGCTTTT TATTAAAGAA A

A65 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)
 Cellular localization: plasma membrane

1 11 21 31 41 51
 MGLPRGPLAS LLLQVQCWLQ CAASEPCRAV FREAEVTLA GGAQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DDFTVRNET VQERRSLKER NPLKIFPSKR ILRRHKRDV VAPISVPENG 120
 KGPPFPRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLNN KPLDREETAK 180
 YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTA 240
 DEDDAIYTYN GVVAYSISHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMGDGSGTT TAVAVVEILD ANDNAPMFDQ QKYEAVHPEN AVGHEVQRLT VTDLDAPNSP 360
 AWRATYLMG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTEGPVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMPD DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540
 VNDHGFVPEP RQITICNQSP VRHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDQYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660
 GAVLALLPFL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFP YGEBGGGEED QDYDITQLHR 720
 GLEARPEVLL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEED

A66 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGATTCCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
 ATTCCTCCAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
 TTTTATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTTCTGGCTT CTGCAGTCAT CAGTGTTTTA 240
 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300
 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
 CCAGAAATCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGGCCG AGACTTGGTT 420
 CCAGGTGATA CAGTTTGGCT TTCTGTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTC 480
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540
 AAGGTGACAG CTCCTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTGAT TGGAAACAGGA 660
 GAAAATTCG AATTTGGGGA GGTTTTAAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
 CCTCTGACA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780
 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840

5
 10
 15
 20
 25
 30

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ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTACAGTG 900
ACGCTAGCTC TTGGTGTTAT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960
ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCTG ATAAACTGG AACACTGACG 1020
AAGAAATGAAA TGACTGTTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTGTATG GTGATGTTGT TCATGGATTC 1140
TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAAATGCTCT TGCAATGAAG 1260
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320
GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
TGTTTTATGA AAGGTGCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAGA GAAGGCACGC 1500
ATGGGCTCAG CGGGACTCAG AGTTCCTGCT TTGGCTTCTG GTCCCTGAAC GGGACAGCTG 1560
ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
ACAACACTCA TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTG ACAGGAGACT 1680
GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTTCCAAA CTTCCTCAGT AGTCTCAGGA 1740
GAGAAATAGT ATGCAATTGA TGTTCAGCAG CTTTCACAAA TAGTACCAA GGTTCAGTA 1800
TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860
TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920
ATTGGAGTTG CGATCGTACA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTTAT 2040
AATAACATTA AAAATTTCGT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACTTTA 2100
ATCTCATTGG CTACATTAAT GAACTTTCCT AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160
ATCAATATTA TTATGGATGG ACCCCAGCTG CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCATTG GTAAAGCTCG TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTTGATA 2280
CTTAAATATC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTTG CTCTGGCGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
TTTTTTGACA TGTTCATATG ACTAAGTTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTCTCTG GATCCATCAT GGGACAATTA 2520
CTAGTTATTT ACTTTCTCTC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTTGT TTCTTTTGGG TCTCAGCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAG 2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTGA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT_GA
  
```

A67 Protein sequence:

35
 40
 45

```

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Protein Accession #: AAF27813
Signal sequence: none found
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
Cellular Localization: not determined
  
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50
 55
 60

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1 11 21 31 41 51
MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI 60
SQFKNPLML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQEYRSEK SLEELSCLVP 120
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS 180
KVTAQPAAAT NGDLASRSNI APMGTLVRCG KAKGVVIGTG ENSEFGEVFK MMQAEAPKT 240
PLQKSMDDLK QLSFYSPFI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGPLIVVTV 300
TLALGVMRMV KKRAIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360
GVGYNQFGEV IVDGDVHGF YNPAVSRIVE AGCVCNDAVI RNNTLMGKPT EGALIALAMK 420
MGLDGLQDQY IRKAEYFPSS EQKWMVAVKCV HRTQQDREPI CFMKGAYEQV IKYCTTYQSK 480
GQTLTLTQQI RDVYQOEKAR MGSAGLRVLA LASGPELGQL TFLGLVGIID PPRTGVKEAV 540
TTLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG EEIDAMDVQQ LSQIVPKVAV 600
FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEAADMI 660
LVDDDFQTIM SAIEBGKGIY NNINKFVRFO LSTSIALLTL ISLATLMNFP NPLNAMQILW 720
INIMDGPFA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
ELRDNVITPR DTTMTFTCFV FDFMFNALSS RSQTSKVFEE GLCSNRMFCY AVLGSIMGQL 840
LVIIYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVERSREKIQ KHVSTSTSSS 900
LEV
  
```

A68 DNA SEQUENCE

65
 70

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Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
Unigene number: Hs.170195
Probeset Accession #: BE616633
Nucleic Acid Accession #: NM_001719
Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)
  
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75
 80

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1 11 21 31 41 51
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCCGCTCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCACGT GCGCTCAGTG CGAGCTGCGG CGCCGCACAG CTTCTGGGCG CTCTGGGCAC 180
CCCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
GCTTCATCCA CCGGCGCCTC GCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTGCCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGCGCGC GGGCCCGGCG 420
GCCAGGGCTT CTCTTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
GCCTGCAAGA TAGCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCGCCGA ATTCGGGATC TACAAGGACT 660
  
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ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
 AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCCTCGG 780
 AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACGAGCAA CCACTGGGTG GTCAATCCGC 840
 GGCACAACTT GGGCCTGCAG CTCTCGGTGG AGACGTGGGA TGGGCAGAGC ATCAACCCCA 900
 AGTTGGCGGG CTTGATTGGG CGGCACGGGC CCCAGAACA GCAGCCCTTC ATGGTGGCTT 960
 TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGAGC AAACAGCGCA 1020
 GCCAGAACC GCTCAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
 AGAACAGCAG CAGCGACCG AGGCAGGCCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG 1200
 AGGGGGAGTG TGCCTTCCCT CTGAATCCTT ACATGAACGC CACCAACCAC GCCATCGTGC 1260
 AGACGCTGGT CCACTTCATC AACCCGGAAG CGGTGCCCAA GCCCTGCTGT GCGCCACGCG 1320
 AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
 TTGGGGCCAA GTTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
 CTGCCTTTTG TGAGACCTTC CCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
 AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
 TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
 GCGGGGCCAG GTCATTGGCT GGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
 TTAGAGCGC CTACCAAGCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
 GGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCTGTGA ATAAATGTCA 1860
 CAATAAACG AATGAATG

A69 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number: Hs.170195

Probeset Accession #: BE616633

Protein Accession #: NP_001710.1

Signal sequence: 1-30

Pfam domains: TGFb_propeptide [37-281]

Transmembrane domains: none found

Cellular Localization: secreted

1 11 21 31 41 51
 | | | | |
 MHVRSRLAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRRLRSQE RREMQREILS 60
 ILGLPHRPRP HLQGHNSAP MFMLDLNLYM AVEBGGGPGG QGFSYPYKAV FSTQGPPLAS 120
 LQDSHFLPDA DMVMSFVNLV EHDKEFFHPR YHHRFREFDL SKIPEGEAVT AAEFRIYKDY 180
 IRERFDNETF RISVYQLQE HLGRESLFL LDRSLWASE EGWLVFDITA TSNHWVNVPR 240
 HNLGLQLSVE TLDQSNINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
 QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAYYCE 360
 GECAEPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
 RNMVVRACGC H

CervicalA70 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)

Unigene number: Hs.87223

Probeset Accession #: AA250737

Nucleic Acid Accession #: NM_001203

Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGCG AGTGC GGAGA CCGCGGCGCT 60
 GAGGACGCGG GAGCCGGGAG CGCAGCGCGG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120
 GTGAAAGGAA AGGAATGCTA TTTATGCCT TGTGATAAA GGTTCAGACT TCTGCTGATT 180
 CATAACCAAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
 TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGG TCCAAAGGTC 360
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCCTTGT GGTCACTTCT 480
 GGTTCGCTAG GACTAGAAGG CTCAGATTTT CAGTGTCTGG ACCTCCCAT TCCTCATCAA 540
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAGACCT ACACCTTACA 600
 CTGCTCCAT TGAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660
 ATATCTGTGA CTGTCTGTAG TTTGCTCTTG GTCTTATCA TATTATTTTG TTACTTCCGG 720
 TATAAAGAC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC 780
 ATTCCTCTTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
 TCAGGCCTCC CTCTGCTGTG CCAAAGGACT ATAGCTAAGC AGATTTCAGAT GGTGAAACAG 900
 ATTGAAAGG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GCGTGGCGGA AAAGGTAGCT 960
 GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
 ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATATG CTGCAGATAT CAAAGGGACA 1080
 GGGTCTCTGA CCAAGTTGTA CTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
 TATCTGAAGT CCACCACTCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200
 AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260
 CATCGAGATC TGAAAGATAA AAACATTTCT GTGAAGAAAA ATGGAAGTTG CTGTATTGCT 1320
 GACCTGGGCC TGGCTGTTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
 ACTCGAGTTG GCACCAACAG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500
 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAAT ACCAGCTTCC TTATCATGAC 1560
 CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620

CGCCCCCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAACTC 1680
 ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740
 ACACCTGCCA AAATGTCAGA GTCCCAGGAC ATTAAACTCT GATAGGAGAG GAAAAGTAAG 1800
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860
 TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC 1920
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTTGTA GCGCGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT

A71 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.72472 / Hs.87223
 Probeset Accession #: AA250737 / U89326
 Protein Accession #: NP_001194
 Signal sequence: 1-13
 Transmembrane domains: 128-144
 PFAM domains: activin_receptor [30-111], protein kinase [204-491]
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFMIEED 60
 DSGLPVVTSGL CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120
 GPIHRRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180
 EQSQSSGSGS GLPLLQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTEEAS 240
 WPRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
 MLKLAYSSVS GLCHLHTEIF STQKPAIAH RDLKSKNIVL KKNGTCCIAD LGLAVKFISD 360
 TNEVDIPNT RVGTRKYMPP EVLDESINRN HFQSYIMADM YSFGILWLV ARRCVSGGIV 420
 EEYQLPYHDL VPSDPSYEDM REIVCIKLR PSFPPNRWSSD ECLRQMGKLM TECWAHPAS 480
 RLTAIRVKKLT LAKMSSESQDI KL

BladderA72 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60
 AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA 120
 CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC 180
 TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
 CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
 GCAGTGGCAG TCGGCCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
 GGGAACTGGT TCTCTGCTTG TTTGACAAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
 GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACTCAAGT 540
 GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
 AGCATCCAGT ACAGACAAAC GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
 CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
 GGCTCAGACA AACTGGGCGC CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
 TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
 ACTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
 GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
 GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
 GCGTACCAGG GGGAAAGTAC CGAGAAGATG ATGTGTGCGA GCATCCCGGA AGGGGGTGTG 1140
 GACACCTGCC AGGCTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
 AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

A73 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_SPc domain: 204-429
 Cellular Localization: plasma membrane/ER

1 11 21 31 41 51
 | | | | |
 MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIV VLIKVILDKY 60
 YFLCGQLPHF IPRQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT 120

GNWFSACFDN FTEALAETAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
 GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHV 240
 LTAAHCFRKH TDVFNWVRA GSDKLGSFPS LAVAKIIIE FNPMPKDNND IALMKLQFPL 300
 TFSGTVRPIK LPFFDEBELT ATPLWIIWGW FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
 AYQGEVTEKM MCAGIPEGV DTCQDSSGGP LMYQSDQWHV VGIVSWGYGC GGFSTPGVYT 420
 KVSAYLNWIY NVWKAEAL

A74 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
 GC CGCGGGGCC GCAGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
 CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCACTGGGG 240
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC 300
 TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCCGGGCCCC CCTGCCCTGC CTGACGTCC 360
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420
 CTCAACCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG 480
 GCGCTCATTA AGCAGCTGTT TGAGGCCGCG GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CCTGGCACTC 600
 AGCCCTTCGA GGTGTGGCGC CCCATCGCAC CCACCTCTCT TGGCTGGAGA CCCC CGGCAG 660
 GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CTTGCCGCCC TTGCCAGATG GGCTCCCCAG 720
 GCCTGCCCCC GGCTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG 780
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCG CTACTACTGG CCGCTGTCAG 840
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCGG TTTCCAGCGG TGCCGCCCTG 900
 GGTCCCATCT TCAGGGAAGG GCACTGCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960
 AGAGGCGCGC GGGCGGCTCC GACGCGGCTC CAAGGCGCAG TTCCCGCTCA ACCAGGCGAC 1020
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080
 GTAAGCGGGG GGTGCCTGCC TGGCTGGGGA GCCCCAGGGA TAGCGGTCCG ACTTCAGGTT 1140
 CTGGCCAAAG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG CGGAGAGCTT 1200
 GGCTGTCATG TGCTCCACAG AGACCTGGGG GTGATGGCCT TCCCCCTCTT GGC CGGAGC 1260
 TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA 1320
 GACAGCTCCC AGGCACGTCA TAGGCAAAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGCG 1380
 CTGGGGTCCCT GCTCACCCCC CTTTGCTCTC ACGCCAGGCC TGTCCCCAGG TTTTCACTGG 1440
 GAGAGGCCAC CTCCCTCAGC CAAGGAAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500
 GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCTACTCC CGCTGGTGCT 1560
 GGAGTACGCA CTGGTGGGGG GGGCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTACACA 1620
 GAACCAAGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCCGGG 1680
 TCAGTGTGTG TGGGGCGCAG GGCCTCCGAT GCGGGGTGAG TGCCTGGGGG GCGCAGGGCC 1740
 CCCGATGCGG GGTGAGTGC TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACCTTTGGT 1800
 ACCTGTGCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCACTC 1860
 CCTTCCGAGT CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTTCC 1920
 TGCTGCACCT GGTGTCAGG GGTGTCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980
 GCCCTCCTAC CTTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCTGG 2040
 ACCTCCTGGG CAGGAAAGGG TGCAGGTCTT GAGGGCCTGT GCCCCACAGC CCCAGCACCC 2100
 AGGTGGACTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGTTCAGCA 2160
 GGCTGGGGTC TGCCCAACAG GGCCTCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCC 2220
 TGGGGGATCC TGGCATCTTT ACTGGAAGTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280
 GGTGACTTCA TCAGGAGACC GCCCACATAG AGCTGGAGCC CGCAGCTGAA GCGGAAATGT 2340
 GAGACAGGCT GGCACCTCCG GAAAAACTGC CTTTCAGCCT TGGTGTTCGG TGCAAGGTGA 2400
 AAAGAAATAG GTCTCTCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAG 2460
 CACGAGGGGA GAATTTAAAG GCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520
 GCAGACCTTG CCTGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580
 GAGCAGCGTC CTTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACAGT 2640
 GCGTGACAC TGATGATGACA CCCGAAATG TCTCAGGATG TTGAATGTG TCCTTGGGGG 2700
 CAGAAGTGTC CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACCA GGCCTCAGGA 2760
 TTTTGTGTTG ATCAAGTTCC AAGGAAAAGG AACATCTCAG CCGGGCGTGG TGGTTCACGC 2820
 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCATCTCT ACAAAAAA AAAAAGAAAG AAAGAAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTTTT ATATATCTAA 3060
 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

A75 DNA SEQUENCE

Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
 Unigene number: Hs.227948
 Probeset Accession #: AB035089
 Nucleic Acid Accession #: AB035089
 Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGGCATGCAG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA 60
 CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAAGAGG 120
 CCAAGAGGAA TAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTGGT 180
 TTGGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG GCAGTGTGGC CAGATAGGA 240

	AGGAGGAAGG	GAGGCAAGAG	ATAATATCAT	TTTCTCTGTG	CTCCAACGTG	ACTTACATAT	300
	GAGACTATTT	CCCTCTCTGC	TTTTCAAACC	TTACTGGAGT	TGTTTTCCCT	CATGAAAACC	360
	AAGAAAGGAA	AGCTAGTTAG	TCTTGTCTCG	AGGTTGTTCA	ATGTATACAT	ATCTATATCT	420
	GTAGACAGAA	TCCTTGGGAA	TACAGTAATT	GACATATATT	CTGTTATTTG	ATGCTTGAAG	480
5	AATCTCCTCC	ACTAACCCAGT	TTCCCTATAG	ATTGCCACAA	GCACATAATA	AGAAACAATA	540
	AATAAAATGT	TCTCTTGACT	TTGTTACTTA	ACAATGCTGA	GAAACCTTTA	CAGCCTTCAT	600
	AAGGAAGTGA	GGTCCAGGAA	AATCTAGGAG	ATATTTCTTA	ACCAATCTAT	AAAGGCATTA	660
	GTAAATGACAG	GATATTTCTT	GAAAGTGTAA	TTTCCCATTT	AGGATTGTTT	TTTAATTTCT	720
10	GGATTCTCTG	AGCCAATGAA	GTTGGTGTAT	GTTTATGAAA	TATCAAGAGA	CATAAGTTGG	780
	CAAGTGTTC	TATGCAAAAA	CTTCTTGGA	TTTCTGAGTT	CTCTGTGGCA	ATATATGACA	840
	TCAGGATATG	TCCAGTCTCA	CACACCAGGA	TATGTCCTTT	CTAGCCTGTC	TATCAGATGC	900
	TAGGAGAACT	ATTTAGGAAC	AGAAAAAAT	GCCTGAAATG	ATTTCTCAT	TGAACATC	960
	CAAGCTTTCT	CTAAATTTAA	GCAAACTCCT	GGTCATTTT	AGTTAGTACC	TTTCTTAAG	1020
15	TTCAACCTTC	AGGGCAAAACC	TCCGTGCCTC	AGACGTTTAG	CCATAGTCTG	AAATTTCTCT	1080
	CCATAGATTG	GTCCCTCTGA	ACCCCGTTT	GTCTCAGCTT	GTTATCTCTG	TTTTTTCTTC	1140
	CCCTCATCTC	CAGGATGAGC	TTGTTGCTTC	TGTCCTATGA	GACATTAGAT	TCCTTTTCTT	1200
	TGGTACCCGA	GTAAATCCAT	CCTACTCCAA	TAGAGGAAGG	TCCATTTTGT	TCTTATAGCG	1260
	CTGGATGCG	ACTCAGCTGA	GAAGACCATT	ATTCATTTT	GGAATTTCTT	ATCTCAGATA	1320
20	TTTCTCTTTC	TTTCTTTTTC	TTCTATCTTT	GGATTTTATG	TCCATCAACG	CCCCATTAGT	1380
	CTATTTCCCG	ACTTCAATCA	GGGAACCTAT	ACCTCTTAAA	CTCATTGAGA	GACTCAAAAC	1440
	ATATATATTG	ATACAGAGCA	CCTAAGAAGA	GCATGTCTTG	GGGTTGAGG	AAACAGGCAG	1500
	GTGAGAAATT	TCCAGATTGG	AAACACAGCT	TCCTTTCTCC	CATCCAGCCC	CTACTTTCAG	1560
	CCTATGTGTT	TCTGGCACCT	TGTTGTAGAT	AAATCTCCCT	TGACTTTGTG	ATGTGCTGAG	1620
25	AAAACAAACT	CACGGCTGGT	GTTAAAAAGG	GCCCATGACA	ATACCAAGTG	TTGGGGAGAA	1680
	TGTGGAGAAA	TCAGAATCTT	ATTCACGGTC	GGTTGGAATG	CACACTTGTG	CAGAATTCTA	1740
	TGGAGAAGAG	TCTGGCATT	CCTCAAAATG	TTAACCTGGA	TTTACCATAT	GACCCAGCGA	1800
	TTTTCTTCAT	AGGTTTATAT	TCAAAAGAAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
	ATGAAAGGTC	ACAACATCAT	TATTCATAAT	AGTAAAAAGG	TGGAAACAAC	ACAAATGTCC	1920
	ATCAACTTAT	CAATTAAGAA	AATCTGGTCT	ATTCATAGAA	TGGAATATTA	TTCCAGCCACA	1980
30	AAAAGGAATG	ATGTACTGAT	CCATGCAATG	ATGTGGACAA	ACCATGAAAA	TAACACTAGA	2040
	TTAAAGAAAG	CAGTCACAAA	AGGACTTACT	GTATGATTCC	ATTTACCTGA	AATGTTTGGG	2100
	ATAGGCAAAAT	CCATAGAAAC	AGGAGGTAGA	TTCTGTGTTT	CCAGGGTCTC	CAGGAAGGGA	2160
	AGAATGAAGT	ACAGATTTTC	TTTTGGAGGT	AGTGAAATG	TTGTGGAATG	AGATCATGAT	2220
	GATGATAGCA	CAGCTTTGTG	AATATAATAA	AATCATTTGA	TTGTACAGTT	GAATTTATGG	2280
35	TATATAAATT	ATATGTTAAT	AAAAAGGGGG	TCCACAAAAC	AAACAGCCCC	CCACTCTGGT	2340
	TGTGAGGAG	ATATTGGATT	AAATGGCCTT	GGACAACAAC	CCCTCTCCCT	GGCCACAGAC	2400
	ATTCTTCAGA	TTACAGAATA	TTCCAGGGGA	AACACTGGAA	TGAGTCTGAA	GCCAGGTGCT	2460
	AAACAGAAGG	ACCATTGAGA	AATGTTGTGA	TCCTGACAGG	TCAAGCAATT	TATTTTTCGG	2520
40	CTTCATTTT	AAATGTAAAA	TTAGAAAGCT	GCCATTTAAA	ATGGCCCGTC	TGTTTCAATT	2580
	GCTCTTCTCA	GTGTCAGCCT	GTTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATACCT	GAGACTGGCA	AGAAAAAGAG	GTTTAAATGG	GCTTAGAGTT	CCACGTGATT	2700
	GGGGAGGCTC	CAGATTCACA	GTAGGAGGCA	AAAGTTATTC	TTACATGGTG	GCTGCAAGAG	2760
	AAGATGAGGA	AGAAGCAAAA	GAAGAAACCC	CTGATAAACC	CATCGGATCT	CCTGAGGCTT	2820
45	ATTAACCTAT	ATGAGAAATG	CACAAGAAAG	ACCGGCCCCC	ATGATTCAAT	TACCTCTACC	2880
	TGGGTCCCTC	CAATAACATG	TGGAAATTCT	GGTAGATACA	ATTCAGTTTG	AGATTTGGGT	2940
	GGGAACACAG	CCAAACCTAT	TCATCTAGCA	AGGCAGATAA	CTTTCTCACT	GAGCCTATGC	3000
	AACAGAAAAC	CATCTGGGAT	GGTTGTAAGG	GGCACAGGAA	GTGACTGGTA	GGATCACTGC	3060
	CAAGCTGAG	CAGTCAGGAG	AAGGCAATAG	AATCCTATT	TCCATAGTAT	GCTATAAGAT	3120
50	ACTGAAGTAC	ACTTCTTCA	TATCTCTTTG	GACTTAGAAT	TAGCACTACA	TTCTTGTGTA	3180
	TACAGAAAAA	TACTATAAGGA	AATTCATAGG	ATGACAAAAA	CTTTCAGAAC	TGAAAAACAG	3240
	GAAATGTAA	CTTTTATGTT	CTTTGGTATT	CGAAGTATGC	CTAAAAGACA	ATGCAAAATC	3300
	CAAGAAAAAG	ATGTTGGGTT	TTTTGTTTGT	TTGGTTTGT	TTTTGTTTGA	CAGCTGGAGT	3360
	AGAAATACAAA	GGGATGGAGT	TGAAACAAAT	GAGAGGAAAT	TGGAATTCTA	AACTTATCTT	3420
55	CATTGGCATT	AGAAAGGCAC	CTACATGTAT	TTCATAGAG	CCGGTGACTG	CTGACTTGCA	3480
	TTCTTATTTT	TTCCCTATAG	ATTAAGAAAG	AGGTACAATG	GTAGAACTGT	AATCCTGTCC	3540
	TTTGTACATA	ATTTTCATAT	TCATAAAGGT	GAGTGTAGC	CCGCTTGTGA	AATCTGAAGT	3600
	TGAGTAACCT	CAATACTATA	CCACAGAGGG	AAAGGCAGCA	AGAGGAGAGG	CATAAATTTA	3660
	GGATCTCACC	CTTCACTTCA	CAGACACACA	CAGCCTCTCT	GCCCACCTCT	GCTTCTCTTA	3720
60	GGAAACACAG	TAAGAGCTTC	AAGCCTCTCC	AGCTTAATAA	CATGAATTAT	TTTTGAGAA	3780
	AATAATGATA	CTGTGTTCTA	TATCATGCAT	CTCCTGCATT	CTGCTGATT	ATATTTTACT	3840
	TATTTCTGCA	GAGCAAAAT	AAAAATACCTA	TTTCATCTGA	TTTGTCCCTT	ATCTAAATTTG	3900
	CTTAGTTTCA	AGTAACCAAA	GGCACTTTTA	GGAACACAGA	GGGAGAGTGC	CTTGACAGCA	3960
	GAGAGTCTTG	AAGGAGATGT	CAGGACGCA	TCTTAACAGC	TGGTTGGATG	TGATCCACAG	4020
65	AGGTCTCCTG	TTAGCATTCA	TTGTAAGGCC	ATCCTACCTA	GCTCTAGTGT	AACCAGCAAT	4080
	GAAAGAAAGA	TAAAGAGGGT	CGATTACTTA	TTTACAATAG	TCTTTAAAAA	CGTAGTTTGT	4140
	TAAGCCTTCT	AATTAGGACA	TTAATATATT	TAATATATGC	ACATTGTAGA	AAGATTGAAG	4200
	CGTTAAAAAT	AAGAGAAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCATTTT	4260
	TTTAAGAAAA	TTGTACTACA	AAATACCAAT	CCATTTATTA	AAGTCATTCT	GACAGGAATC	4320
70	TGATGCTTTT	CCAGGAGTTC	CAGATCACAT	CGAGTTCACC	ATGAATTCAC	TCAGTGAAGC	4380
	CAACACCAAG	TTCATGTTCC	ATCTGTTTCA	ACAGTTCAGA	AAATCAAAAG	AGAACAACAT	4440
	CTTCTATTCC	CCTATCAGCA	TCACATCAGC	ATTAGGATG	GTCCCTCTAG	GAGCCAAAGA	4500
	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCTGTTGCAG	4560
	TTTTTCTCTG	GTTCCGTCGG	CTAGCACGCA	GATGGTAATA	GATGTGGTGG	TCTGATGGGT	4620
75	AGCACAGGGG	GCTGTGCGAG	AATTCCTATA	ACTGTGAGAC	CAGTCACTTA	AACAGATCTT	4680
	TTGAGTAAAG	TTTTCTTGTC	CCGCTTCATG	TCTCTCCAG	GTCTTCACT	TTGATCAAGT	4740
	CACAGAGAAG	ACCACAGAAA	AAGCTGCAAC	ATATCATGTG	AGTCACAGAG	CAGTCTGATT	4800
	CAGCTTTAGA	TCCCTGAACA	GGTCATAGTT	TAAACCTGGA	ACTTCACAAA	AACATAAGAAA	4860
	AGGCCAGTTT	TAGGGAATAA	CTTGGAACACA	AAGATTGAGA	CATACAGAGT	GGGTTGGCAT	4920
80	TTTCATGGCAG	ATAATTATTA	TTCTCATTTT	CTGCGTTACT	AAAAGACAGT	CAGCACTGTA	4980
	CCTCAGAGCA	TAGGTCTGGA	TCAGGATAGG	CTGGGTTTCA	ACTCCAGCTT	TGCTCTTCAC	5040
	AAATGATGAA	TAAAGACAGG	ACACAACCTGC	TCGGAGTCCC	AGTGACCTCA	TCCCAGAAAA	5100
	CTAAGGGTAA	GAAAAAATCT	GACTCAATAC	ATGCAAAATG	ATGCAAAATG	TTACAACAGT	5160
	GCCTTGCCCA	TAAAGTGCAT	AATAAATGTT	ATTATTATTA	TAAAGTAGCT	ATAATTATAC	5220
	TAATCATAAAT	AATGTGAAAA	TAATTTAATT	TTCATTGAGT	CATTAAATGAG	ATTCAGAGGA	5280

	ATAAGCACAA	GTCCAAGTAT	ATTTTGAAAA	ATGATTGCTA	TGGAATATAT	TGGTTTAGAG	5340
	CCTTAATAGT	GCAAAATGCT	TTGCTGGAAG	GTAGAAAGTT	CTAGATTTAA	ACAGGCTTAG	5400
	GTTCAAAACT	TGGCCTTCT	AATTTATGTC	TCTATAAACA	GGGTTTTTTT	CCCCATTCTC	5460
5	TGAGCTTTCT	TGTGTTCACT	TGAATTGAAC	TAAAGACTTA	GAGTTACCCA	TGTAAGTCC	5520
	TTAGCCATGG	ACCTGGCATA	CACCTCTCTT	ACGTGCAGAG	AATGACCATC	ATGAGGAAAG	5580
	AGCCACAGAT	CAGTCAATGT	GTCCTACAAG	ATAATAGCAC	CAACAGGTAT	AACAGGGCTT	5640
	CCTGGCATAA	TCTATTAAAA	ATATCCAACC	TTCAACATAC	TCGTATCCTT	GATGACTGTT	5700
	AGAAGTGAAA	TATGGTCCCT	GCCATAAGG	AGCTGAGAGT	TTAACTGGGA	AGCTAAACCT	5760
10	AACCCCTTAA	ACCAACAAGG	AGAAAACTTA	CTGGTAGACA	GCGCTGCATC	TTTAGTTTCA	5820
	AAGAGAAAAA	ATTGCAGTAC	GTTAGAGCAA	GAAGAAATTT	CTGGAAGAAG	TCAAATATAA	5880
	GGTGGATTTT	GAAGGGTATT	TGAGGTGAAA	TACACCAATT	ATCAGGGAAT	AACATCAAAAG	5940
	GTCTCTCAAT	AGACTACCAG	CATTTAGGGA	CTGATCTAAC	AGACTTAGCA	TGGGTTTAGT	6000
	ATTTACATTG	ATACAGCAAT	TGAATGATCT	CCTTTTTTGA	TGTTTGAAGG	TTGATAGGTC	6060
	AGGAAATGTT	CATCACCAGT	TTCAAAAGCT	TCTGACTGAA	TTCAACAAAT	CCACTGATGC	6120
15	ATATGAGCTG	AAGATCGCCA	ACAAGCTCTT	CGGAGAAAAG	ACGTATCAAT	TTTTACAGGT	6180
	AAATTCACCT	GGCCTACCCA	CATTTCAATT	GCATCCTGAT	GTCTGTGTCT	CTGAGTGGCC	6240
	AAATGGAAGA	AAGCAAGGCA	GATGAGCCTG	GCCGACCCAG	GTGGAGAGCA	TTTACTCAGA	6300
	GTGCATTAGC	TCCATTTCCA	CAACTCTCCC	CCACTGGAGT	GTCCCAGACC	CCAACGATAC	6360
20	ATCACTGAAG	TGTGGATTTA	GGGATAATCT	TGTGATAAAA	GAGGAGGTTG	TGTAATAGAG	6420
	TGAGTAAGAG	TAATAAGTAA	TAAGATACCA	TCGATAAACT	GGCACTGACT	CAGTCAACATA	6480
	CGATACATCT	TGTGGGAAAA	TGTATGACTA	ATGGGATATT	ATTGGAATGG	GCAGGCTTGG	6540
	GTGAGTTCTT	GAGAATAGTT	GAGGAAGTAC	CAGGAATAT	TGAATGCACA	GGATGAAAGA	6600
	CAAAAAAACA	GATCAGAAAC	ATCATGGTTA	AAATTACTGG	AGAGAAGTCT	GAGAAGCAAT	6660
25	GAATCTCCTT	CAGGGAAGCC	TGCTCTGCAG	TTTGCAAAACC	ACAGCCTCTT	CTGCTTCTGC	6720
	CTTTTGCCAA	GATGATATTG	ACCTTCAGTG	ACCTCTTTCT	TGTGCCAGCC	CACATTCCTC	6780
	TTTTGCATTG	CCTACATGAC	ACCTGTATAA	AAATATCCAT	GGACAGGAGA	TACTGCATCT	6840
	ATTCAGGGTC	TGGATTGAGC	TTACTGTTGT	TACAAATAAG	TAAGTTTGGT	AATATATAGT	6900
	TACATAAATT	ACTCCTAATT	CCTACTTCTT	CCTTCATATC	TCAAAGGAAT	ATTTAGATGC	6960
30	CATCAAGAAA	TTTTACAGAA	CCAGTGTGGA	ATCTACTGAT	TTTGCAAAATG	CTCCAGAAGA	7020
	AAGTCGAAAG	AAGATTAACT	CCTGGGTGGA	AAGTCAAAAG	AATGGTAGGA	GAGCCACCCA	7080
	TTATAGAAAC	ACCTTTGAGA	AACCTATGCC	AGTGAGCCTT	GTGCTTGACA	CTGCATGGGG	7140
	GAACAGGTGT	GGGAGTTGAG	ATGGGTTTGC	AGGGAGGGCT	GAAGAGGGCA	CTCCAGATGA	7200
	AGGATTTGTC	CAATGAATTA	TGAAGAGAGC	CTAGGGGAGC	CAAGGAGGAA	ATCACAGGAA	7260
35	GCCAAATTAGA	TGGAACAACA	CTGGAGAAT	TATTTGCTTA	TGGCCCTGCA	TGACAAATAG	7320
	TTTGTGGATC	CCCTGTCTCC	GCTCAGACCT	ATTTTGAGAT	CATATCCTTT	ACTTTAAATC	7380
	AGACTCAAAAT	TTTTATGATG	AATATTTAAT	AGAAAAAATT	AGAAAGCGTC	TCTCGTCTCC	7440
	TTTACTAATT	GGGAAACCAAG	CAGCTCTCTG	GTAAATCACC	CTTTTGTCTC	TGAGCTGGAG	7500
	CTGCCTGGAT	CACATCTGTA	GCCAAATGTT	TCTGCAGGGA	TTATCAGAGC	TCTCTTCCCC	7560
40	ATCAAGGGCA	AAGAGCTTGA	CAAAGTCTCC	ATTCTACAGA	CATCTTTCTT	ACCTCCACCC	7620
	TCTCATTACA	GGCCAAACTC	ACAGCACTC	AACATGAGAG	TGAATAGGAA	GATACCCCGG	7680
	GAAGTAGTGT	CTGACAGCAG	AGGACATGCG	TTTCATATTA	CAGAGCTCAA	GTCACTCATC	7740
	CTAAATAGCA	ATCAGGGCCT	CCTTCCTCTG	AATGGGGACC	CCGTAGTTAA	AAAAAATAA	7800
	AAGTAGGAAG	AGGAGGGGAG	GAGAAAGGAA	AGACACATGT	TGGAAGAGTA	GACAAATCA	7860
45	GTTTATCAGT	ATTCCAAATC	AGATGATTGG	AGACATTCAT	ACACAGAGAA	CGTGAACCTC	7920
	TTCTCTATCA	CAAGAAGTGA	TGTTCTCCATC	AAGGGTAACT	TTATACGACT	GGAGCCTTGA	7980
	AGAAAGCTGC	ATCTGGTGAA	CCACTGGTCA	GTGAGTCTAA	CAATTCAAAG	ATCAAAGTCA	8040
	GTGAGTCTCA	AGCAGGGATT	TGGGTCAATA	ATTAACGATC	AGTCACGAAC	ATTTGCAAAG	8100
	CATCTTCCAG	ACAAGCCATT	TGTAGCTTGT	GTAAAAGACT	CTTTTATTCT	TTCCCTTGCA	8160
50	GAAAAAATTA	AAAACTTATT	TCCTGATGGG	ACTATTGGCA	ATGATACGAC	ACTGGTTCTT	8220
	GTGAACGCAA	TCTATTTCAA	AGGGCAGTGG	GAGAATAAAT	TTAAAAAAGA	AAACACTAAA	8280
	GAGGAAAAAT	TTTGGCCAAA	CAAGGTATTG	TCTATATTTT	ATTTATATAG	TGTAATATGT	8340
	TAATACATGG	AATGTTAAAC	ATTTCTGATG	GAATGTAAAC	TGATAAGTAA	AAAAATAAAA	8400
	TGTTCTAGTG	CTGTTAATTT	GTTGTTTTAC	TCTTATAACT	TTATTAGTTT	AGGAATACCT	8460
55	GAAAAAATAT	TGTTTCTAAC	TCAATGGAAT	CCTGGGTTAT	TTCTTAGAAG	AAGAAGGATG	8520
	TGTTGCTATC	TCAATAATAT	TATCTTTTTT	GTCTTGTGTT	TCAGTGTGTA	TTTGTTTGAC	8580
	ACATTGATTT	ATGTCAGAAAT	ACATACAAAT	CTGTACAGAT	GATGAGGCAA	TACAATTCCT	8640
	TTAATTTTGC	CTTGCTGAGG	GATGTACAGG	CCAAGGTCTT	GGAAATACCA	TACAAAGGCA	8700
	AAGATCTAAG	CATGATTGTG	CTGCTGCCAA	ATGAAATCGA	TGCTCTGCAG	AAGGTAAGAA	8760
60	CTTGATCTCA	CAACTCTTCC	TTCTACTGCC	GGACATTTT	CCAAAGATAC	CAAGTTTAAA	8820
	CAAGGTAATA	GCTTATGACC	GAGTTGCCTC	AAAATGATGA	AAAATCTAA	ATGAGGAATG	8880
	ATGACTCACC	TTCAATATTAC	AAATATTTGA	GCATAGGGCC	TGACACAAAC	TGAAAGCTTA	8940
	GTTTTTGTGT	GTTTGTGTTG	TTTTATTATT	ATTATTATAA	TACTTTAAGC	TTTAGGGTAC	9000
	ATGTGCACAA	TGTGCAGGTT	AGTTACATAT	GTATACATGT	GCCATGCTGG	TGTGCTGCAC	9060
65	CCATTAACTC	ATCATTTAGC	GTTAGGTATA	TCTCCTAATG	CTATCCCTCC	CCCCCTCCCC	9120
	CACCCCAACA	CAGTCTCTAG	AGTGTGATGT	TACCTTCTCG	TGTCCAAGTG	TTCTCATTTG	9180
	TCAATTCCCA	TCTATGATTT	AATTCATCT	ATGGCTTAGT	TAATGATTAA	TTTATTAGAG	9240
	TTACATGCAT	TGGATATCAA	TTTGATGATA	TTATTATGCA	GCAATTTAAA	CTTGACTGGG	9300
	AGAAATATAT	ACCAATGTGA	GGAAAGTTTA	CAAATAGGCC	GAGTAGAAAA	GGGAATACAA	9360
70	ATTTAGGAAT	TTAGGGAATT	ACAATTTAAT	AATTGCAATG	TGTACTAAAT	AATGTATACA	9420
	GAAAAATATG	ATGAGCCTAT	TAAAAATGTA	CACATGTAGT	AGGCTGTTGG	CACAAGAAAT	9480
	AGTGATACAT	ACAGTTCAAT	GTGTACAAAA	TAATGTAATC	ATATTTTACA	TGTGTATCAT	9540
	ACAGTTGTAT	ACATACATAT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600
	ACATACATGT	ATATACATAT	ACACATATAA	CCCAATGTAT	TTATATATTC	AGGACTCATA	9660
75	TTTTACCTAT	TAGAATAATA	ATGCTATTAA	AAGTGAACCT	TCTGTATTTC	ACATTTATTG	9720
	CCAAATAAAC	GAATCTCCAC	ATAGTCAATT	CATTGTAAAG	GTGTATTAGA	GATCGACAGT	9780
	TAGTCATATC	AGTTTCTTTT	TTCCATTGTT	ATAGCTTGAA	GAGAACTCA	CTGCTGAGAA	9840
	ATTGATGGAA	TGGACAAGTT	TGCAGAATAT	GAGAGAGACA	TGTGTCGATT	TACACTTACC	9900
	TCGGTTCAAA	ATGGAAGAGA	GCTATGACCT	CAAGGACACG	TTGAGAACCA	TGGGAATGGT	9960
80	GAATATCTTC	AATGGGGATG	CAGACCTCTC	AGGCATGACC	TGGAGCCACG	GTCTCTCAGT	10020
	ATCTAAAGTC	CTACACAAGG	CCTTTGTGGA	GGTCACTGAG	GAGGGAGTGG	AAGCTGCAGC	10080
	TGCCACCGCT	GTAGTAGTAGT	TCGAATTATC	ATCTCCTTCA	ACTAATGAAG	AGTTCTGTTG	10140
	TAATCACCTT	TTCCATTCTT	TCATAAGGCA	AAATAAGACC	AACAGCATCC	TCTTCTATGG	10200
	CAGATTCTCA	TCCCATAGA	TGCAATTAGT	CTGTCACTCC	ATTTAGAAAA	TGTTCACTTA	10260
	GAGGTGTTCT	GGTAAACTGA	TTGCTGGCAA	CAACAGATTG	TCTTGCTTCA	TATTTCTTTT	10320

CTATCTCATC TTGATGATGA TAGTCATCAT CAAGAATTTA ATGATTAAAA TAGCATGCCT 10380
 TTCTCTCTTT CTCTTAATAA GCCACATAT AATGTACTT TTCCTTCCAG AAAAATTTCC 10440
 CTTGAGGAAA AATGTCCAAG ATAAGATGAA TCATTTAATA CCGTGTCTTC TAAATTTGAA 10500
 ATATAATTCT GTTCTTGACC TGTTTTAAAT GAACCAAAACC AAATCATACT TTCTCTTCAA 10560
 ATTTAGCAAC CTAGAAACAC ACATTTCTTT GAATTTAGGT GATACCTAAA TCCTTCTTAT 10620
 GTTCTTAAAT TTTGTGATTC TATAAAACAC ATCATCAATA AAATAATGAC ATAAAAATCAT 10680
 TTTTGTCTTA CCTGTTTCT CTCTGGAAAG GGCAAGTGT CAGTTACACA TAGGAAAGAT 10740
 AATTTAGAGA TATATTAATC ATATATAAAG GAAAATTAAA AACAGAGTAG TTCATGATGA 10800
 GCCTGGAGTA GAAGGCATAT CCCAGAACAG GAGGAGCCTT GTAAACCACA TAGGAACTTC 10860
 CTATTTTATG CTAAGGGAT AAGAACTCA TTACAGGCTT TGATGGTGT TTGTCAAAGA 10920
 GGGGCATAAA ATTATCATAT CCACATCTAG AAAATACATC TCTGGCTACG CTGATATCAA 10980
 TGGATGCGAG GAAAGAACAG TGTGGTTACC ATATATAAAT TAGGAAATCA TTAGAGTATT 11040
 GGGAGTGGAA ATGGAGAGAA AGAAAGAGCC TGGGGGAATT ATTTAGGAAA TAATAGTTAC 11100
 AGAAAGACAT CTAAGTTGCT GACCTATCTG ACTGGATGGA TGAAGAATA TCTTGTCTTCT 11160
 GAGAGAAAAA AAGACTTTGG GTTTAAATTT GTACTTGATG AATTAAGGTA CTTTAAATAT 11220
 TCAAATGGAT TTGCCTGGCA GGCACCTGAA GATATTAGTC TAAATCTCAG AAACAGAATA 11280
 TGATCTGAAG CTCTAAATTT GTGATATTC ATATAAATAC TTTAGAGTCA TTGGGATAAA 11340
 TATGTTAGTT GTGCTAAAAA GCAAAATAA GATACTAGGG AGAAAGGATA AAGTTAGAAG 11400
 AAAGAAGAAT CTAGAATTGA CCTTGAAGTA TATCAGCATG TGTAAAGATC AGGAATTGAT 11460
 CATTTTATT TTCCAGAAAG TAGCTTTTCT TAGGGTTCCA TATTTACTCC CATAGATTCT 11520
 TCCC

A76 Protein sequence:

Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
 Unigene number: Hs.227948
 Probeset Accession #: AB035089
 Protein Accession #: BAB21525
 Signal sequence: none found
 Transmembrane domains: none found
 Serine Proteinase Inhibitor domain: 13-390
 Cellular Localization: secreted

1 11 21 31 41 51
 | | | | |
 MNSLSEANTK FMFDLFQQFR KSKENNIFYS PISITSALGM VLLGAKDNTA QQISKVLHFD 60
 QVTENTTEKA ATYHVDNRSGN VHHQFQKLLT EFNKSTDAYE LKIANKLFE KTYQFLQEYL 120
 DAIKKFYQTS VESDFDFANAP BESRKKINSW VESQINEKIK NLFPDGTIGN DTTLVLVNAI 180
 YFKGQWENKF KKENTKEEFK WPNKNTYKSV QMMRQYNSFN FALLEDVQAK VLEIPYKGD 240
 LSMIVLLPNE IDGLQKLEEK LTAELKMEWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300
 TMGMVNIENG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAAATAVV VVELSSPSTN 360
 EEFCCNHFFL FFIRQNKTNIS ILFYGRFSSP

A77 DNA SEQUENCE

Gene name: hypothetical protein FLJ13459
 Unigene number: none found
 Probeset Accession #: XM_047266
 Nucleic Acid Accession #: XM_047266
 Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CTGACCTCAA GTGATCCACC CACCTCTGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC 60
 CACCATGCCA GGCCCTCTTA ACCTCTTCAA GTCTGTTTTC TCATCTGCAA AACAGAGGTA 120
 ATAAGATCAG TATCTTCTTA ATGGAAGCAC CTGGACTACA TTTTCTTCAT TCATTGTTAT 180
 CATAAATGAG GACTAACCTG TCTCCCGTTG GGAGTTTGA ACCTAGACCT CATGTCTTCA 240
 TGACGTCACT ACTGCCCCAG GCCCAGCTGT GTCCCTACAC CAGCCCCAGC TGACGCATCT 300
 TCTTTTCTG CCGTAGAGTA TGGTTACAAAT GCCTGCGCTG ATGCATTCTG GCCTTCGCAG 360
 ATCCTGGCGG GGCTGTGCCA ACGCTGTGGC CTCCCTGCCC CTGAATACCG AGCCGGTGCT 420
 GTCAAGGTGG GCAGCAAAGT CTTCTGACA CCACCGAGA CCCTGCCCC AGGGATCTCT 480
 TCACATGTGG ATTGACATCT TTCCTCAAGA TGTGCTGCT CCACCCCAAG TTGACATCAA 540
 GCCTCGGCAG CCAATCAGCT ATGAGCTCAG AGTTGTATC TGGAAACACGG AGGATGTGGT 600
 TCTGGATGAC GAGAAATCCAC TCACCGAGA GATGTCGAGT GACATCTATG TGAAGAGCTG 660
 GGTGAAGGGG TTGGAGCATG ACAAGCAGGA GACAGACGTT CACTTCAACT CCCTGACTGG 720
 GGAGGGGAAC TTCAATTGGC GCTTTGTGTT CCGCTTTGAC TACCTGCCCA CGGAGCGGGA 780
 GGTGAGCGCT TGGCGCAGGT CTGGACCTTT TGCCCTGGAG GAGGCGGAGT TCCGCGAGCC 840
 TGCAGTGTG TCCTGCAGG TCTGGGACTA TGACCGCATC TGTGCCAATG ACTTCTTTGG 900
 ATCCCTGGAG TTGCAGCTAC CAGACATGGT GCGTGGGGCC CGGGGCCCGG AGCTCTGCTC 960
 TGTGCAGCTG GCCCGCAATG GGGCCGGGCC GAGGTGCAAT CTGTTTCGCT GCCGCCGCTC 1020
 GAGGGGCTAG TGGCCGTTAG TGAAGCTGAA GGAGGCAGAG GACGTGGAGC GGGAGGCGCA 1080
 GGAGGCTCAG GCTGGCAAGA AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GGCCAGAAGA 1140
 CCTGGAGTTC ACAGACATGG GTGGCAATGT GTACATCCTC ACGGGCAAGG TGGAGGCAGA 1200
 GTTTGAGCTG CTGACTGTGG AGGAGGCCGA GAAACGGCCA GTGGGGAAGG GCGGGAAGCA 1260
 GCCAGAGCCT CTGGGAGAAC CCAGCCGCCC CAAAACCTCC TTCAACTGTT TTGTGAACCC 1320
 GCTGAAGACC TTTGTATCTT TCATCTGGCG CCGGTACTGG CGCACCTTGG TGCTGCTGCT 1380
 ACTGGTGCTG CTCACCGTCT TCCTCTCTCT GGTCTTCTAC ACCATCCCTG GCCAGATCAG 1440
 CCAGGTCACT TTCCGTCGCC TCCACAAGTG ACTCTGCTG ACCTTGGACA CTCACCCAGG 1500
 GTGCCAACCC TTCAATGCCT GCTCCTGGAA GTCTTTCTTA CCCATGTGAG CTACCCCAAGA 1560
 GTCTAGTGCT TCCTCTGAAT AAACCTATCA CAGCCACTG

A78 Protein sequence:

Gene name: hypothetical protein FLJ13459

Unigene number: none found
 Probeset Accession #: XM_047266
 Protein Accession #: XP_047266
 Signal sequence: none found
 Transmembrane domains: 291-313
 C2 domain: 27-86
 Cellular Localization: plasma membrane / ER

1 11 21 31 41 51
 | | | | |
 MWIDIFPQDV PAPPFVDIKP RQPISEYELRV VIWNTEDVVL DDENPLTGEM SSDIYVKSUV 60
 KGLEHDKQET DVHFNLSLTGE GNFNWRFVFR FDYLPTEREV SVWRRSGPFA LEEAEFRQPA 120
 VLVLQVWDYD RISANDFLGS LELQLPDMVR GARGPELCSV QLARNAGAGPR CNLFRCCRRLR 180
 GWWPVVKLKE AEDVEREAQE AQAGKKRKQ RRRKGRPEDL EFTDMGGNVY ILTGKVEAEF 240
 ELLTVEAEAK RPVGKGRKQP EPLEKPSRPK TSFNWFVNPL KTFVFFIWR RYWRTLVLLLL 300
 VLLTVFLLLV FYTIPGQISQ VIFRPLHK

A79 DNA SEQUENCE

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Nucleic Acid Accession #: AL137708
 Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60
 GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCTTTCTGT CTGTCTCCTT GCTCTGCCCC 120
 AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180
 ATGGCCTGGG CTGGGCCCTT GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAGG 240
 CTCTTGTGGG CAAAGCAGGG GAGGCCCAA TGTGGAGGAA CAGAGTCTCC TGGTGGCTG 300
 CTGTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCCTG 360
 GGGTCACCGT AGGCCCATG TAGCACCTG GTTCCCCTGC CTGTAGGTGA CAGGAGCCAG 420
 CCCAGCCAGG TGTGCTCCTT CCCAGGGCCC TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480
 CGCCCGCCCC ACCTTCTCTC CCACCCACAT GCCGAAGGGT GGCCAGGCAG GCAGGTGGAC 540
 GAGTCCAGGC AGCGGGCTGAG TCAGTGTGTG TGGAAATGTT TGGCCGCCTC CAGCTGCACC 600
 CTGCCCTTAC CTGCCACAC CTACCTTCA TCCTCAGGCG CTGCCGCCCT GAGCCCCCTG 660
 CAGGAATGCA CCTTTAGCCC AGGCCTGCTC AGTGAGCTCC GCCGACAGCC AGCCCTGCTC 720
 CTCCCGCCAT GACCTGCGAG ACCCTCTGG GCTTCCAAGT TCCTGGGGGC TGCAGTGAAC 780
 ATGCTCCACC TGCATGGCTG GCAAACCATG GTGGGCCCCA GCTGTGGTGC GTGCTGGGGT 840
 AGAGGCAAGG AAGTGATGGG ACCGCAGAGA TGAGACCCCC AGGGATGAGA TGGGACCCCC 900
 AGGACGGGCC CAGGGTCCAG GGCCAGGAG AGAGAAGCAG GGAGGGAGAG AGCTTCTTGG 960
 TGGAGGACGC ATCCTACAGT GGGGGCAAGG GTGCTCTGAG GTCCGGTGAA GGCAGGGACT 1020
 AGGCTGCCCA GGCCTGCCTT GCTTGGCTGG GGCTGGGGGC TGCTGGGAGG TGGCTGGGAG 1080
 GCTGGGCTTG GGCAGCTAAG CTGGAGCTTT GGCCAGGGTC CAGAGCCTCC CTCCCTTCAG 1140
 CTCTCTGCTG CACAGAACCT TCGCCCTTGG CCACCCCTGT CTGCCTCCTT GCCCTGGCAG 1200
 ACCCAGCACT GAGTGTCTGT AGTCAGATGG GGTAGCGGGC AGGGGCCGGA GGGGCCACCC 1260
 TCCCAGCTGA CCCAGCCTCC TGGGCGGCTT CTTCCAAACC AGCAGGGTAG AAAGATGGGG 1320
 CACCCACAGG TCTCTCCAGC TGCCCGGGCC CCAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380
 ATTCCAGACC TTGTGCGCGG GACCCCTGTG GAGTTGTGGG ATTCCCAAGA GGGGTGTGGG 1440
 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC 1500
 CCAGGGCCCC GCTGGGCTCT CATTGCCGGC GCCCTTGCCG CGGGCGTCTT CCTCGTCTCC 1560
 TGCCCTCTCT GTGCTGCTGC CTGCTGTGTC CGCCGCCACA GGAAGAAGCC CAGGACCAAG 1620
 GAGTCCGTGA GTCTGGGCTG TGCCCGCGGC ACCACCACCA CCCACCTGGT GAGGAGCGGC 1680
 TCCTTGCTCA CTCAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740
 GGCAGATTCA GCCCAGGGA TGGTTAACC CCCACAGAGG CAGGGCGTIG AGGACCTTCC 1800
 TGGCAGGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCCAT 1860
 GGGCCCCAGG GAGCCACAGC GGGTTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT 1920
 TTTGGGTGGG TTTGGCCGGT CTCACAGAGC GAAGCCGACG ATTTGTGCC TTTGGGTGGC 1980
 CTGGCCTGGA GGCGGGGGTT CTTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCCAGGG 2040
 CTCTGATGAG GCATGATGTC AGCACCACCT GCCCCTTGTC CCAACTCACT CCAGGTGCAA 2100
 CCTGATGTGG ATGGCCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCCCTGCA 2160
 CTCTCCCTGG AGTTTCACTT TGGAGCCAG GAGGTGAAGG GCCCGCTGC GCAGGACCA 2220
 CGGTTCTGCG AGTTTCCGGA AAGGGTGACG GGGGAAGGGC AGACCCCATG CCCTGGGTGG 2280
 TGGGAGCTG ACAGGGCAGG GGCCCTTGGC TGAGCCCAAC CGCTGGGCTC CCAGATCAGG 2340
 GTGGGCTTGA GGCAGCAGC CGACCTGAGG CTGGGGGCA CCGTGGACCC CTATGCCCGG 2400
 GTCAGCGTGT CCACCCAGGC CGGACACAGA CATGAGACAA AAGTGACACG AGGCACGCTC 2460
 TGCCCGTGT TTGACGAGAC CTGCTGCTTC CACGTGAGTC AGGGATGGTC GGCTGGGTGG 2520
 GCCTGGACGG CTGGAATGGG CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGCCTGGGCA 2580
 GCTGGGTGGG CTGAGCTAG GGCAGCAGGG CCTGGCTCAC GCCGTGCTC CAGATCCCCG 2640
 AGGCGGAGCT GCCAGGGGCC ACCCTGCAGG TGCAGCTTTT CAACTTCAAG CGCTTCTCGG 2700
 GGCATGAGCC CTGGGTGAG CTCCGTCTGC CACTGGGCAC CGTGGATCTG CAGCATGTTC 2760
 TGGAGCACTG GTACCTGCTG GGCCCGCCGG CTGCCACTCA GGTGAGGTGC TGGTCACCAG 2820
 GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CCTGCCCTAT GGGCCATCGG AAAGACAGGC 2880
 CTGATGGGCA GCATTTTCGG GGGTCTGAGC CCCAACTCGG CCAGAATCAC CCTCCCGGGC 2940
 TGAAGCCCTT CTGCTGCCC ACAGCCGAG CAGGTGCGGG AGCTGTGCTT CTCTCTCCGG 3000
 TACGTGCCCA GCTCAGGCCG GTGACCGTGT GTGGTGTCTG AGGCTCGAGG CTGCGTCCA 3060
 GGACTTGCAG AGCCCTTACG GAAGGTCCAG CTCATGCTGA ACCAGAGGAA GTGGGAAGAG 3120
 AGAAAGACAG CCACCAAAA GGGCACGGCG GCCCCTACT TCAATGAGGC CTTCACTTTC 3180
 CTGGTGCCTT TCAGCCAGGT CCAGAATGTG GACCTGGTGC TGGCTGTCTG GGACCGCAGC 3240
 CTGCCCTCC GAACTGAGCC CGTAGGCAAG GTGCACCTGG GTGCCCGGGC CTCGGGGCAG 3300

CCCCTGCGAGC ACTGGGCGAGA CATGCTGGCC CACGCCCGGC GGCCCATTCG CCAGCGGCAC 3360
 CCCCCTGCGGC CAGCCAGGGA GGTGGACCGC ATGCTGGCCC TGACGCCCCG CCTTCGCGCTG 3420
 CGCCTGCCCT TGCCCCACTC CTGAATGCAC CACATGCCCT TGTCTCCCGC CTGAGCCCGAG 3480
 GCACTTGCCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC

A80 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Protein Accession #: CAB70885
 Signal sequence: none found
 Transmembrane domains: 69-85
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MGHPVPSPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAKWGL QLSTDALSLA 60
 STFGPRWALI AGALAAGVLL VSCLLCAACC CCRHRKRPK DKESVGLGSA RGTTHLVR 120
 SGLLTQSRE GLKSRLQSPG QRGEFSRDRG LTPTEAGR

A81 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51
 | | | | |
 GCGGAACACC GCGCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
 TCCTCTCGTG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCACGG 120
 CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGAGG GCGGGAGGCG 180
 CGGAGCAGGA GCCCGGCCAG CGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTCCT 480
 ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
 AGACAGGCTG GTTGTGTTGG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA 660
 TCATCGTGAG CGACCAAGT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCAGGGA 720
 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
 AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
 CCAGTGGGCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
 ACAATGCTCC CATGTTTGAC CCCAGAAGT ACGAGGCCCA TGTGCTGAG AATGCAAGTGG 1080
 GCCATGAGGT CCAGAGGGTG ACGGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC 1140
 GTGCCACCTA CTTATCATG GCGCGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTTCAG GCCAAAAACC 1260
 AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCCCTT TGTGCTGAAG CTCCCAACCT 1320
 CCACAGCCAC CATATGGTTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
 CTGCAGAAGA CCCTGACAAG GAGAATCAAA AGATCAGTA CCGCATCCTG AGAGACCCAG 1500
 CAGGTGGCTT AGCCATGGAC CCAGACAGTG GGCAGGTAC AGCTGTGGGC ACCCTCGACC 1560
 GTGAGGATGA GCATTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
 ATGGAAGCCC TCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGCCC AGTCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC 1740
 ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCCCTTC CAGGCCGAGC 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG 1920
 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
 ATGTCGAAAC CTGCCCTGGA CCCTGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
 TCCTGGCTCT GCTGTTCTTC CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
 TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
 AGGCCAGGCC GGAGTGTTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
 AGGCGGCTAA CACAGACCCC ACAGCCCCGC CTAACGACAC CCTCTTGGTG TTCGACTATG 2400
 AGGGCAGCGG CTCGACGCC GGTCCCTGAC GCTCCCTCAC CTCCTCGGCC TCCGACCAAG 2460
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGTGGGCGG GGAGGACGAC TAGGGCGGCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC 2580
 CACAGAGCAT CTCGAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640
 GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
 TCCTTAGCCT TTCAGGATG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760
 CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCCAGAA GCCTCTTACC TGCCGTAAAA 2820
 TGCTCAACCC TGTGTCCTGG GCCTGGGCTC GCTGTGACTG ACCTACAGTG GACTTCTCTC 2880
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940
 TCAAAACGTT AGAGAAAGTT CTTCAAAGT GCAGCCGAGA GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060
 ATACTGAGGT TGCCTAGGTT GCCCTTATT TTTTATTTTC CCGTGTGCGT TGCTATAGAT 3120
 GAAGGTGTAG GACAACTGCT TATATGTACT AGAATTTTTT TATTAAAGAA A

A82 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)

Cellular localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
KGPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREEIAK 180
YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGLVP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TMDMGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEV AVGHEVQRLT VTDLDAPNSP 360
AWRATYLMG GDDGDHFTIT THPESNQGIL TTRKGLDPEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
DPAGWLANDP DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLLD 540
VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPHSTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKLFL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660
GAVLALLFL LLLLLLVKRL RKIKEPLLLP EDDTRDNVFI YGEEGGGEED QDYDITQLHR 720
GLEARPEVVL RNDVAPTII PPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
DYEAGSGDAA SLSSLTSSAS DQDQDYDYLW EWGSRFKKLA DMYGGGEDD

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A83 DNA SEQUENCE

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Probeset Accession #: F07953
 Nucleic Acid Accession #: NM_016334
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCAGCGTG CTGTGGCCTC 60
GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA 120
CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTTTGGG TTTGGGTGGC TTTTCTTCAT 180
GCCGCAATTG TTTAAAGACT ATGAGATACG TCAGATATGT GTACAGGTGA TCTTCTCCGT 240
GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
GAATAGCAGC TCCCGTTATT TTTCACTGGAA AATGAACCTG TGCCTAATTC TGCTGATCCT 360
GGTTTTCATG GTGCTTTTTC ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA 420
TAAACAACGA CTGCTTTTTT CCTGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
ACTAGGAGAT CCGTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTTCCTTCTG GATTGGGTGC 600
TGTCAACTGC CCATACACTT ACATGTCTTA CTTCCTCAGG AATGTGACTG ACACAGATAT 660
TCTAGCCCTG GAACGGCGAC TGCTGCAAAC CATGGATATG ATCATAAGCA AAAAGAAAAA 720
GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG 780
TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAG ATCTTACTCT 840
TATTCAACAG GAAGTGGATG CTTTGGGAAG ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAATATTTT 960
TAAATTTCTT GGTTCATTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020
CAATATTGTT TTTGATCGAG TTGGGAAAAA GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080
TGTGAATTAT CTGGGAATCC AATTGTATGT GAAGTTTGTG TCCCAACACA TTTCTTTCAT 1140
TCTTGTGGGA ATAATCATCG TCACATCCAT CAGAGGATTG CTGATCACTC TTACCAAGTT 1200
CTTTTATGCC ATCTCTAGCA CTAAGTCCTC CAATGTCATT GTCCTGCTAT TAGCACAGAT 1260
AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTGAATA 1320
CCGCACCATA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACCGTTGGTT 1380
TGATGTGATC TTCCTGGTCA GCGCTCTCTC TAGCATACTC TTCTCTTATT TGGCTCACA 1440
ACAGGCACCA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTTAGAGGC 1500
CAGTGGTTTC AAAATTTAGA TATAAGAGGG GGGAAAAATG GAACCAGGGC CTGACATTTT 1560
ATAAACAAC AAAATGCTAT GGTAGCATTT TTCACCTTCA TAGCATACTC CTTCCCTCTC 1620
AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAACCTAAG 1680
ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG 1740
CCAAGAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGGTAGC 1800
TGAGCCAAC ACGTAGGATT TCCGTTTAA GGTTCACATG GAAAAGGTTA TAGCTTTGCC 1860
TTGAGATTGA CTCATTAAAA TCAGAGACTG T

```

A84 Protein sequence

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Protein Accession #: NP_057418.1
 Signal sequence: none found
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402,
 424-446
 Cellular Localization: plasma membrane

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1      11      21      31      41      51

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	MSFLIDSSIM	ITSQILFFGF	GWLFFMRQLF	KDYEIRQYVV	QVIFSVTFAF	SCTMFELIIF	60
	EILGLNSSSS	RYFHWKMNLC	VILLILVFMV	PFIYGYFIVS	NIRLLHKQRL	LFSCLLWLTF	120
5	MYFFWKLGDP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFAGVNCP	YTYMSYFLRN	180
	VTDTDILALE	RRLQLQMDMI	ISKKKRMAMA	RRTMFQKGEV	HNKPSGFWMG	IKSVTTSASG	240
	SENLTLIQGE	VDALIELSRQ	LFLETADLYA	TKERIEYSKT	FKGKYFNFLG	YFFSIYCVWK	300
	IFMATINIVF	DRVGKTDVPT	RGIEITVNYL	GIQFDVKFWS	QHSIFILVGI	IIVTSIRGLL	360
10	ITLTKFYFAL	SSSKSSNVIV	LLLAQIMGMV	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
	FYHRWFDVIF	LVSALSILF	LYLAHQAPE	KQMAP			

A85 DNA SEQUENCE:

Gene name: TTK protein kinase

Unigene number: Hs.169840

Probeset Accession #: M86699

Nucleic Acid Accession #: NM_003318

Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

20	1	11	21	31	41	51	
	GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACTC	TTGTTGGCCA	GGCTGGAGTG	60
	CAATGGCACA	ATCTCAGCTT	ACTGCAACCT	CCGCCTCCCG	GGTTCAAGCG	ATTCTCCTGC	120
	CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACTAATTT	180
25	CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCTG	240
	ACCTCAGGTG	ATCCACTTGC	CTTGGCCTCC	CAAAGTGCTA	GGATTACAGC	CGTGAAACTG	300
	TGCTCGCTG	ATTCTTTTTT	TGTTGTTGGA	TTTTTGAAAC	AGGGTCTCCC	TTGGTCGCCC	360
	AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACTATAACC	TCCACCTCCT	GGTTTCAAGT	420
	GATCCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	GCGTGCACCA	CCACACCCGG	480
30	CTAATTTTTG	TATTTTATT	AGAGACAGGG	TTTCACCATG	TTGGCCAGGC	TGTTCTCAAA	540
	CTCCTGGACT	CAAGGGATCC	GCCTGCCTCC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
	AGTCACCATG	CCTGACCTTA	TAATTCCTAA	GTCTTTTTTT	CTGGTCCATT	TCTTCCTTAG	660
	GGTCCTCACA	ACAAATCTGC	ATTAGGCGGT	ACAATAATCC	TTAACTTCAT	GATTCACAAA	720
	AGGAAGATGA	AGTGATTATC	GATTAGAAAA	GGGGAAGTAG	TAAGCCCACT	GCACACTCCT	780
35	GGATGATGAT	CTTAATCCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
	TTTGGTTTAA	ATTAATTATC	TAAATATCTA	AAAACATTTT	TGGATACATT	GTTGATGTGA	900
	ATGTAAGACT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCCTCAG	960
	TGCAGTTTTC	TGTAGAAATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGATT	1020
	CCATAATGAA	CAAAGTGAGA	GACATTAAAA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
40	AACTAAGCTT	GAATAAAAT	TCTGCTGATA	CTACAGATAA	CTCGGGAAT	GTTAACCAAA	1140
	TTATGATGAT	GGCAAAACAAC	CCAGAGGACT	GGTTGAGTTT	GTTGCTCAAA	CTAGAGAAAA	1200
	ACAGTGTTCC	GCTAAGTGAT	GCTCTTTTAA	ATAAATTGAT	TGGTCGTGAC	AGTCAAGCAA	1260
	TTGAAGCGCT	TCCCCAGAT	AAATATGGCC	AAAATGAGAG	TTTTGCTAGA	ATTCAAGTGA	1320
	GATTGCTGTA	ATTAAGAGCT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAAAATG	1380
45	CCAGAGCAAA	CTGCAAGAAA	TTTGCTTTTG	TTCATATATC	TTTTGCACAA	TTTGAACTGT	1440
	CACAAGGTAA	TGTCAAAAAA	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CGTGGAGCAG	1500
	TACCACTAGA	AATGCTGGAA	ATTGCCCTGC	GGAATTTAAA	CCTCCAAAAA	AAGCAGCTGC	1560
	TTTCAGAGGA	GGAAAGGAAG	AATTTATCAG	CATCTACGGT	ATTAACCTGC	CAAGAATCAT	1620
	TTTTCCGGTTC	ACTTGGGCAT	TTACAGAATA	GGAACAACAG	TGTGATTGCC	AGAGGACAGA	1680
50	CTACTAAAGC	CAGGTTTTTA	TATGGAGAGA	ACATGCCACC	ACAAGATGCA	GAAATAGGTT	1740
	ACCCGAATTC	ATTGAGACAA	ACTAACAAAA	CTAAACAGTC	ATGCCCATTT	GGAAGAGTCC	1800
	CAGTTAACTC	TCTAATATGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTTGTACCTT	1860
	GTTTTATGAA	AAGACAAACC	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
	AACCAAGTGG	AAATGATTCC	TGTGAATTAA	GAAATTTAAA	GTCTGTTCAA	AATAGTCATT	1980
55	TCAAGGAAC	TCTGGTGCA	GATGAAAAGA	GTTCTGAATC	TATTATTACT	GATTCAATAA	2040
	CCCTGAAGAA	TAAACGGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
	AAGAACCAGA	GGTTCCAGAG	AGTAACCAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
	GTATTAAACA	GAATCCTGCT	GCATCTTCAA	ATCACTGGCA	GATTCGGGAG	TTAGCCCGAA	2220
	AAGTTAATAC	AGAGCAGAC	CATACCACTT	TTGAGCAACC	TGCTTTTTCA	GTTTCAAAAC	2280
60	AGTCACCACC	AATATCAACA	TCTAATGGT	TTGACCCAAA	ATCTATTTGT	AAGACACCAG	2340
	GCAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTGTAGAA	TCCAGTTGTA	AAGATGACT	2400
	TTCCACCTGC	TTGTCAGTTG	TCAACACCTT	ATGGCCAACC	TGCCTGTTTC	CAGCAGCAAC	2460
	AGCATCAAT	ACTTGCCACT	CCACTTCAAA	ATTTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
	ATGAATGCAT	TTGGTTTAA	GGAAGAATTT	ATTCATATT	AAAGCAGATA	GGAAGTGGAG	2580
65	GTTCAAGCAA	GGTATTTTCA	GTGTTAAATG	AAAAGAAACA	GATATATGCT	ATAAAATATG	2640
	TGAACCTAGA	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	CCGGAACGAA	ATAGCTTATT	2700
	TGAATAAACT	ACAACAACAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAAATCACGG	2760
	ACCAGTACAT	CTACATGGTA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAAA	2820
	AGAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAAAAATATG	TTAGAGGCAG	2880
70	TTCAACAAT	CCATCAACAT	GGCATTGTTT	ACAGTGATCT	TAAACCAGCT	AACTTCTCTGA	2940
	TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATTGC	AAACCAAAATG	CAACCAGATA	3000
	CAACAAGTGT	TGTTAAAGAT	TCTCAGTTTG	GCACAGTTAA	TTATATGCCA	CCAGAAGCAA	3060
	TCAAAGATAT	GTCTTCTCTC	AGAGAGAATG	GGAATCTTAA	GTCAAAGATA	AGCCCCAAAA	3120
	GTGATGTTTG	GTCTTAGGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCATTTC	3180
75	AGCAGATAAT	TAATCAGATT	TCTAAATTAC	ATGCCATAAT	TGATCCTAAT	CATGAAATTG	3240
	AATTTCCCGA	TATCCAGAG	AAAGATCTTC	AAGATGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
	ACCCAAAAAC	GAGGATATCC	ATTCCTGAGC	TCCTGGCTCA	TCCATATGTT	CAAATTCAAA	3360
	CTCATCCAGT	TAACCAAAATG	GCCAAGGGAA	CCACTGAAGA	AATGAAATAT	GTTCTGGGCC	3420
	AACTTGTTGG	TCTGAATTCT	CCTAATCCCA	TTTTGAAAGC	TGCTAAAAC	TTATATGAAC	3480
	ACTATAGTGG	TGGTGAAAGT	CATAATTCTT	CATCCTCCAA	GACTTTTGAA	AAAAAAAGGG	3540
80	GAAAAAAATG	ATTTCAGATT	ATTCGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGAGT	3600
	GTTTACTCTT	TGAATCCCTG	TGGAAATCTA	CATTTGAAGA	CAACATCACT	CTGAAGTGT	3660
	ATCAGCAAAA	AAAAATTCAGT	GAGATTATCT	TTAAAAAGAA	ACTGTAAGAA	TAGCAACCCAC	3720
	TTATGGCACT	GTATATATTG	TAGACTTGT	TTCTCTGTTT	TATGCTCTTG	TGTAATCTAC	3780
	TTGACATCAT	TTTACTCTTG	GAATAGTGGG	TGGATAGCAA	GTATATTTCTA	AAAAACTTTG	3840

TAAATAAAGT TTTGTGGCTA AATGA

A86 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

1	11	21	31	41	51	
MNKVRDIKKN	FKNEDLTDEL	SLNKISADTT	DNSGTVNQIM	MMANNPEDWL	SLLLKLEKNS	60
VPLSDALLNK	LIGRYSQAIE	ALPPDKYQON	ESFARIQVRF	AELKAIQEPD	DARDYFQMAR	120
ANCKKFAFVH	ISFAQFELSQ	GNVKKSKQLL	QKAVERGAVP	LEMLEIALRN	LNLOKKQLLS	180
EEEKQNLAS	TVLTAQESFS	GSGLHLQNRN	NSCDSRGQTT	KARFLYGENM	PPQDAEIGYR	240
NSLRQTNKTK	QSCPFGRVPV	NLLNSPDCDV	KTDSDSVVPCF	MKRQTSRSEC	RDLVVPKSKP	300
SGNDSCELRN	LKSVQNSHFK	EPLVSDEKSS	ELIITDSITL	KNKTESLLA	KLEETKEYQE	360
PEVPESNQKQ	WQAKRKSECI	NQNPAASSNH	WQIPELARKV	NTEQKHTTPE	QPVFSVSKQS	420
PPISTSKWFD	PKSICKTPSS	NTLDDYMSCF	RTPVVKNDFF	PACQLSTPYG	QPACFQQQHQ	480
QILATPLQNL	QVLASSSANE	CISVKGRIYS	ILKQIGSGGS	SKVFQVLNEK	KQIYAIKIVN	540
LEEADNQTLN	SYRNEIAYLN	KLQQHSKII	RLYDYEITDQ	YIYMVMCEGN	IDLNSWLKKK	600
KSIDPWERKS	YWKNNLEAVH	TIHQHGIVHS	DLKPANFLIV	DGMLKLIDFG	IANQMOPDIT	660
SUVKDSQVKT	VNYMPEATK	DMSSRENGK	SKSKISPKSD	VWSLGCILY	MTYKGTPEFQ	720
IINQISKLHA	IIDPNHEIEF	PDIPEKDLQD	VLKCCCLKRDP	KQRISIPPELL	AHPYVQIQTH	780
PVNQMAKGT	EEMKYVLGQL	VGLNSPNSIL	KAAKTLYEHY	SGGESHNSSS	SKTFEKKRGR	840
K						

A87 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

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GGGCGCAGCG	GGGCCCCGTCT	GCAGCAAGTG	ACCGACGGCC	GGGACGGCCG	CCTGCCCCCT	60
CTGCCACCTG	GGGCGGTGCG	GGCCCGGAGC	CCGGAGCCCG	GGTAGCGCGT	AGAGCCGGCG	120
CGATGCACGT	GCCTCACTG	CGAGCTGCGG	CGCCGCACAG	CTTCGTGGCG	CTCTGGGCAC	180
CCCTGTTTCT	GCTGCGCTCC	GCCCTGGCCG	ACTTCAGCCT	GGACAACGAG	GTGCACTCGA	240
GCTTCATCCA	CCGGCGCTTC	CGCAGCCAGG	AGCGGCGGGA	GATGCAGCGC	GAGATCCTCT	300
CCATTTTGGG	CTTGCCCCAC	CGCCCGCGCC	CGCACCTCCA	GGGCAAGCAC	AACTCGGCAC	360
CCATGTTTCT	GCTGGACCTG	TACAACGCCA	TGGCGGTGGA	GGAGGGCGGC	GGGCCCCGGC	420
GCCAGGGCTT	CTCCTACCCC	TACAAGGCCG	TCTTCAGTAC	CCAGGGCCCC	CCTCTGGCCA	480
GCCTGCAAGA	TAGCCATTTC	CTCACCGACG	CCGACATGGT	CATGAGCTTC	GTCAACCTCG	540
TGGAACATGA	CAAGGAATTC	TTCCACCCAC	GCTACCACCA	TCGAGAGTTC	CGGTTTGATC	600
TTTCCAAGAT	CCCAGAAGGG	GAACTGTCA	CGGCAGCCGA	ATTCCGGATC	TACAAGGACT	660
ACATCCGGGA	ACGCTTCGAC	AATGAGACGT	TCCGGATCAG	CGTTTATCAG	GTGCTCCAGG	720
AGCACTTGGG	CAGGGAATCG	GATCTCTTCC	TGCTCGACAG	CCGTACCCTC	TGGGCCTCGG	780
AGGAGGGCTG	GCTGGTGTTC	GACATCACAG	CCACCAGCAA	CCACTGGGTG	GTCAATCCGC	840
GGCACAACTT	GGGCTCTGAC	CTCTCGGTGG	AGACGTGGA	TGGGCAAGAG	ATCAACCCCA	900
AGTTGGCGGG	CCTGATTGGG	CGGCACGGGC	CCCAGAACAA	GCAGCCCTTC	ATGTTGGCTT	960
TCTTCAAGGC	CACGGAGGTC	CACTTCCGCA	GCATCCGGTC	CACGGGGAGC	AAACAGCGCA	1020
GCCAGAACCG	CTCCAAGACG	CCCAGAAACC	AGGAAGCCCT	CGCGATGGCC	AACGTGGCAG	1080
AGAACAGCAG	CAGCGACCAG	AGGCAGGCCT	GTAAGAAGCA	CGAGCTGTAT	GTCAAGCTTC	1140
GAGACCTGGG	CTGGCAGGAC	TGGATCATCG	CGCCTGAAGG	CTACGCCGCC	TACTACTGTG	1200
AGGGGGAGTG	TGCCTTCCCT	CTGAATCCT	ACATGAACGC	CACCAACCCAC	GCCATCGTGC	1260
AGACGCTGGT	CCACTTCATC	AACCCGGAAG	CGGTGCCCAA	GCCCTGTCTG	GCGCCACGCG	1320
AGCTCAATGC	CATCTCCGTC	CTCTACTTCG	ATGACAGCTC	CAACGTATAT	CTGAAGAAAT	1380
ACAGAAACAT	GGTGGTCCGG	GCCTGTGGCT	GCCACTAGCT	CCTCCGAGAA	TTCAGACCCT	1440
TGCGGGCCAA	GTTTTTCTGG	ATCCTCCATT	GCTCGCCTTG	GCCAGGAACC	AGCAGACCAA	1500
CTGCCTTTTG	TGAGACCTTC	CCCTCCCTAT	CCCCAACTTT	AAAGGTGTGA	GAGTATTAGG	1560
AAACATGAGC	AGCATATGGC	TTTTTGATCAG	TTTTTCAGTG	GCAGCATCCA	ATGAACAAGA	1620
TCCTACAAGC	TGTGCAGGCA	AAACCTAGCA	GGAAAAAATA	ACAACGCATA	AAGAAAAATG	1680
GCCGGGCCAG	GTCATTGGCT	GGGAAGTCTC	AGCCATGCAC	GGACTCGTTT	CCAGAGGTAA	1740
TTATGAGCGC	CTACCAGCCA	GGCCACCCAG	CCGTGGGAGG	AAGGGGGCGT	GGCAAGGGGT	1800
GGGCACATTG	GTGTCGTGTC	GAAAGGAAAA	TTGACCCGGA	AGTTCTCTGA	ATAAATGTCA	1860
CAATAAAACG	AATGAATG					

A88 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Protein Accession #: NP_001710.1
 Signal sequence: 1-30
 Pfam domains: TGFb_propeptide [37-281]
 Transmembrane domains: none found
 Cellular Localization: secreted

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1      11      21      31      41      51
5      |      |      |      |      |      |
      MHVRSRLRAA PHSFVALWAP LFLRLRSALAD FSLDNEVHSS FIHRRRLRSQE RREMQREILS 60
      ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
      LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHREFRFDL SKIPEGEAVT AAEFRIYKDY 180
      IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVEFDITA TSNHWVVPNR 240
      HNLGLQLSVE TLDGQSINPK LAGLIGRHGF QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
      QNRSKTPKNQ EALRMANVAE NSSSDQROAC KKHLYVSFR DLGWQDWIIA PEGYAAYCE 360
10     GECAFFLNSY MNATNHAIVQ TLVHFINFET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
      RNMVVRACGC H

```

A89 DNA SEQUENCE:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
 Unigene number: Hs.27373
 Probeset Accession #: F13036
 Nucleic Acid Accession #: AC012478
 Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

```

20     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGCGCGCCG TGCCGCTGCC CGCCCCGCTC CTGCCGCTGC TGCTGCTCGC GCTCCTGGCC 60
      GCTCCCGCCG CCGCGGCCAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120
      CGCGAGTCGC GGCACCGGCC CGGCCCGGGG CCGGGGAACA CCACCCGGTT TGGGTCTGGG 180
      GCGGCGGGCG GCAGCGGCAG CTCCAGCTCC AACAGCAGTG GCGACGCCTT GGTGACCCGC 240
      ATTTCATCC TCTCTCGCGA CCTACCCACC CTCAAGGCAG CGGTGATCGT GGCCTTCGCC 300
      TTTACACCC TCTCATCGC CTGCCTGCTG CTGCGCGTCT TCAGGTTCGGG AAAGAGGTTA 360
      AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGCGCCA 420
      CTAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
      TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT 540
      GTGCCCCCAG CCTTCATCCT CGACATTGAC CTTCAGCAAA GATGCACTGG AAGGCCTGAT 600
      GGTGGAATCA GAACTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAAGTTGG 660
      TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGCGT CGGAGGTGTT 720
35     GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTC AGGCATCTGC 780
      TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCAACCAA TGGAGTTGCT TCTGCCACCC 840
      TTTGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG 900
      CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTAGCCA GAAACACCCG GGTCCATCT 960
      GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGTG CTGAAAGTGA CCTTCCAAAT 1020
      CCTTGGTGGC CATTTAGCGC CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAAACATG 1080
      AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGGCCAGC GGGGCACCTT TTGTGAAGAC 1140
      AGAGCAGTGA CTAAGTTTCT CCAGGTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
      GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
      ACCCATCTGT TCAGGTGGG TCGTTAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
45     AGGGTGTTC GCGTCCGCG GCAGTCTCTG CATGGCGGAG GGTCAAGCGG TACCGCAACT 1380
      TGCCTTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTCTACAAA 1440
      ATCTGTCTCC CCTGCTGTGC CGTGGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
      GTCCCTTGGT CATTTAGCGC GAGCCACAAA AAGGCAGCTG CTGCCCACGG GGAGCCTGTC 1560
      AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
50     GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCACGTGA GGATGTCACT 1680
      CACCCTGGAG GAGACTTGA TGGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740
      GATGGCAGAT GCCAGAAGT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
      TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTCTCCTT 1860
      TCCCCCGGAC AGCCCTGTT TCTGTCCAGG CCCTGA

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A90 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
 Unigene number: Hs.27373
 Probeset Accession #: F13036
 Protein Accession #: FGENESH predicted
 Signal sequence: 1-27
 Transmembrane domains: 94-115, 448-469
 Cellular Localization: not determined

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65     1      11      21      31      41      51
      |      |      |      |      |      |
      MRVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTRFGSG 60
      AAGSGSSSSS NSSGDALVTR ISILLRDLPT LKAIVIVAF FTTLLIACLL LRVFRSGKRL 120
      KKTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGQCTLLTVP 180
      VPPPFILDI LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV 240
      ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPPP FGHPEKVPFT STPHGFRQLQ 300
      LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAAESDLFN PWWHFSATGS PIKTLYTQTM 360
      STLGLDVFCG AQQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESFGPHHL RLLRECPPLS 420
75     THPVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
      ICLPCCAHEH LREAKRSSVT VLASFQSPQ KAAAHGEPV KRGPSCQLTR HTCPGWGITH 540
      ANLQTIPTDQ GQEGREDVT HPGGDLGVA NFYLEEEGFQ DGRQCQKMLM SEEGPPSLTG 600
      CERLTGSHHF SSHSKWSWFL SPRQLFLSR P

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EWING**A91 DNA SEQUENCE**

Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942

Probeset Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5
 10
 15
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 65
 70
 75
 80

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1      11      21      31      41      51
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60
CTCGCGGTCA GGTATGGTTTT CTCTGTCAAG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
GTTTTACTGA CGTTCAAGAT ATTCCCTGTG ATCATTGTGC TTCATGTCGT TCTGGTAACA 180
TCCCTGGAAG AAGATACTGA TAATTCAGT TTGTCAACC CACCTGCTAA ATTATCTGTT 240
GTCAGTTTTG CCCCTCTCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
AGCTTACTCC TTTCAAACGA AACAGAAAAA ACTAAATCA CTATAGTAAA AACCTTCAAT 360
GCTTCAGGCG TCAAACCCCA GAGAAATATC TGCAATTGT CATCTATTG CAATGACTCA 420
GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAA 480
CAACATATAA CGAATGGCAC CTTAACCTGA GTCCTGTCTC TAAGTGAATT AAAACGCTCA 540
GAGCTCAACA AAACCTTCCA AACCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
GAGGCCAAAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA 660
TGCTGTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTTCGAC CAATGGAACA CTGCTGCTGT 720
TCTGTCAAGA TACCCTGCCC TTCTTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATTTTC TTCCAGCCAA 840
TCCATCCAGG TGGTGCCTCG GGCCACTGTG CTTTCCCAGG TCCCCAAAGC TACCTCTTTT 900
GCTGAGCCCTC CAGATTATTC ACCTGTGACC CACAATGTTT CCTCTCCAAT AGGGGAGATT 960
CAACCCCTTT CACCCCAAGC TTCAGCTCCC ATAGCTTCCA GCCCTGCCAT TGACATGCCC 1020
CCACAGTCTG AAACGATCTC TTCCCTATG CCCCACAAACC ATGTCTCCGG CACCCCACT 1080
CCTGTGAAAG CCTCATTTTC CTCTCCCACC GTGTCTGCCC CTGCGAATGT CAACACTACC 1140
AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTTCTGA TCTTGAGAAC 1200
CAAGTGTGTC AGATGGAGAA GGCTCTGTCC TTGGGCAGCC TGGAGCCTAA CCTCGCAGGA 1260
GAAATGATCA ACCAAGTCAG CAGACTCTTT CATTCGCCGC CTGACATGCT GGGCCCTCTG 1320
GCTCAAGATG TGCTGAAAGT AGTGGATGAC ATTGGCCTAC AGCTGAACCT TTCAACACG 1380
ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
TTCAACACAA CTACCTTTGT GGCCCAAGAC CCTGCAATC TTCAGGTTT TCTGGAAACC 1500
CAAGCTCCTG AGAACGATAT TGGCACAATT ACTCTTCTCT CATCGCTGAT GAATAATTAT 1560
CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTITTTG AACACCTGCT 1620
TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTAT ATCATCGAGT 1680
GTTGCAGAAC TGACCGTCAG GAACCTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
AAACCGAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGGT 1800
GGCAGAGGAG GCTGGTCAGA CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAAACC 1860
ATCTGTACCT GTAGCCATCT AACAAGCTTC GCGCTTCTGC TGGACCTATC TAGGACATCT 1920
GTGCTGCCTG CTCAAATGAT GGCTCTGACG TCCATTACAT ATATTGGTTG TGGGCTTTCA 1980
TCAATTTTTT TGTCTGTGAC TCTTGTAAAC TACATAGCTT TTGAAAGAT CCGGAGGGAT 2040
TACCCTTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CTGTGCTTCT 2100
CTCCTGGACT CGTGGATTGC TCTGTATAAG ATGCAAGGCC TCTGCATCTC AGTGGCTGTA 2160
TTTCTTCATT ATTTTCTCTT GGTCTCATTC ACATGGATGG GCCTAGAAGC ATTCCATATG 2220
TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATCTCTG 2280
ATTGTGCGTT GGGGGGTACC AGCTGTGGTT GTGACCATCA TCCTGACTAT ATCCCCAGAT 2340
AACTATGGGC TTGGATCCTA TGGGAAATTC CCCAATGGTT CACCGGATGA CTTCTGCTGG 2400
ATCAACAACA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTTG 2460
CTGAACGTCA GCATGTTTAT TGTGGTCTCT GTTCAGCTCT GTGCAATTAA AAAGAGAAG 2520
CAACTGGGAG CCCAGCGAAA AACCAGTATT CAAGACCTCA GGAGTATCGC TGGCCTTACA 2580
TTTTTACTGG GAATAACTTG GGGCTTTGCC TTCTTTGCC TGGGACCAGT TAACGTGACC 2640
TTCATGTATC TGTTTGCCAT CTTTAATACC TTACAAGGAT TTTTCATATT CATCTTTTAC 2700
TGTGTGGCCA AAGAAATGTT CAGGAAGCAA TGGAGGCGGT ATCTTTGTTG TGGAAAGTTA 2760
CGGCTGGCTG AAAATTTCTG CTGGAGTAAA ACTGCTACTA ATGGTTTAAA GAAGCAGACT 2820
GTAACCAAGG GAGTGTCCAG CTCTTCAAAT TCCTTACAGT CAAGCAGTAA CTCACATAAC 2880
TCCACCACAC TGTATGATGA TAATGATTGC TCAGTACACG CAAGCGGGAA TGGAAATGCT 2940
TCTACAGAGA GGAATGGGGT CTCTTTTAGT GTTCAGAAATG GAGATGTGTG CCTTACAGAT 3000
TTCACTGGAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCCGT 3060
ATGGCTCTCA GAAGGACTTC AAAGCGGGGA AGCTTACACT TTATTGAGCA AATGTGATTC 3120
CTTTCTTCTA AATCAAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA 3180
CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT 3240
AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300
TTTAGACATT TCTGATTGG TTTCTTATCT TTCAATTTAT AAGAAGGTTG GTTTTAAACA 3360
ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420
TTTAAAGAGG CTAAGTTATC TTTGATAACA TCATATAAAG CAACTGTTGA CTTACAGCTG 3480
TTGGTGAGTT TAGTTGTGCA TGCCTTTGTG GTATATAAGC TAAATTCTAG TGACCCATGT 3540
GTCAAAAATC TTACTTCTAC ATTTTITTTG ATTTATTTTC TACTGTGTA ATGTATTCTC 3600
TTGTAGAAATC ATGGTTGTTT TGTCTCACGT GATAATTGAG AAAATCCTTG CTCGTTCCGC 3660
AAATCCTAAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA 3720
TCAAGAAATA ATGATCCCAG CCAGACTGAG AAAATGTAAG CAGACAGTGC CACAGTTAGC 3780
TCATACAGTG CCTTTGAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840
TGGGTCTATGG TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900
GTGCACGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCCATCCC CTGACCCGAT 3960
CCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020
AGAGGGATGA ACTGTCATCC AGACCATGTG TCAGGAAAT TGTGAACGTA GATGAGGTAC 4080
ATACACTGCC GCTTCTCAAA TCCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC 4140
CTTCTCTTAA AAAGGTACAT ATATATGGA AAAAAATCATA TTGCCGTTCT TTAAGAGGCA 4200
ACTGCATGGT ACATGTTTGA TTGTTATGAC TGGTACACTC TGGCCAGGCC AGAGCTATAA 4260
TTGTTTTTTT AATGTTCTTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320
GGGAAGTCTC CTACACTGCT ATTGTTGCTA CATGTATCGA GCCTTGATTG CTCCTAGTTA 4380
TATACAGGCT CATCTTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCCTC AAGTACATCC 4440
TTATTAGGAA CATTCTTAAC CCCTTTTAGT TAAGTCTTTC ACTAAGGTTT TCTTGATATC 4500
ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560
CTGACTTGTC TTTGCAATAT TTCTTTTCTG ATTTATTTAA TTTTCTTGTA TTTATATGTT 4620

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AAAATCAAAA ATGTTAAAAAT CAATGAAATA AATTTGCAGT TAAGA

A92 Protein sequence

Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MVFSVRQCGH	VGRTEEVLIT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSPF	PAKLSVVSFA	60
PSSNEVETTS	LNDVTLSELL	SNETEKTKIT	IVKTFNASGV	KPQRNICNLS	SICNDSAFFR	120
GEIMFQYDKE	STVPQNQHIT	NGTLTGVLSL	SELKRSELNK	TLQTLSETYF	IMCATAEAQS	180
TLCNCTFTIKL	NTMTNACAAI	AALERVKIRP	MEHCCCSVRI	PCPSSPEELG	KLQCDLQDPI	240
VCLADHPRGP	PFSSSQSIPV	VPRATVLSQV	PKATSFAPFP	DYSPVTHNVP	SPIGEIQPLS	300
PQPSAPIASS	PAIDMPPQSE	TISSPMPQTH	VSGTPPPVKA	SFSSPTVSAP	ANVNTTSAPP	360
VQTDIVNTSS	ISDLENQVLQ	MEKALSLGSL	EPNLAGEMIN	QVSRLHSP	DMLAPLAQRL	420
LKVVDIDIGLQ	LNFSNTTISL	TSPSLALAVI	RVNASSFNIT	TFVAQDPANL	QVSLETQAPE	480
NSIGTTTLP	SLMNNLPAHD	MELASRVQFN	FFETPALFQD	PSLENLSLIS	YVISSSVANL	540
TVRNLTNRVT	VTLKHNPSQ	DELTIVRCVFW	DLGRNGGRGG	WSDNGCSVKD	RRINETICTC	600
SHLTSFGVLL	DLSTRTSVLPA	QMMALTFITY	IGCGLSSIFL	SVTLVTYIAF	EKIRRDYPSK	660
ILIQLCAALL	LLNLVFLDLS	WIALYKMQGL	CISVAVFLHY	FLLVSFYWMG	LEAFHMYLAL	720
VKVENTYIRK	YILKFCIVGW	GVPVAVVTII	LTISPDPNYGL	GSYGKFPNGS	PDDFCWINNN	780
AVFYITVVG	FCVIFLLNVS	MFIVVLVQLC	RIKKKKQLGA	QRKTSIQDLR	SIAGLTFLLG	840
ITWGAFAFFW	GPVNVTFMYL	FAIFNTLQGF	FIFIFYCVAK	ENVRKQWRRY	LCCGKRLRLAE	900
NSDWSKTATN	GLKKQTVNQG	VSSSSNSLQS	SSNSTNSTTL	LVMNDCSVHA	SGNGNASTER	960
NGVSFSVQNG	DVCLHDFTGK	QHMFNEKEDS	CNGKGRMALR	RTSKRGSLSHF	IEQM	

Fibrosis

A93 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 ProbeSet Accession #: N67551
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
CCGCAGAGGA	GCCTCGGCCA	GGCTAGCCAG	GGCGCCCCCA	GCCCCCTCCC	AGGCCGCGAG	60
CGCCCCCTGCC	CGCGTGCTCTG	GCCTCCCCCTC	CCGAGACTGCA	GGGACAGCAC	CCGGTAACATG	120
CGAGTGGAGC	GGAGGACCCC	AGCGGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
GGGTCCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
ATGCCTCTGC	CCTGGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
GGGAACGCGG	CCAGTGCAGG	GCATCAGCGG	TTGTTAGCAT	CGGCACGTCA	GCCTGGGGTC	360
TGTCACATATG	GAACCTAACT	GGCCTGCTGC	TACGGCTGGA	GAAGAAACAG	CAAGGGAGTC	420
TGTGAAGCTA	CATGCGAACC	TGGATGTAAG	TTTGGTGAGT	GCGTGGGACC	AAACAAATGC	480
AGATGCTTTC	CAGATAACAC	CGGGAACACC	TGCAGTCAAG	ATGTGAATGA	GTGTGAATG	540
AAACCCCGGC	CATGCCAACA	CAGATGTGTG	AATACACACG	GAAGCTACAA	GTGCTTTTGC	600
CTCAGTGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
ATAAATCTGT	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCCT	GTGTCCATCC	720
TCAGGACTCC	GCCTGGCCCC	AAATGGAAGA	GACTGTCTAG	ATATTGATGA	ATGTGCTCT	780
GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTGGAAG	CTACTACTGC	840
AAATGTACATA	TTGCTTTCGA	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
AATGAATGTA	CTATGGAATG	CCATACGTGC	AGCCACCATG	CCAATTGCTT	CAATACCCAA	960
GGGTCCCTTCA	AGTGTAATAG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCG	GTGTTCTGCT	1020
ATCCCTGAAA	ATTCTGTGAA	GGAAGTCCTC	AGAGCACCTG	GTACCATCAA	AGACAGAATC	1080
AAGAAGTTGC	TTGCTCACAA	AAACAGCATG	AAAAAGAAGG	CAAAAAATTA	AAATGTTTACC	1140
CCAGAACCCCA	CCAGGACTCC	TACCCCTAAG	GTGAACCTGC	AGCCCTTCAA	CTATGAAGAG	1200
ATAGTTTCCA	GAGGCGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GAAAATGAAA	1260
GAGGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
AGCCTGCGAG	GAGATGTGTT	TTTCCTTAAG	GTGAATGAAG	CAGGTGAATT	CGGCTTGATT	1380
CTGCTCCAAA	GGAAAGCGCT	AACTTCCAAA	CTGGAACATA	AAGATTTAAA	TATCTCGGTT	1440
GACTGCAGCT	TCAATCATGG	GATCTGTGAC	TGGAAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
TGGAATCCTG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGSCA	1560
GGTCACAAGA	AAGACATTGG	CCGATTGAAA	CTTCTCCTAC	CTGACCTGCA	ACCCCAAGC	1620
AACTTCTGTT	TGCTCTTTGA	TTACCGGCTG	GCCCGAGACA	AAGTCGGGAA	ACTTCGAGTG	1680
TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCACGAGTGA	GGATGAAAAG	1740
TGGAAGACAG	GGAAAATTCA	GTTGTATCAA	GGAAGTATG	CTACCAAAAG	CATCATTTTT	1800
GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
TCAGGCTTAT	GTCCAGATAG	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
TTGACTTTGT	ATGTCAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCATT	1980
TTAGAATTAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCTT	2040
TCTTGATATA	GATATGCCAA	TATTTGCTTT	AAATATCATA	TCAGTGTATC	TTCTCAGTCA	2100
TTTCTGAATC	TTTCCACATT	ATATTATAAA	ATATGGAAAT	GTCACTTTAT	CTCCCTCCT	2160
CAGTATATCT	GATTTGTATA	AGTAAGTTGA	TGAGCTTCTC	TCTACAACAT	TTCTAGAAAA	2220
TAGAAAAAAA	AGCACAGAGA	AATGTTTAA	TGTTTGACTC	TTATGATACT	TCTTGGAAGC	2280
TATGACATCA	AGAGTAGACT	TTTGCTTAAG	TGGCTTAGCT	GGGTCTTTCA	TAGCCAAACT	2340
TGTATATTAT	AATCTTTTGT	AATAATAATA	TCCAAATCAT	CAAAAAAATA	AAAAAATA	

A94 Protein sequence:

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Protein Accession #: NP_056322.2
 Signal sequence: 1-21
 Transmembrane domains: none found
 MAM domain: 402-546
 EGF domain: 80-259
 Cellular Localization: secreted

1	11	21	31	41	51	
MPLPWSLALP	LLLSWVAGGF	GNAASARHHG	LLASARQPGV	CHYGTKLACC	YGWRRNSKGV	60
CEATCEPGCK	FGCEVGNPKC	RCFPGYTGKT	CSQDVNECGM	KPRPCQHRVC	NTHGSYKFC	120
LSGHMLMPDA	TCVNSRTCAM	INCQYSCEDT	EEGPQCLCPS	SGLRLAPNGR	DCLDIDECAS	180
GKVICPYNRR	CVNTFGSYYC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SHHANCFTNQ	240
GSFKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KKLLAHKNSM	KKKAKIKNVT	300
PEPTRTPTEPK	VNLQPFNYEE	IVSRGGSNSHG	GKKGNBEEKMK	EGLEDEKREE	KALKNDIEER	360
SLRGDVFPPK	VNEAGEFGLI	LVQRKALTSK	LEHKDLNISV	DCSFNHGICD	WKQDREDDFD	420
WNPADRDNAI	GFYMAVPALA	GHKKDIGRLK	LLLPDLQFQS	NFCLLFYDYL	AGDKVGLLRV	480
FVKNSNNALA	WEKTTSEDEK	WKTGKIQLYQ	GTDATKSIIF	EAERGKGKTG	EIAVDGVLLV	540
SGLCPDSSL	VDD					

GLIOBLASTOMAA95 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1	11	21	31	41	51	
AGCAACGACG	CCGGGCGACG	GGAGCGGCGG	CCGCGCCATG	TGGCTGCTGG	GGCGGCTGTG	60
CCTGCTGCTG	AGCAGCGCCG	CGGAGAGCCA	GCTGCTCCCC	GGGAACAACT	TCACCAATGA	120
GTGCAACATA	CCAGGCAACT	TCATGTGCAG	CAATGGACGG	TGCATCCCGG	CGCGCTGGCA	180
GTGTGACGGG	CTGCTGACT	GCTTCGACAA	GAGTGATGAG	AAGGAGTGCC	CCAAGGCTAA	240
GTGGAATGT	GGCCCAACCT	TCCTCCCTG	TGCCAGCGGC	ATCCATTGCA	TCATTGGTCG	300
CTTCCGGTGC	AATGGGTTTG	AGGACTGTCC	CGATGGCAGC	GATGAAGAGA	ACTGCACAGC	360
AAACCCCTCT	CTTTGCTCCA	CCGCCCGCTA	CCACTGCAAG	AACGGCTCT	GTATTGACAA	420
GAGCTTCATC	TGCGATGGAC	AGAATAACTG	TCAAGACAAC	AGTGATGAGG	AAAGCTGTGA	480
AAGTTCTCAA	GAAACCCGCG	GTGGGCAGGT	GTTTGTGACT	TCAGAGAACC	AACTTGTGTA	540
TTACCCAGC	ATCACCTATG	CCATCATCGG	CAGCTCCGTC	ATTTTTGTGC	TGGTGGTGGC	600
CCTGCTGGCA	CTGGTCTTGC	ACCACCAGCG	GAAGCGGAAC	AACCTCATGA	CGCTGCCCGT	660
GCACCGGCTG	CAGCACCTCG	TGCTGCTGTC	CCGCTCGGTG	GTCCTGGACC	ACCCCCACCA	720
CTGCAACGTC	ACCTACAACG	TCAATAATGG	CATCCAGTAT	GTGGCCAGCC	AGGCGGAGCA	780
GAATGCGTCG	GAAGTAGGCT	CCCCACCTCT	CTACTCCGAG	GCCTTGCTGG	ACCAGAGGCC	840
TGCGTGGTAT	GACCTTCTCT	CACCGCCCTA	CTCTTCTGAC	ACGGAATCTC	TGAACCAAGC	900
CGACCTGCCC	CCCTACCGCT	CCCGTCCGG	GAGTGCCAAC	AGTGCCAGCT	CCCAGGCAGC	960
CAGCAGCCTC	CTGAGCGTGG	AAGACACCAG	CCACAGCCCG	GGGCGAGCTG	GCCCCAGGA	1020
GGGCACTGCT	GAGCCAGGGG	ACTCTGAGCC	CAGCCAGGGC	ACTGAAGAAG	TATAAGTCCC	1080
AGTTATTCCA	AAGTCCATAT	GGGTTAATCT	GCTCTGACTT	GTTGCCATTTC	TAACAAATTG	1140
TGCTCATGGG	AAGCTCTTTA	AGCACCTGTA	AGGATGTCTC	AAGTTACAGT	TTGGGATATT	1200
AACTATCTCT	GCATTCCTCT	CCTCCCCAG	ACTTCAGAGA	TGTTTTTCTG	CGGTCTCAGT	1260
TGACATGATC	TGTTGTGCGT	CTTTTCTGTC	AGGTCACTCT	TCCCTTGGGA	CCCAGATCA	1320
CACCTCATTT	TTTCACATTA	TTCTGTTTCT	GTTGGAGAGA	CAGCATATAA	AACAGTATTG	1380
AAATAGGCTG	GGAGAGAGCA	ATGTTTCTGT	GCTATATTGG	ATGCTCAGAA	GTGCAGGAGA	1440
CGCTGGACCC	AATTCTCTCT	GCTGGGTAGT	TACCTTATAG	CATTGGGGA	TTTGGGTAG	1500
ATGATCTAAC	CAGGAGGCCA	TCACTGGATG	GTCAACCCCC	CAAAAAAATT	CCATTTGAGC	1560
ATCAAAACCT	GCTTTGCACA	ATCCTATTGG	ATGCCCCAG	TTCAGCAGAG	TCAGTGGCCA	1620
AAGAAAACCT	TGGACGTGAG	TAACACCTTT	CAGCAGTCGC	AACGTTATTT	TGGTTTGTG	1680
AAGGACTCTG	AAACCATCTA	CCCTGTATAA	ATTCTGGCTT	TAGAAATTGG	CCCAAGAATG	1740
CTCATTTCTG	GAGCTTTCTC	CAGCAGCATA	TATCATCAGC	CTCATCTTAA	AATAGGCAGG	1800
GAGCCCTCCG	CATGAGTTTA	TCCAAGTTCT	CAGCTCCTAA	AATGCAGGCT	GCCAAGACCC	1860
TACACCTGCC	CTGGCTCTAC	AGCCACITAC	CTGGTTTCTG	GACTGTCAAC	CTCCAGCTG	1920
ACCTGCCCGT	AGCCAAGGAA	TGAGGACCTA	ACTTGAGTTG	GCCCAAGTCT	TGACCTGGCT	1980
GTATGTCCCT	GTGGCCACAC	CCCAGCCTGT	CTTGCTCATT	CATGCAGCCT	CAACACTGGC	2040
CTCCAAAGTT	CCCTTAACAC	TTGCAAGTCT	CTTTTACCT	GTGCATTTGG	ACTTGAGGAC	2100
ACTGGTTTCT	ATCACAGGTG	AGAGCCATGT	TCAATACCTC	CAGCAAGCTC	TCCTGGCTCC	2160
CTGCACGTGT	CACGCTCCTC	TTCCCAAGGT	CCCAATACCA	GCACCTCTAG	TTAGAGTTAG	2220
GGTCAGGGTC	AGGCCTCTCC	CAACATCCCA	GTAGTTTCTC	CTCTGAGACA	CATGGGCAAG	2280
AGACAATTGG	GAGTCAAGAT	TTTCCATTGG	GATCTATTTT	AAATCTTTTA	GAAATGCATT	2340
TGAAACAGTG	TGTTTGTTTT	TTCCCTTCTA	GTTAAGGGAC	TATTTATATG	TGTATAGGAA	2400
AGCTGTCTCT	TTTTTTGTTT	TTCTTTTAAC	AAGGTCCAAA	GAAAGATGCA	AAAGGAGATC	2460
ACACCTCTGC	CCCGCTGAGC	CCCGTGATAA	CAAGTCACTC	CAGACTAACC	TGTGTGCCAG	2520
ACATTGTGTC	ATTGTTGCAC	TTTGAGGTTA	TTATTATCA	AGTTCCTGAA	GGAAGCAGAA	2580
AGAGGGACTC	CTCTCTCCCT	CCGTGTATAG	TCTCTATGTT	TGTGCTAGTT	TTTCTTTTTT	2640
TTCTCTGTGT	CCAGTCAGCC	ACAGGGCCCG	CCTCCCTGCA	GGAATAAGGG	GTAACACGTT	2700
AGGTGTTGTT	TGGCAAGAAA	CCCACTGAC	TGATGAGGGG	TAAATGGAA	CCAGGTAGAG	2760
CCACTCCGGG	CAGCTGTCAA	CCATTTCAG	CTTCTTCCG	CAGCTGAAGA	AATGTTCACT	2820
AACCTGTTTG	ACGCTAATTA	AAACAGAGCC	TGCAGGAAGT	GGGCTAAAG	TGGCATTTCAG	2880

TGATCCTGTT CTGTAGACTT TTCTTCTTT TTTTAACCAA ATCCAAAGGA TGTTACAGAA 2940
 AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA 3000
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAAGAA CTTTGTATGA CAGCCAGAAT GTGTAGAAC TCTGGCTGAA 3120
 CATTTTCATCT CTTGTAGAGT AGAAGGGCTT TATTTCTCCC TTGTATGGG CCCCTTCTTC 3180
 TTCTCGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTTAGT 3300
 AGATAAGGGA TGCCCTACTAA TGCTTTTTTA AAACAAACAG GGACATTTT ATTATAGATT 3360
 TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAA CCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCCAG 3540
 AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAACTG 3720
 GAAAGGTTGT GTGTCTGTGC TTTTGTGTT TGGTTAGGC TTGGTTTTGT TTTTAAATT 3780
 TTATACCTTC TAATAAATT GCAGTTTCAT TCTTCTGTG TGTGCAAAWG GWMCTAMARM 3840
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTCGGAAGAA GTTTTAAACA CCACCTCGGG 3900
 TGGGGCGGG GGGCCACCT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAAG 3960
 GAAACCTGG CCAAGAAAAA GGTGGCGAGA ATTCCTCCAC CCAAGAAAAA ACGCCCGGG 4020
 GGAAACCGCA GAGTGTGCG TAAACCACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

A96 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MWLLGLPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60
 EKECPKAKSK CGPTFFPCAS GIHCLIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNGLCIDKSF ICDGNNCCD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180
 VIFVLVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240
 YVASQAEQNA SEVGSPPSYS EALLDQRPW YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEEV

LUNG

A97 DNA SEQUENCE

Gene name: putative GPCR, Weakly similar to dJ365012.1
 Unigene number: Hs.256897
 Probeset Accession #: BE001836
 Nucleic Acid Accession #: BE001836
 Coding sequence: 1-2955 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGGCCGTC AATCTTTTTC CTTCACACT GGGATGATG GGCTAGACCC AGACCCAATC 60
 ATGTTAAGTA TGATAGGGAT CAGTGGCCCA GCTGGTGTGG AAGACAAAGT GGTCACTCTG 120
 GGTTTAGGCC CACATAGCAC TAAAGGTCTT CAACATGCAA TTAGAAGCTC AAATGTTGAC 180
 GGGAAATATG TTCACCTCTA AAAAGATGTT TCTATTAGAA TTTACTTACT CTTTCATGAA 240
 AACATAGATG CTTCCTCTTT CTTGATTAGT GATGGCCATC AGTTAAACCA AGTGCACCTCA 300
 GAGAAGTCAA ATCTGACAC AATCCAGCAA GTAACATATA AAACGTATGG CCCAGTCGAA 360
 GAATATCAGC TGCTGCTTCA GGTGACCTAT AGAGATTCCA AGGAGAAAAG AGATTGAGA 420
 AATTTTCTGA AGCTCTTGAA GCCTCCATTA TTATGGTCAC ATGGGCTAAT TAGAATTATC 480
 AGAGCAAAGG CTACCACAGA CTGCAACAGC CTGAATGGAG TCCTGCAGTG TACCTGTGAA 540
 GACAGCTACA CTTGGTTTCC TCCCTCATGC CTGTATCCCC AGAACTGCTA CCTTCACACG 600
 GCTGGAGCAC TCCCAAGCTG TGAATGTCAT CTCAACAACC TCAGCCAGAG TGTCAATTTT 660
 TGTGAGAGAA CAAAGATTGG GGGCACTTTC AAAATTAATG AAAGGTTTAC AAATGACCTT 720
 TTGAATTCAT CTTCTGCTAT ATACTCCAAA TATGCAAAAT GAATTGAAAT TCAACTTAAA 780
 AAAGCATATG AAAGAATTCA AGGTTTGTAG TCGGTTTCAG TCACCCAATT TCGAAATGGA 840
 AGCATCGTTG CTGGGTATGA AGTTGTTGGC TCCAGCAGTG CATCTGAAC TCTGTCTGAG 900
 ATTGAACATG TTGCCGAGAA GGCTAAGACA GCCCTTCACA AGCTGTTTCC ATTAGAAGAC 960
 GGCTCTTTCA GAGTGTTCGG AAAAGCCCAG TGTAATGACA TTGTCTTTGG ATTTGGGTCC 1020
 AAGGATGATG AATAATACCT GCCCTGCAGC AGTGGCTACA GGGGAACAT CACAGCCAAG 1080
 TGTGAGTCCT CTGGGTGGCA GGTCTATCAGG GAGACTTGTG TGCTCTCTCT GCTTGAAGAA 1140
 CTGAACAAGA ATTTAGTAT GATTGTAGGC AATGCCACTG AGGCAGCTGT GTCATCCTTC 1200
 GTGCAAAATC TTTCTGTCAT CATTGGGCAA AACCCATCAA CCACAGTGGG GAATCTGGCT 1260
 TCGGTGGTGT CGATTCTGAG CAATATTTCA TCTCTGTAC TGGCCAGCCA TTTCAAGGTG 1320
 TCCAATTCAA CAATGGAGGA TGTCTATCAGT ATAGCTGACA ATATCCTTAA TTCAGCCTCA 1380
 GTAACCAACT GGACAGTCTT ACTGCGGGAA GAAAAGTATG CCAGCTCACG GTTACTAGAG 1440
 ACATTAGAAA ACATCAGCAC TCTGGTGCCT CCGACAGCTC TTCTCTGAA TTTTCTCGG 1500
 AAATTCATG ACTGGAAAGG GATTCCAGTG AACAAAAGCC AACTCAAAG GGGTACAGC 1560
 TATCAGATTA AAATGTGTCC CCAAAATACA TCTATTCCTA TCAGAGGCCG TGTGTTAATT 1620
 GGGTCAGACC AATTCAGAG ATCCCTTCCA GAAACTATTA TCAGCATGGC CTCGTGTACT 1680
 CTGGGGAACA TTCTACCCGT TTCCAAAAT GGAAATGCTC AGGTCAATGG ACCTGTGATA 1740

TCCACGGTTA TTCAAACCTA TTCCATAAAT GAAGTTTTC TATTTTTTTC CAAGATAGAG 1800
 TCAAACCTGA GCCAGCCTCA TTGTGTGTTT TGGGATTTC GTCAATTGCA GTGGAACGAT 1860
 GCAGGGCTGCC ACCTAGTGAA TGAAACITCAA GACATCGTGA CGTGCCAATG TACTCACTTG 1920
 5 ACCTCTTCTT CCATATTGAT GTCACTTTT GTCCCTCTA CAATCTTCCC CGTTGTAAAA 1980
 TGGATCACCT ATGTGGGACT GGGTATCTCC ATTGGAAGTC TCATTTTATG CCTGATCATC 2040
 GAGGCTTGT TTTGGAAGCA GATTAAAAAA AGCCAAACCT CTCACACACG TCGTATTATG 2100
 ATGGTGAACA TAGCCCTGTC CCTCTTGATT GCTGATGTCT GGTATTATGT TGGTGCCACA 2160
 GTGGACACCA CGGTGAACCC TTCTGGAGTC TGCACAGYTG CTGTGTTCCT TACACACTTC 2220
 10 TTCTACCTCT CTTTGTTCCT CTGGATGCTC ATGCTTGGCA TCCTGCTGGC TTACCGGATC 2280
 ATCCTCGTGT TCCATCACAT GGCCAGCAT TTGATGATGG CTGTTGGATT TTGCCTGGGT 2340
 TATGGGTGCC CTCTCATAT ATCTGTGATT ACCATTGCTG TCACGCAACC TAGCAATACC 2400
 TACAAAAGGA AAGATGTGTG TTGGCTTAAC TGGTCCAATG GAAGCAAACC ACTCCTGGCT 2460
 TTTGTTGTCC CTGCACTGGC TATTGTGGCT GTGAACCTCG TTGTGGTGCT GCTAGTTCTC 2520
 15 ACAAAGCTCT GGAGGGCCGAC TGTGTTGGGAA AGACTGAGTC GGGATGACAA GGCCACCATC 2580
 ATCCGCGTGG GGAAGAGCCT CCTCATCTG ACCCCTCTGC TAGGGCTCAC CTGGGGCTTT 2640
 GGAATAGGAA CAATAGTGGA CAGCCAGAAT CTGGCTTGGC ATGTTATTTT TGCTTTACTC 2700
 AATGCATTCC AGGGAATTTT TATCTTATGC TTGGAATAC TCTTGACAG TAAGCTGCGA 2760
 CAACTTCTGT TCAACAAAGT GTCTGCCTTA AGTTCTTGGG AGCAAAACAGA AAAGCAAAA 2820
 20 TCATCAGATT TATCTGCCAA ACCCAAATTC TCAAAGCCTT TCAACCCACT GCAAAACAAA 2880
 GGCCATTATG CATTTTCTCA TACTGGAGAT TCCTCCGACA ACATCATGCT AACTCAGTTT 2940
 GTCTCAAATG AATAA

A98 PROTEIN SEQUENCE

Gene name: putative GPCR, Weakly similar to dJ365012.1
 25 Unigene number: Hs.256897
 Protein Accession #: none found
 Signal sequence: 1-17
 Pfam domain: 7tm_2 [561-820]
 30 Transmembrane domains: 545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 35 | | | | |
 MHALLLCFSV LNASGLSL QSPVEEYQLL LQVTYRDSKE KRDLRNFLKL LKPPLLWSHG 60
 LRRIIRAKAT TDCNSLNGVL QCTCEDSYTW FPPSCLDPQN CYLHTAGALP SCECHLNLS 120
 QSVNFCERTK IWGTFKINER FTNDLLNSSS AIYSKYANGI EIQLKKAYER IQGFESVQVT 180
 40 QFRNGSIVAG YEVVSSSSA ELLSAIEHVA EKAKTALHKL FPLEDGSFRV FGKAQCNDIV 240
 FFGSGKDEY TTPCSSGYRG NITAKCESSG WQVIRETCVL SLLEELNKNF SMIVGNATEA 300
 AVSSFVQNL S VIIRQNPST VGNLASVVS LSNISLSLSA SHFRVSNSTM EDVISTADNI 360
 LNSASVTNWT VLLREEKYAS SRLLLETLENI STLVPPTALP LNFSRKFIDW KGIPVNKSQL 420
 KRGYSYQIKM CPQNTSIPIR GRVLIGSDQF QRSLPETIIS MASLTGLNIL PVSKNAGNAV 480
 NGPVIISTVIQ NYSINBVFLE FSKIESNLISQ PHCVWFDFSH LQWNDAGCHL VNETQDIVTC 540
 45 QCTHLTSFSI LMSPPFVPTI FPVVKWITYV GLGISIGSLI LCLIIIEALFW KQIKKSQTS 600
 TRRICMVNIA LSLLIADWVF IVGATVDTTV NPSGVCTAAV FPTHFFYLSL FFWMLMLGIL 660
 LAYRIILVPH HMAQHLMMAV GFCLGYGCPL IISVITIAVT QPSNTYKRKD VCWLWNWSNGS 720
 KPLLAFVPPA LAIVAVNFV VLLVLTKLWR PTVGERLSRD DKATIIRVGK SLLILTPLLG 780
 LTWGFIGITI VDSQNLAWHV IFALLNAFQV RTVTITYCIV K

A99 DNA SEQUENCE

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 55 Probeset Accession #: F07953
 Nucleic Acid Accession #: NM_016334
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 60 | | | | |
 AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCAGCGTGG CTGTGGCCTC 60
 GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA 120
 CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTTTGA TTTGGGTGGC TTTTCTTCAT 180
 65 GCGCCAATTG TTTAAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCTTCTCCGT 240
 GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTGAAATCT TAGGAGTATT 300
 GAATAGCAGC TCCCGTTATT TCACTGGAA AATGAACCTG TCGTAATTC TGCTGATCCT 360
 GGTTFTCATG GTGCCTTTTT ACATTGGCTA TTTTATTTTG AGCAATATCC GACTACTGCA 420
 TAAACAACGA CTGCTTTTTT CTGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
 70 ACTAGGAGAT CCCTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
 CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTTCTTTCTG GATTTGGTGC 600
 TGTCAACTGC CCATACACTT ACATGTCCTA CTCTCTCAGG AATGTGACTG ACACAGATAT 660
 TCTAGCCCTG GAACGCGCAC TGCTGCAAAC CATGGATATG ATCATAAGCA AAAAGAAAAG 720
 GATGGCAATG GCACGAGAAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG 780
 75 TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAA ATCTTACTCT 840
 TATTCAACAG GAAGTGGATG CTTTGAAGA ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
 TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAAATATT 960
 TAATTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020
 80 CAATATTGTT TTTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080
 TGTGAATTAT CTGGGAATCC AATTTGATGT GAAGTTTGGG TCCCAACACA TTTCTTTCAT 1140
 CTTTGTGGA ATAATCATCG TCACATCCAT CAGAGGATTG CTGATCACTT TTACCAAGTT 1200
 CTTTATGACC ATCTCTAGCA GTAAGTCCTC CAATGTCAAT GTCCTGCTAT TAGCACAGAT 1260
 AATGGGCATG TACTTGTCT CTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTAGAATA 1320
 CCGCACATA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACCGTTGGTT 1380
 TGATGTGATC TTCTTGGTCA GCGCTCTCTC TAGCATACTC TTCCTCTATT TGGCTACAA 1440

ACAGGCACCA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTTAGAGGC 1500
 CAGTGGTTTC AAAATTTAGA TATAAGAGGG GGGAAAAATG GAACCAGGGC CTGACATTTT 1560
 ATAAACAAAC AAAATGCTAT GGTAGCATTT TTCACCTTCA TAGCATACTC CTTCCCCCTC 1620
 AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAACCTCAAG 1680
 ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG 1740
 CCAAGAAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGGTAGC 1800
 TGAGCCAAAC ACGTAGGATT TCCGTTTAA GGTTCACATG GAAAAGGTTA TAGCTTTGCC 1860
 TTGAGATTGA CTCATTAAAA TCAGAGACTG T

A100 Protein sequence

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Protein Accession #: NP_057418.1
 Signal sequence: none found
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MSFLIDSSIM ITSQILFFGF GWLFFMRQLF KDYEIRQYVV QVIFSVTFAP SCTMPFELIIF 60
 EILGLVNSSS RYFHWKMLNC VILLILVFMV PFYIGYFIVS NIRLLHKQRL LFSCLLWLTF 120
 MYFFWKLGDG PFILSPKHGI LSIEQLISRV GVIGVTLMAL LSGFGAVNCP YTYMSYFLRN 180
 VDTDILALE RRLQTMDMI ISKKRMAMA RRTMFQKGEV HNKPSGFWCM IKSVTTSASG 240
 SENLTLIQQE VDALEELSRL LPLETADLYA TKERIEYSKT PKGKYFNFLG YFFSIYCVWK 300
 IFMATINIVF DRVGKTDPTV RGIETVNYL GIQFDVKFWS QHISFILVGI IIVTSIRGLL 360
 ITLTFFFYAI SSSKSSNVIV LLLAQIMGY FVSSVLLIRM SMPLEYRTII TEVLGELQFN 420
 FYHRWFDVIF LVSLSSILF LYLAKHQAPE KQMAP

A101 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
 CTGGGCCAGC GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTGCG GGGAGCTGCT GGCTGCAGCC 300
 TGTGCCAGCG GGGCCCTGCC CCGCTCCTCC TCCGGGCCCC CCTGCCCTGC CTGACGTCC 360
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG 480
 GCGCTCATTA AGCAGCTGTT TGAGGCCCCG GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGGCC CAGGGGCCAG CTGGCACTC 600
 AGCCCTTCGA GGGTGGGCGC CCCATCGCAC CCACCTCTC TGGCTGGAGA CCCCCGCGAG 660
 GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CCTGCGCCCC TTGCCAGATG GGCTCCCCAG 720
 GCCTGCCCCC GGCTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG 780
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGAG CTACTACTGG CCGCTGTCTAG 840
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCGG TTTCAGCGG TGCCGCCCTG 900
 GGTCCCATCT TCAGGGAAG GCACCTGCCA CGCCAGGCTG CACTTCCAAC AACGGGCGAGC 960
 AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080
 GTAAGCGGGG GGTGCTTGGC TGGCTGGGGA GCCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140
 CTGGCCAAGG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200
 GGCCTGCATG TGCCTCCCAC AGACCTGGGG GTGATGGCCT TCCCCCTCTT GGCCGGGACG 1260
 TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA 1320
 GACAGCTCCC AGGCACGTCA TAGGCAAAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380
 CTGGGGTCTC GCTCACCCCC CTTTGCTCTC ACGCCAGACC TGTCCCCAGG TTTCACTGCG 1440
 GAGAGGCCAC CTCCCTCAGC CAAGGAAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500
 GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT 1560
 GGAGTACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTACCCA 1620
 GAACCAAGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680
 TCAGTGTGTG TGGGCGCGAG GGCCTCCGAT GCGGGGTGAG TGCGTGGGGG GCGCAGGGCC 1740
 CCCGATGCGG GGTACGTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACCTTGGT 1800
 ACACTGTCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC 1860
 CCTTCCGGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920
 TGCTGCACCT GGTCTGCAGG GGTGTCCCAG GACAGGCCCA AGTCAGGCCA GCATGCAGCT 1980
 GCCCTCTTAC CTTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCTGG 2040
 ACCTCTCTGG CAGGAAAGGG TGCAGTCTCT GAGGGCCTGT GCCCCACAGC CCCAGCACCC 2100
 AGGTGGACTC CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCCGTGAGC 2160
 GGCTGGGGTC TGCCACCCAG GGCCTCCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCCC 2220
 TGGGGGATCC TGGCATCTTT ACTGGAGTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280
 GGTGACTTCA TCAGAGAGCC GCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340
 GAGACAGGCT GGCACCTCCG GAAAACTGCT CTTTCAGCCT TGGTGTTCGG TGCAAGGTGA 2400
 AAAGAAATAG GTCCCTCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAC 2460
 CACGAGGGGA GAATTTAAAG GCCCGGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520
 GCAGACCCCT CTTGAGCTCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580
 GAGCAGCGTC CTTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACACGT 2640
 GCGTGCACAC TGTGATGACA CCCGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700
 CAGAAGTGTC CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA 2760
 TTTTGTGTTG ATCAGTTTCC AAGGAAAAGG AACATCTCAG CCGGGCGTGG TGGTTCAGGC 2820

CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCCATCTCT ACAARAATAA AAAAAGAAAG AAAGAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060
 AGAAATAAAA GAGATTCTCG GAAACATGAA AAAAAA

A102 DNA SEQUENCE

Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTATGCCCC GTGTGAGCCA 60
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA AACTGTGTGC CTACTATCTC TTCCGTGGTG 120
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCCGATGTC 180
 AGAGGTCTCG AAAAATGAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAATAA GTCCTGTGTC ACCAGATGCA 300
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGTGGTTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCAATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAAAATGT TGCTGTGCCC CACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT TCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCTCTG GCCACGTGTT TACCTTGACG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTTA TGAATTGTAC CTCCTCAAGT CATGGAACAT CCAGGTGGGT 1020
 CTAGTTTCCC TGTGAGCAA TCCAGCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACCTCCCC 1200
 GATGGAAGAG TGTGCTGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 TCCCTGTCC TGAACCAACG GCGCTCCCT TTGATTTCCA ACAAGATCTG CAACCACAGG 1320
 GACGTGTACG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA 1620
 TCCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCTTGG GAGCTCTGAG 1680
 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCTTTCCA TCTGATTCCA GCACAACTT 1740
 CAAGCTGCTT TTTGTTTTTGA GGTGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
 TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCAACCC CAACTAATTT 1920
 TTGTATTTT AGTAGAGACA GGGTTTCACT ATGTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 CCTCAATGA TGTGCTGCT TCAGCCTCCC ACAGTCTGG GATTACAGGC ATGGGCCACC 2040
 ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
 AGGGGCGGCT TTCCCACTGT TCTCTCTCCA GGGGCTTGTG AAAATTCCTG 2160
 ACGAGATAAG CAGTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCAGTT TCTACTCTA GGGACCAAG 2280
 CCAAACCCAC CCTTCTACT TCCAAGACTT ATTTTACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGGCCAT TTTATGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400
 TTGTCTTTG ATTCCAATA ATATGTTTCC TTCCCTCAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAA

A103 Protein sequence:

Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_SPC domain: 216-444
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MGENDPFAVE APFSFRSLFG LDDLKISVPA PDADAVAAQI LSLLPLKFFP IIVIGIIALI 60
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEVRCVRV GGQNAVQLQVF 120
 TAASWKTMCs DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 VTALHHSVIV REGCASGHVY TLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQFQGYH 240
 LCGSVITPL WIITAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGA GDASPLVNHA 360
 AVPLISNKIC NHRDVGYGII SPSMLCAGYL TGGVDSCQGD SGGPLVCQER RLWKLVGATS 420
 FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT

A104 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)
 Unigene number: Hs.208229
 Probeset Accession #: AI819198
 Nucleic Acid Accession #: NM_032551.1
 Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
10  ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCTCTGGG GGGCACCAGGC CAACGCCTCC 60
    GGCTGCCCCG GCTGTGGCGC CAACGCCTCG GACGGGCCAG TCCCTTCGCC GCGGGCCGTG 120
    GACGCCTGGC TCGTGCCGCT CTCTCTCGCG GCGCTGATGC TGCTGGGCCT GGTGGGGAAC 180
    TCGCTGGTCA TCTACGTCA CTGCCGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240
15  ATGCCCAACC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGCGTCCC CTTCACGGCC 300
    CTGCTGTACC CGCTGCCCCG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT CGTCAACTAC 360
    ATCCAGCAGG TCTCGGTGCA GGGCACGTGT GCCACTCTGA CCGCATGAG TGTGGACCGC 420
    TGGTACGTGA CGGTGTTCCC GTTGCGCGCC CTGCACCGCC GCACGCCCGC CCTGGCGCTG 480
    GCTGTACGCC TCAGCATCTG GGTAGGCTCT GCGGCGGTGT CTGCGCCGGT GCTCGCCCTG 540
20  CACCGCCTGT CACCGGGGCC GCGCGCCTAC TGCAGTGAGG CCTTCCCCAG CCGCGCCCTG 600
    GAGCGCGCCT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCCGCT GCTCGCCACC 660
    TGCGCTGTCT ATGCGGCCAT GCTGCGCCAC CTGGGCGCGG TCGCCGTGCG CCCCGCGCCC 720
    GCCGATAGCG CCCTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGGCCAAAG 780
    GTCTCGCGCG TGGTGGCGCG CGTGGTCCTG CTCTTCGCGC CTGCTGGGGG CCCATCCAG 840
25  CTGTTCTCTG TGCTCAGCGC GCTGGGCCCC GCGGGCTCCT GGCACCCAG CAGTACGCC 900
    GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCCTACA GCAACTCCCG GCTGAACCCG 960
    CTGCTCTACG CCTTCTCTGG CTGCACTTTC CGACAGGCC TCCGCCGGGT CTGCCCTTGC 1020
    GCGCGCGCGC GCCCGCGCGC CCGCGGCCGT CCGGACCCCG AGCCCCACAC 1080
    GCGGAGCTGC ACCGCTGGG GTCCCAACCG GCCCGCGCA GGGCGCAGAA GCCAGGGAGC 1140
30  AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA
  
```

A105 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA
 Unigene number: Hs.208229
 Protein Accession #: AI819198
 Signal sequence: none found
 Pfam domains: 7tm_1 [59-323]
 Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
45  MHTVATSGPN ASWGAPANAS GCPGCGANAS DGPVPSRAV DAWLVPLFFA ALMLLGLVGN 60
    SLVIYVICRH KPMRTVTNFI IANLAATDVT FLCCVPFPTA LLYPLPGWVL GDFMCKFVNY 120
    IQQVSVQATC ATLTAMSVDR WYVTVFPLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180
    HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240
    ADSALQGQVL AERAGAVRAK VSRLVAAVVL LFAACWGP IQ LFLVLQALGP AGSWHPRSYA 300
50  AYALKTWAHC MSYNSALNPN LLYAFLGSHF RQAFRRVCPA APRRRRRRRR PGPSDPAAPH 360
    AELHRLGSHP APARAQKPGS SGLAARGLCV LGEDNAPL
  
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A106 DNA SEQUENCE

Gene name: integrin, beta 8
 Unigene number: Hs.52620
 Probeset Accession #: AA479726
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
60  CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCTTGGCC AGCCAGGACG 60
    CTGCCGACTT GTCTTTGCCG GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
    GTTGGCCTCC CTGCCCACTT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT 180
65  TCCCTTCGAC CTCGCCGGCG TACCCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
    TAGGGTGGTT TCCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300
    CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAG CTCTTTTCTT 360
    TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT 420
    TGGCCGTCGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCCGTGCC GAGCCGGGAG 480
70  GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGGCC GCTTACCTGC ACCGCTTGCT 540
    CCGAGCCGCG GGGTCCGCCT GCTAGGCCTG CGGAAAACGT CCTAGCGACA CTCGCCCGCG 600
    GGCCCGGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGGCG 660
    GGGCGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTTTTACC GCTGCATTGT 720
    TCTGCCTGCA AAACGACCGG CGAGGTCCCG CCTGTTCTCT CTGGGCGAGC TGGGTGTTT 780
75  CACTTGTCTT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGATCTTCA AATGCAGCAT 840
    CCTGTGCCAG GTGCCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTC 900
    TTTCAAGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTTAATA AGCAAAGGCT 960
    GCTCAGTTGA TTCAATAGAA TACCCATCTG TGATGTTTAT AATACCCACT GAAAATGAAA 1020
80  TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT CCGTCCAGGA GCCGAAGCTA 1080
    ATTTTATGCT GAAAGTTTAT CCTCTGAAGA AATATCTGT GGAATCTTAT TATCTTGTGT 1140
    ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTGGA AACGATTAT 1200
    CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTCTGCTTGG ATTTGGCTCA TACGTTGATA 1260
    AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT 1320
    ACAATTTAGA CTGCATGCCT CCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA 1380
    TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440
  
```

5	AAGGAGGTTT	TGACGCCATG	CTTCAGGCAG	CTGTCTGTGA	AAGTCATATC	GGATGGCGAA	1500
	AAGAGGCTAA	AAGATTGCTG	CTGGTGATGA	CAGATCAGAC	GTCCTCATCTC	GCTCTTGATA	1560
	GCAAAATTGGC	AGGCATAGTG	GTGCCCCAATG	ACGGAAACTG	TCATCTGAAA	AACAACGTCT	1620
	ACGTCAAATC	GACCAACCATG	GAACACCCCT	CACCTAGGCCA	ACTTTCAGAG	AAATTAATAG	1680
	ACAACAACAT	TAAATGTCATC	TTTGCAGTTC	AAGGAAAACA	ATTTTCATGG	TATAAGGATC	1740
	TTCTACCCCT	CTTGCCAGGC	ACCATTGCTG	GTGAAATAGA	ATCAAAGGCT	GCAAACTCA	1800
	ATAATTTGGT	AGTGAAGGCC	TATCAGAAGC	TCATTTTCAGA	AGTGAAAGTT	CAGGTGGAAA	1860
	ACCAGGTACA	AGGCATCTAT	TTTAACATTA	CCGCCATCTG	TCCAGATGGG	TCCAGAAAGC	1920
	CAGGCATGGA	AGGATGCAGA	AACGTGACGA	GCAATGATGA	AGTTCTTTTC	AATGTAACAG	1980
10	TTACAATGAA	AAAATGTGAT	GTCACAGGAG	GAAAAAATA	TGCAATAATC	AAACCTATTG	2040
	GTTTTAATGA	AACCGCTAAA	ATTTCATATAC	ACAGAACTG	CAGCTGTGAG	TGTGAGGACA	2100
	ACAGAGGACC	TAAAGGAAAG	TGTGTAGATG	AAACTTTTCT	AGATTCCAAG	TGTTTCCAGT	2160
	GTGATGAGAA	TAAATGTCAT	TTTGATGAAG	ATCAGTTTTC	TTCTGAGAGT	TGCAAGTCAC	2220
15	ACAAGGATCA	GCCTGTTTGC	AGTGGTCGAG	GAGTTTGTGT	TTGTGGGAAA	TGTTTCATGTC	2280
	ACAAAATTAA	GCTTGGAAAA	GTGTATGGAA	AATACTGTGA	AAAGGATGAC	TTTTCTTGTC	2340
	CATATCACC	TGGAAATCTG	TGTGCTGGGC	ATGGAGAGTG	TGAAGCAGGC	AGATGCCAAT	2400
	GCTTCAGTGG	CTGGGAAGGT	GATCGATGCC	AGTGCCCTTC	AGCAGCAGCC	CAGCACTGTG	2460
20	TCAATTCAA	GGGCCAAGTG	TGCAGTGGAA	GAGGCACGTG	TGTGTGTGGA	AGGTGTGAGT	2520
	GCACCGATCC	CAGGAGCATC	GGCCGCTTCT	GTGAACACTG	CCCCACCTGT	TATACAGCCT	2580
	GCAAGGAAAA	CTGGAATTGT	ATGCAATGCC	TTCAACCTCA	CAATTTGTCT	CAGGCTATAC	2640
	TTGATCAGTG	CAAAACCTCA	TGTGCTCTCA	TGGAACAACA	GCATTATGTC	GACCAAACTT	2700
	CAGAATGTTT	CTCCAGCCCA	AGCTACTTGA	GAATATTTT	CATCATTTTC	ATAGTTACAT	2760
	TCTTGATTGG	GTTCCTTAAA	GTCTCTGATCA	TTAGACAGGT	GATACTACAA	TGGAATAGTA	2820
25	ATAAAATTAA	GTCTCTCATCA	GATTACAGAG	TGTCAGCCTC	AAAAAAGGAT	AAATTGATTTC	2880
	TGCAAAAGTGT	TTGCACAGA	GCAGTCACCT	ACCGACGTGA	GAAGCCTGAA	GAAATAAAAA	2940
	TGGATATCAG	CAAAATTAAAT	GCTCATGAAA	CTTTCAGGTG	CAACTTCTAA	AAAAAGATTTC	3000
	TTAAACACTT	AATGGGAAAC	TGGAATTGTT	AATAATTGCT	CCTAAAGATT	ATAATTTTAA	3060
	AAGTCACAGG	AGGAGACAAA	TTGCTCACGG	TCATGCCAGT	TGCTGGTGT	ACACTCGAAC	3120
30	GAAGACTGAC	AAGTATCCTC	ATCATGATGT	GACTCACATA	GCTGCTGACT	TTTTTCAGAGA	3180
	AAAATGTGTC	TTACTACTGT	TTGAGACTAG	TGTCGTTGTA	GCACCTTACT	GTAATATATA	3240
	ACTTATTTAG	ATCAGCATAG	AATGTAGATC	CTCTGAAGAG	CACCTGATTAC	ACTTTACAGG	3300
	TACCTGTTAT	CCCTACGCTT	CCCAGAGAGA	ACAATGCTGT	GAGAGAGTTT	AGCATTGTGT	3360
	CACCTACAAGG	GTACAGTAAT	CCCTGCACCTG	GACATGTGAG	GAAAAAATA	ATCTGGCAAG	3420
35	TATATTCTAA	GGTTGCCAAA	CACCTCAACA	GTTGGTGGTT	GAATAGACAA	GAACAGCTAG	3480
	ATGAATAAAT	GATTCGTGTT	TCACCTCTTC	AAGAGGTGAA	CAGATACAAC	CTTAATCTTA	3540
	AAAGATTATT	GCTTTTAAAA	GTGTGTAGTT	TTATGCATGT	GTGTTTATGG	TTTGCTTATT	3600
	TTTGCAGATG	GGATACATA	TCCAGCATTC	TCTCCTCTTT	GCCTTTATGT	TTTGTCTTCT	3660
	TTTTTACAGG	ATAAGTTTAT	GTATGTCCAC	GATGACTGGA	TTAATTAAGT	GCTAAGTTAC	3720
40	TACTGCCATA	AAAAACTAAT	AATACAATGT	CACCTTATCA	GAATACTAGT	TTTAAAAGCT	3780
	GAATGTAA						

A107 Protein sequence:

45	Gene name:	Integrin, beta 8
	Unigene number:	Hs.52620
	Probeset Accession #:	AA479726
	Protein Accession #:	NP_002205.1
	Signal sequence:	1-39
50	Transmembrane domains:	682-704
	EGF domain:	552-584
	INB domain:	54-469
	Cellular Localization:	plasma membrane

55	1	11	21	31	41	51	
	MCGSALAFFT	AAFVCLQNDR	RGPASFLWAA	WVFSVLVLGLG	QGEDNRCASS	NAASCARCLA	60
60	LGPECGWCVQ	EDFISGGGRS	ERCDIVSNLI	SKGCSVDSIE	YPSVHVIIPT	ENEINTQVTP	120
	GEVSIQLRPG	AEANFMLKVH	PLKKYPVDLY	YLVDVSASMH	NNIEKLNSVG	NDLSRKMAFF	180
	SRDFRLGFGS	YVDKIVSPYI	SIHPERIHQ	CSDYNLDCMP	PHGYIHVLSL	TENITEFEKA	240
	VHRQKISGNI	DTPEGGFDAM	LQAAVCESHI	GWRKEAKRL	LVMTDQTSHL	ALDSKLAGIV	300
	VPNDGNCHLK	NNVYVKSTM	EHPSLGQLSE	KLIDNNINVI	FAVQKQFHW	YKDLLPLLEF	360
65	TIAGEIESKA	ANLNNLVEA	YQKLISEVKV	QVENQVQGIY	FNITAICPDG	SRKPGMEGCR	420
	NVTSNDEVL	NVTVMKKCD	VTGGKNYAI	KPIGFNETAK	IHIHRNCSCQ	CEDNRGPKGK	480
	CVDETFLDSK	CFQCDENKCH	FDQDQFSSES	CKSHKQDPVC	SGRGVCVCGK	CSCHKIKLGK	540
	VYGYKCEKDD	FSCPYHHGNL	CAGHGECEAG	RCQCFSGWEG	DRQCPCPSAA	QHCVNSKGQV	600
	CSGRGTCVCG	RCECTDPRSI	GRFCEHCPTC	YTACKENWNC	MQCLHPHNLS	QAILDQCKTS	660
70	CALMBQQHYV	DQTSECFSSP	SYLRIFFIIF	IVTFLIGLLK	VLIIRQVILQ	WNSNLIKSSS	720
	DYRVSASKKD	KLILQSVCTR	AVTYRREKPE	EIKMDISKLN	AHETFRCNF		

A108 DNA sequence

75	Gene name:	ESTs
	Unigene number:	Hs.128899
	Probeset Accession #:	AA983251
	Nucleic Acid Accession #:	AA983251
	Coding sequence:	1-1749 (underlined sequences correspond to start and stop codons)

80	1	11	21	31	41	51	
	ATGCTGTCTG	GCTTCTTGAT	GAGTCCCAGT	ACCCAGCAC	GAGCACAGTA	CACTCCCAGG	60
	GGAAAGAAAC	TTCCGTGGGA	GGCTTCCATC	GGTGCACACA	CCTCCGAGG	GCGAGGCAGC	120
	GACCGGGAGA	GGGAGAGCCG	GCCGGAGGCT	GCCGGGCTCC	TGTGGGACCG	CGCTGCAGCC	180
	GGGGAGGCGG	AGAAAGGGAA	CCGGGCGCAG	CCGCCCGCCT	GGATCCGCGC	CCAGCAGCAG	240

5 CCGCGGCCGC CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGGCGC GCAGGACCCT 300
 CGCTGCGTC CTGGACGTTT CCGGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360
 TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCATC AGCGAGTGCA 420
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
 GCTCCTGGAC CTAGGGCCCG GCGTCGTGCG CTCTGGGCG TCGCGGCAGA GGGGAGTGCG 540
 CCGCGCGGAA AGCGCGCGCG GACAGTCAGT GACGAGGCCG GGGGGTCGCC GGGGCCAAGA 600
 CTCTCTGGAG ACCGTCTGCT GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660
 TGTGGGGCGC TCGCCGCTCG TCCGTCTCCT CATCCTGGAA CGCGGCTTCG CTCCTGCAGC 720
 TGCTGCTGGC TGCCTGCTG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780
 10 TGGCTGGACG CGCAGGCGCT CTGGCGCATC GGTTCAGT GTCCCGAGCG CTTCGACGGC 840
 GGCAGCGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGCGGCTGG CGAGCCTGGC 960
 CGGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020
 15 GGAGACGGCG AGGGTGCGCC CCCACCGGTG AGGGCCTGGC AGCGGTGCTC CCCTGAAGGC 1080
 TCCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCGG TGCCAGACGC 1140
 CGCGGATTCC CATCTTCTCC ACGCGCGCGC CCCTCTCCCC TGACGCGGCC CGCCTTGCCC 1200
 ATCTACGTGC CGTTCCTCAT TGTGTGGCTCC GTGTTTGTG CTTTATCAT CTGTGGGTCC 1260
 CTGGTGGCAG CCTGTTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCA GCAGAGCCGA 1320
 20 GCCCCAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACTCC 1380
 CGGGGGTCTG CTTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440
 GGGGCCCGGG CGCCCCCAAC AAGGTACAG ACCAACTGTT GCTTGCCGGA AGGGACCATG 1500
 AACACGTGT ATGTCAACAT GCCACGAAT TTCTCTGTG TGAATGTCA GCAGGCCACC 1560
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCCAT ACGTGGGGTA CACGGTGACG 1620
 25 CAGCACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCCTGGCTAC 1680
 AGGCAGATTC AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
 ACTGTATAAC CGAGAGTCAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAAGTCC GCACATGTG GTGGTATTTA TGGCAGGATT CCTTTGGATG 1860
 GCTTCATTTG CCCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920
 CATCCAGGGT ATCATTTGATT TATGATGGAA AACCGGCCTC AGCTGGAGAT GACTGTGATG 1980
 30 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
 AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100
 TTGTTGTTGA TCGCACAGGA TCAAAATGCC TGTATCTCTC CTTTACTCGG GACTTTTFTT 2160
 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCCAGGC TGGAGTGACG 2220
 35 TGGTGCATC TCGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCAACA CTCTGCCTC 2280
 AGCTCCACAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTTATTTT 2340
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGTCTGGTCT ACTCTCTGTA CCTCAAGCAA 2400
 TCTGCTGTG TCAGCCTCCC AAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
 TGAGCCTTTT TTTTTTTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAA TAACAGGACT 2520
 40 ATTCATAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATCCACA 2580
 GGCACACCTT AATTCATTG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640
 GGGCCTATTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
 TTAATAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCATT CATCCCTTTC 2820
 45 TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTTCTTTT 2880
 TATATTGAAT TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940
 TGGTTATGGT TTGGCGTTTC CTCTCTGTTG GTTTTCAGAG CCCCATGTCT ATATAGTCTC 3000
 GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060
 50 AAAAAATTTT TTTGCTTAGT TATAAAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
 TAGCTCTCTA GCCATAACCT GAGACTTGGG ATGAAATTTA AACAGATAC GATTACTTTT 3180
 GCAGATCATA AGGCTTTTTA TACTCTTGT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240
 GATTGTAAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTCTCCAC ACTGTTCTTG 3300
 ATTTCTCTC TCTTTCAGG CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360
 CAAATTCAGG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAGAT AACTTTAAGG 3420
 55 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACAGTATT TTGTAATTA ACAATCGCT 3480
 GTATGGTATG TCTTCTTACA CATTTATGTC TATAGATATC TATGATCAT CTTTCTATTC 3540
 TGTTCATGA CTGAATAATG TAAACCAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
 TTTTTTAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
 TGAATAAATA AAAAAAATA AAAAAAATA

A109 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular Localization: not determined

70 1 11 21 31 41 51
 | | | | | |
 MLSGFLMSPS TQHRAQYTFG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
 GEAEGKNRGE PPAPWIRAQQ PRPPFAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPEA 120
 75 SGRQPRGPSD CIPRFPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG 180
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAAPRVVP CGALAAAPSP HPPTPLRSCS 240
 CCWLRCWRRG RGPSGEYCHG WLDAQGVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300
 ARLDQGGCDN DRQQGAGEPG RADKDGPRL GRASCLRGTQ GDGEGAPPV RAWQRCSPG 360
 SPKGRQLLRA FPGLPRARR RGFPSSPRGG PSPLQRPALP IYVPLIVGS VFVAFILGS 420
 80 LVAACCCRL RPQDPPQSR APGNNRLMET IPMIPASSTS RGSSSRQSST AASSSSANS 480
 GARAPPTRSQ TNCCLPEGTM MNVVMPTN FSVLNCQAT QIVPHQGYL HPPIVGYTVQ 540
 HDSVFMTAVP PFMDGLQPGY RQIQSPFPHT NSEQKMYPAV TV

A110 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]

Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

5

```

1      11      21      31      41      51
|      |      |      |      |      |
10 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTCTGAGAG AGTCTCTAGA AGACATGATG 60
   CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTCACAG TTTCTTCCAA CCTTGCCATT 120
   GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
   ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTATGTCTC AAAAAAGTAA GAAGCCATTA 240
   ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGCCC 300
   CAAATGAAG  AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
   GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
   GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
   TATGAGCCTC GGGATTATAC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
   CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTCAT 600
   GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
   TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
   TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

```

25 A111 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 30 Transmembrane domains: none found
 Cellular Localization: secreted

```

35 1      11      21      31      41      51
   |      |      |      |      |      |
   MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
   PLMVIHLED  CQYSQALKKV FAQNEEQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM 120
   FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

```

40 A112 DNA SEQUENCE
 Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 45 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

```

50 1      11      21      31      41      51
   |      |      |      |      |      |
   ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
   AAACCCCGTA TCCCACATGA GACCTTCAGA AAGGTGGGGA TCCCACATCAT CATAGCACTA 120
   CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC 180
   TACTTCTCT  GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
   CTGGAAGTGC CTTGGGGGGA GGAACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
   55 GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
   GGGAACTGGT TCTCTGCTTG TTTCGACAA TCCACAGAAG CTCTCGCTGA GACAGCCTGT 420
   AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
   GATCTGGATG TGTTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGATGCG GAACTCAAGT 540
   GGGCCCTGTC TCTCAGGCTC CTGCTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG 600
   60 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
   AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCCTGGGTC 720
   CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
   GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
   65 TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCCTC 900
   ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
   GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
   GACATACTGC TGACGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
   GCGTACCAGG GGGAAAGTCAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
   70 GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
   GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
   AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

```

75 A113 Protein sequence:
 Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 80 Transmembrane domains: 31-53
 LDLA domain: 54-94
 Tryp_SpC domain: 204-429
 Cellular Localization: plasma membrane/ER

1	11	21	31	41	51	
MLQDPDSDQP	LNSLDVKPLR	KPRIPMETFR	KVGIPIIIAL	LSLASIIIVV	VLIKVILDKY	60
YFLCGQLPHF	IPRKQLCDGE	LDCPLGEDEE	HCVKSFPEGP	AVAVRLSKDR	STLQVLDSAT	120
GNWFSACFDN	FTEALAEFAC	RQMGYSKPT	FRAVEIGPDQ	DLDVVEITEN	SQELRMRNSS	180
GPCLSGSLVS	LHCLACGKSL	KTPRVVGEE	ASVDSWPQV	SIQYDKQHVC	GGSLDPHVV	240
LTAACHFRKH	TDVFNWKVRA	GSDKLGSFPS	LAVAKIIIE	FNPMPKDND	IALMKLQFPL	300
TFSGTVRPIC	LPFFDEELTP	ATPLWIIGWG	FTKQNGGKMS	DILLQASVQV	IDSTRCNADD	360
AYQGEVTEKM	MCAGIPEGGV	DTCQGDGSGP	LMYQSDQWHV	VGIWSWGYGC	GGPSTPGVYT	420
KVSAYLNWIY	NVWKAEL					

A114 DNA SEQUENCE:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACTC	TTGTTGGCCA	GGCTGGAGTG	60
CAATGGCACA	ATCTCAGCTT	ACTGCAACCT	CCGCCTCCCG	GGTTCAAGCG	ATTCTCCTGC	120
CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACCTAATTT	180
CTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCTG	240
ACCTCAGGTG	ATCCACTTGC	CTTGGCCTCC	CAAAGTGCTA	GGATTACAGC	CGTGAAACTG	300
TGCTTGGCTG	ATTCTTTTTT	TGTTGTTGGA	TTTTTGAAAC	AGGGTCTCCC	TTGGTCGCCC	360
AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACATAAACC	TCCACCTCCT	GGTTTCAAGT	420
GATCCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	CGCTGCACCA	CCACACCCGG	480
CTAATTTTTT	TATTTTTTAT	AGAGACAGGG	TTTCAACATG	TTGGCCAGGC	TGTTCTCAAA	540
CTCCTGGACT	CAAGGGATCC	GCCTGCCTCC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
AGTCACCATG	CCTGACCTTA	TAATTTCTAA	GTCAATTTTT	CTGGTCCATT	TCTTCCCTAG	660
GGTCTCCACA	ACAAATCTGC	ATTAGGCGGT	ACAATAATCC	TAACTTTCAT	GATTACAAAA	720
AGGAAGATGA	AGTGATTCCAT	GATTTAGAAA	GGGGAAGTAG	TAAGCCCACT	GCACACTCCT	780
GGATGATGAT	CCTAAATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
TTTGGTTTAA	ATTAATTATC	TAAATATCTA	AAAACATTTT	TGGATACATT	GTTGATGTGA	900
ATGTAAGACT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCCTCAG	960
TGCAGTTTTT	TGTAGAAATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGATT	1020
CCATAATGAA	CAAAGTGAGA	GACATTAAAA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
AACTAAGCTT	GAATAAAATT	TCTGCTGATA	CTACAGATAA	CTCGGGAAGT	GTTAAACCAA	1140
TTATGATGAT	GGCAAAACAAC	CCAGAGGACT	GGTTGAGTTT	GTTGCTCAAA	CTAGAGAAAA	1200
ACAGTGTTC	GCTAAGTGAT	GCTCTTTTAA	ATAAATTGAT	TGGTCGTTC	AGTCAAGCAA	1260
TTGAAGCGCT	TCCCCAGAT	AAATATGGCC	AAAATGAGAG	TTTTGCTAGA	ATTCAAGTGA	1320
GATTTGCTGA	ATTAAGAGCT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAATGG	1380
CCAGAGCAAA	CTGCAAGAAA	TTTGCTTTTG	TTTATATATC	TTTTGCACAA	TTTGAAGTGT	1440
CACAGGTAA	TGTCAAAAAA	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CGTGGAGAG	1500
TACCACTAGA	AATGCTGGAA	ATTGCCCTGC	GGAATTTTAA	CCTCCAAAAA	AAGCAGCTGC	1560
TTTCAGAGAA	GGAAAAGAAG	AATTTATCAG	CATCTACGGT	ATTAAGTACC	CAAGAATCAT	1620
TTTCCGGTTT	ACTTGGGGCAT	TTACAGAATA	GGAAACAACAG	TTGTGATTCC	AGAGGACAGA	1680
CTACTAAAGC	CAGTTTTTTT	TATGGAGAGA	ACATGCCACC	ACAAGATGCA	GAAATAGGTT	1740
ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAAACAGTC	ATGCCCAATT	GGAAGAGTCC	1800
CAGTTAAGCT	TCTAATATAGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTTGTACCTT	1860
GTTTATGAA	AAGACAAACC	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
AACCAAGTGG	AAATGATTCC	TGTGAATTAA	GAAATTTTAA	GTCTGTTCAA	AATAGTCATT	1980
TCAAGGAACC	TCTGGTGTC	GATGAAAAGA	GTTCTGAAGT	TATTATTACT	GATTCAATAA	2040
CCCTGAAGAA	TAAACCGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
AAGAACCAGA	GGTTCCAGAG	AGTAACCAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
GTATTAAACA	GAATCCTGCT	GCATCTTCAA	ATCACTGGCA	GATTCCGGAG	TTAGCCCGAA	2220
AAGTTAATAC	AGAGCAGAAA	CATACCACCT	TTGAGCAACC	TGCTTTTCAA	GTTTCAAAAC	2280
AGTCAACACC	AATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTGTT	AAGACACCAA	2340
GCAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTGTAGAA	TCCAGTTGTA	AAGAATGACT	2400
TTCCACCTGC	TTGTCAAGTT	TCAACACCTT	ATGGCCAACC	TGCTGTGTTT	CAGCAGCAAC	2460
AGCATCAAT	ACTTGCCACT	CCACTTCAAA	ATTTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
ATGAATGCAT	TTCCGTTTAA	GGAAGAATTT	ATTCCATATT	AAAGCAGATA	GGAAGTGGAG	2580
GTTCAAGCAA	GGTATTTTCA	GTGTTAAATG	AAAAGAAACA	GATATATGCT	ATAAAATATG	2640
TGAACCTTAGA	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	CCGGAACGAA	ATAGCTTATT	2700
TGAATAAACT	ACAACAACAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAAATCACGG	2760
ACCAGTACAT	CTACATGATA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAAA	2820
AGAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAAAAATATG	TTAGAGGCGA	2880
TTCAACAAT	CCATCAACAT	GGCATTTGTC	ACAGTGATCT	TAAACCAAGT	AACCTTCTGA	2940
TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATTGC	AAACCAATG	CAACCAAGATA	3000
CAACAAGTGT	TGTTAAAGAT	TCTCAGGTTG	GCACAGTTAA	TTATATGCCA	CCAGAAGCAA	3060
TCAAAGATAT	GTCTTCTCTC	AGAGAGAATG	GGAAATCTAA	GTCAAAGATA	AGCCCCAAAA	3120
GTGATGTTTG	GTCTTATAGG	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCAATTG	3180
AGCAGATAAT	TAATCAGATT	TCTAAATTAC	ATGCCATAAT	TGATCTTAAT	CATGAAATGG	3240
AATTTCCCGA	TATCCAGAG	AAAGATCTTC	AAGATGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
ATCCAAAAA	GAGGATATCC	ATTCCTGAGC	TCCTGGCTCA	TCCATATGTT	CAAAATTCAAA	3360
CTCATCCAGT	TAACCAAAATG	GCCAAAGGAA	CCACTGAAGA	AATGAAATAT	GTTCTGGGCC	3420
AACCTTGTGG	TCTGAATTC	CCTAACTCCA	TTTTGAAAGC	TGCTAAAACT	TTATATGAAC	3480
ACTATAGTGG	TGGTGAAGT	CATAATTCTT	CATCCTCCAA	GACTTTTGAA	AAAAAAGGG	3540
GAAAAAATG	ATTTCAGATT	ATTCGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGACT	3600
GTTTACTACT	TGAATCCCTG	TGGAATCTTA	CATTGAAGA	CAACATCACT	CTGAAGTGT	3660
ATCAGCAAAA	AAATTCAGT	GAGATTATCT	TTAAAGAAA	ACTGTAAAAA	TAGCAACAC	3720

TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC 3780
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAAGTTTG 3840
 TAAATAAAGT TTTGTGGCTA AAATGA

A115 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

1	11	21	31	41	51	
MNKVRDIKKN	FKNEDLTDEL	SLNKISADTT	DNSGTVNQIM	MMANNPEDWL	LLLLKLEKNS	60
VPLSDALINK	LIGRYSQAIE	ALPPDKYGQN	ESFARIQVRF	AELKAIQEPD	DARDYFQMAR	120
ANCKKFAFVH	ISFAQFELSQ	GNVKKSKQLL	QKAVERGAVP	LEMLEIALRN	LNQKKQLLS	180
EEKKNLAS	TVLTAQESFS	GSLGHLQNRN	NSCDSRGQTT	KARFLYGENM	PPQDAEIGYR	240
NSLRQTNKTK	QSCPFGRVPV	NLLNSPDCDV	KTDDSVVPCF	MKRQTSRSEC	RDLVVPKSKP	300
SGNDSCELRN	LKSVQNSHFK	EPLVSDEKSS	ELIITDSITL	KNKTESSLLA	KLEETKEYQE	360
PEVPESNQKQ	WQAKRKSECI	NQNPAASSNH	WQIPELARKV	NTEQKHTTFF	QPVFVSVKQS	420
PIISTSKWFD	PKSICKTPSS	NTLDDYMSCF	RTPVVKNDFF	PACQLSTPYG	QPACFQQQOH	480
QILATPLQNL	QVLASSSANE	CISVKGRIYS	ILKQIGSGGS	SKVFQVLNEK	KQIYAIFYVN	540
LEEADNQTLN	SYRNEIAYLN	KLQHSKDKII	RLYDYEITDQ	YIYVMVECGN	IDLNSWLKKK	600
KSIDPWKRS	YWKMLAEAVH	TIHQHGVHS	DLKPANFLIV	DGMLKLIDFG	IANQMOPDIT	660
SVVKDSQVGT	VNYMPEAIK	DMSSSRENGK	SKSKISPKSD	VWSLGCILYY	MTYKGTFFQQ	720
IINQISKLHA	IIDPNHEIEF	PDIEPKDLQD	VLKCKLKRDP	KQRISIPELL	AHPVYVQIQT	780
PVNQMAKGT	BEMKYVLGQL	VGLNSPNSIL	KAAKTLYEHY	SGGESHNSSS	SKTFEKKRGK	840
K						

OVARIANA116 DNA SEQUENCE

Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Nucleic Acid Accession #: NM_001508
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
ATGGCTTCAC	CCAGCCTCCC	GGGCAGTGAC	TGCTCCCAA	TCATTGATCA	CAGTCATGTC	60
CCCGAGTTTG	AGGTGGCCAC	CTGGATCAAA	ATCACCTTA	TTCTGGTGTA	CCTGATCATC	120
TTCTGTATGG	GCCTTCTGGG	GAACAGCGCC	ACCATTGCGG	TCACCCAGGT	GCTGCAGAAG	180
AAAGGATACT	TGCAGAAGGA	GGTGACAGAC	CACATGGTGA	GTTTGGCTTG	CTCGGACATC	240
TTGGTGTTCC	TCATCGGCAT	GCCCATGGAG	TTCTACAGCA	TCATCTGGAA	TCCCCTGACC	300
ACGTCCAGCT	ACACCTTGTC	CTGCAAGCTG	CACACTTTCC	TCTTCGAGGC	CTGCAGCTAC	360
GCTACGCTGC	TGCACGTGCT	GACACTCAGC	TTTGAGCGCT	ACATCGCCAT	CTGTCACCCC	420
TTCAGGTACA	AGGCTGTGTC	GGGACCTTGC	CAGGTGAAGC	TGCTGATTGG	CTTCGTCTGG	480
GTCACTCCCG	CCCTGTGGGC	ACTGCCCTTG	CTGTTTGCCA	TGGGTACTGA	GTACCCCTCG	540
GTGAACGTGC	CCAGCCACCG	GGGTCTCACT	TGCAACCGCT	CCAGCACCCG	CCACCACGAG	600
CAGCCCGAGA	CCTCCAATAT	GTCCATCTGT	ACCAACCTCT	CCAGCCGCTG	GACCGTGTTT	660
CAGTCCAGCA	TCTTCGGCGC	CTTCGTGGTC	TACCTCGTGG	TCCTGCTCTC	CGTAGCCTTC	720
ATGTGCTGGA	ACATGATGCA	GGTGCTCATG	AAAAGCCAGA	AGGGCTCGCT	GGCCGGGGGG	780
ACGCGGCCTC	CGCAGCTGAG	GAAGTCCGAG	AGCGAAGAGA	GCAGGACCGC	CAGGAGGCAG	840
ACCATCATCT	TCCTGAGGCT	GATTGTTGTG	ACATTGGCCG	TATGCTGGAT	GCCCAACCAG	900
ATTGCGAGGA	TCATGGCTGC	GGCCAAACCC	AAGCACGACT	GGACGAGGTC	CTACTTCCGG	960
GCGTACATGA	TCCTCCTCCC	CTTCTCGGAG	ACGTTTTTCT	ACCTCAGCTC	GGTCATCAAC	1020
CCGCTCCTGT	ACACGGTGTC	CTCGCAGCAG	TTTCGGCGGG	TGTTCTGTGA	GGTGTGTGTC	1080
TGCCGCTGTG	CGCTGCAGCA	CGCCAACCAC	GAGAAGCGCC	TGCGCGTACA	TGCGCACTCC	1140
ACCACCGACA	GCGCCCGCTT	TGTGCAGCGC	CCGTGTCTCT	TCGCGTCCCG	GCGCCAGTCC	1200
TCTGCAAGGA	GAAGTGAAGG	GATTTTCTTA	AGCACTTTTC	AGAGCGAGGC	CGAGCCCCAG	1260
TCTAAGTCCC	AGTCATTGAG	TCTCGAGTCA	CTAGAGCCCA	ACTCAGGCGC	GAAACACGCC	1320
AATTCTGCTG	CAGAGAAATG	TTTTTCAGGAG	CATGAAGTTT	<u>GA</u>		

A117 Protein sequence:

Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Protein Accession #: NM_001508, NP_001409
 Signal sequence: none found
 Pfam domains: 7tm_1 [72-172, 224-344]
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MASPSLPGSD	CSQIIDHSHV	PEFEVATWIK	ITLILVYLII	FVMGLLGNSA	TIRVTQVLQK	60

KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120
 ATLLHVLTLF FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL 180
 VNVPSHRGLT CNRSSTRHHE QPETSNSMIC TNLSSRWTFV QSSIFGAFVY YLVVLLSVAF 240
 MCWNMQVLM KSQKGSLLAGG TRPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCWMPNQ 300
 IRRIMAAAKP KHDWTRSYFR AYMLLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC 360
 CRLSLQHANH EKRLRVHAHS TTDGARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPE 420
 SKSQSLSLSE LEPNSGAKPA NSAAENGFEQ HEV

A118 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.87223
 Probeset Accession #: AA250737
 Nucleic Acid Accession #: NM_001203
 Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGCG AGTGC GGAGA CCGCGGCGCT 60
 GAGGACGCGG GAGCCGGGAG CGCAGCGCGG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120
 GTGAAAGGAA AGGAAGATCA TTTTCATGCCT TGTGTGATAA GGTTCAGACT TCTGCTGATT 180
 CATAACCAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
 TGCCATAAGT GAGAGCAAAA CTTCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC 360
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480
 GGTTCGCTAG GACTAGAAGG CTGAGATTTT CAGTGTGCGG ACACCTCCAT TCCTCATCAA 540
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCCTACA 600
 CTGCTCCCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660
 ATATCTGTGA CTGCTCTGTAG TTTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCCGG 720
 TATAAAGAGC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC 780
 ATTCCTCCTG GAGATCCCTT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
 TCAGGCTCC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTGAGAT GGTGAAACAG 900
 ATTGAAAAAG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GGCCTGGCGA AAAGGTAGCT 960
 GTGAAAGTGT TCCTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
 ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080
 GGGTCCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
 TATCTGAAGT CCACCACCTT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTCTGTC 1200
 AGTGGCTTAT GTCATTTTAA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260
 CATCGAGATC TGAAAGTAA AAACATTCTG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320
 GACCTGGGCC TGGCTGTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
 ACTCGAGTTG GCACCAACAG CTATATGCCT CCAGAAAGTGT TGGACGAGAG CTTGAACAGA 1440
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCTCAT CTCTTGGGAG 1500
 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560
 CTAGTGCCCA GTGACCCCTT TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAAGTTA 1620
 CGCCCTCAT TCCCAAAACG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAAACCT 1680
 ATGACAGAAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740
 ACACCTGCCA AAATGTCAGA GTCCAGGAC ATTAACTCT GATAGGAGAG GAAAGTAAG 1800
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA 1860
 TAAGCATCCA CAGTACAAGC CTGGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAG 1920
 CTTTCAAGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTGTA GCGGAGAAA CCGTGGGTA ACTTGTTCAT GATATGATGC AT

A119 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.72472 / Hs.87223
 Probeset Accession #: AA250737 / U89326
 Protein Accession #: NP_001194
 Signal sequence: 1-13
 Transmembrane domains: 128-144
 PFAM domains: activin_receptor [30-111], protein kinase [204-491]
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED 60
 DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120
 GPIHHRALL SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180
 EQSQSSSGSGS GLPLLVRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTTTEAS 240
 WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
 MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNLLV KNGTCCCIAD LGGLAVKFISD 360
 TNEVDIPPNP RVGTRKRYMP EVLDESLNRN HFQSYIMADM YSFGILILWEV ARRCVSGGIV 420
 EBYQLPYHDL VSPDSPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGLKM TECWAHNPAS 480
 RLTLRLVKKT LAKMSESQDI KL

A120 DNA SEQUENCE

Gene name: L1V-1 protein, estrogen regulated
 Unigene number: Hs.79136
 Probeset Accession #: U41060
 Nucleic Acid Accession #: NM_012319.2
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60

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|CTCGTGGCGA|ATTCGGGCACG|AGACCGCGTG|TTCGCGCCTG|GTAGAGATTT|CTCGAAGACA|60
CCAGTGGGGCC|CGTGTGGGAAC|CAAACCTGCG|CGCGTGGCCG|GGCCGTGGGA|CAACGAGGCC|120
GCGGAGACGA|AGCGGCAATG|GCGAGGAAGT|TATCTGTAAT|CTTGATCCTG|ACCTTTGCCC|180
TCTCTGTAC|AAATCCCCTT|CATGAACATA|AAGCAGCTGC|TTTCCCCAG|ACCAGTGAGA|240
AAATTAGTCC|GAATTGGGAA|TCTGGCATT|ATGTTGACTT|GGCAATTTCC|ACACGGCAAT|300
ATCATCTACA|ACAGCTTTTC|TACCGCTATG|GAGAAAATAA|TTCTTTGTCA|GTGTAAGGGT|360
TCAGAAAAAT|ACTTCAAAT|ATAGGCATAG|ATAAGATTAA|AAGAATCCAT|ATACACCATG|420
ACCACGACCA|TCACTCAGAC|CACGAGCATC|ACTCAGACCA|TGAGCGTCAC|TCAGACCATG|480
AGCATCACTC|AGACCACGAG|CATCACTCTG|ACCATGATCA|TCACTCTCAC|CATAATCATG|540
CTGCTTCTGG|TAAAAATAAG|CGAAAAGCTC|TTTCCCCAGA|CCATGACTCA|GATAGTTCAG|600
GTAAGATGCC|TAGAAACAGC|CAGGGGAAAG|GAGCTCACCG|ACCAGAACAT|GCCAGTGGTA|660
GAAGGAATGT|CAAGGACAGT|GTTAGTGCTA|GTGAAGTGAC|CTCAACTGTG|TACAACACTG|720
TCTCTGAAGG|AAGTCACTTT|CTAGAGACAA|TAGAGACTCC|AAGACCTGGA|AAACTCTTCC|780
CCAAAGATGT|AAGCAGCTCC|ACTCCACCCA|GTGTCACTAT|AAAGAGCCGG|GTGAGCCGGC|840
TGGCTGGTAG|GAAAACAAAT|GAATCTGTGA|GTGAGCCCCG|AAAGGCTTTT|ATGTATTCCA|900
GAAACACAAA|TGAATCCTT|CAGGAGTGTT|TCAATGCATC|AAGCTACTG|ACATCTCATG|960
GCATGGGCAT|CCAGGTTCCG|CTGAATGCAA|CAGAGTTCAA|CTATCTCTGT|CCAGCCATCA|1020
TCAACCAAAT|GTATGCTAGA|TCTGTCTGA|TTCATACAAG|TGAAAAGAAG|GCTGAAATCC|1080
CTCCAAAGAC|CTATTCATTA|CAATAGCCTT|GGGTGGTGG|TTTTATAGCC|ATTTCCATCA|1140
TCAGTTTCTT|GTCTCTGCTG|GGGTTATCT|TAGTGCCTCT|CATGAATCGG|GTGTTTTTCA|1200
AATTTCTCCT|GAGTTTCTTT|GTGGCACTGG|CCGTTGGGAC|TTTGAGTGGT|GATGCTTTTT|1260
TACACCTTCT|TCCACATTT|CATGCAAGTC|ACCACCATAG|TCATAGCCAT|GAAGAACCAG|1320
CAATGGAAAT|GAAAGAGGGA|CCACTTTTCA|GTCATCTGTC|TTCTCAAAAC|ATAGAAGAAA|1380
GTGCTATTTT|TGATTCACG|TGAAGGGTC|TAACAGCTCT|AGGAGGCTG|TATTTTCATG|1440
TTCTTGTGA|ACATGCTCTC|ACATTGATCA|AACAATTTAA|AGATAAGAAG|AAAAAGAATC|1500
AGAAGAAACC|TGAAATGAT|GATGATGTGG|AGATTAAAGAA|GCAGTTGTCC|AAGTATGAAT|1560
CTCAACTTTC|AACAATGAG|GAGAAAGTAG|ATACAGATGA|TCGAAGCTGAA|GGCTATTATC|1620
GAGCAGACTC|ACAAGAGGCC|TCCCACTTTG|ATTCTCAGCA|GCCTGCAGTC|TTGGAAGAAG|1680
AAGAGGTCAT|GATAGCTCAT|GCTCATCCAC|AGGAAGTCTA|CAATGAATAT|GTACCCAGAG|1740
GGTGCAAGAA|TAAATGCCAT|TCACATTTCC|ACGATACACT|CGGCCAGTCA|GACGATCTCA|1800
TTCACCCAAA|TCATGACTAC|CATCATATTC|TCCATCATCA|CCACCACCAA|AACCACCATC|1860
CTCAGAGTCA|CAGCCAGGCG|TACTCTCGGG|AGGAGCTGAA|AGATGCCGGC|GTCGCCACTT|1920
TGGCCTGGAT|GGTGATAATG|GGTGATGGCC|TGCACAATTT|CAGCGATGGC|CTAGCAATTG|1980
GTGCTGCTTT|TACTGAAGGC|TTATCAAGTG|GTTTAAAGTAC|TTCTGTTGCT|GTGTTCTGTC|2040
ATGAGTTGCC|TCATGAATAA|GGTGACTTTG|CTGTTCTACT|AAAGGCTGGC|ATGACCGTTA|2100
AGCAGGCTGT|CCTTATAAT|GCATTGTCTG|CCATGCTGGC|GTATCTTGGG|ATGGCAACAG|2160
GAATTTTCAT|TGCTCATTAT|GCTGAAAATG|TTTCTATGTG|GATATTTGCA|CTTACTGCTG|2220
GCTTATTCAT|GTATGTTGCT|CTGGTTGATA|TGGTACCTGA|AATGCTGCAC|AATGATGCTA|2280
GTGACCATGG|ATGTAGCCGC|TGGGGGTATT|TCTTTTACA|GAATGCTGGG|ATGCTTTTGG|2340
GTTTTGGAAT|TATGTTACTT|ATTTCCATAT|TTGAACATAA|AATCGTGTTC|CGTATAAAT|2400
TCTAGTTAAG|GTTTAAATGC|TAGAGTAGCT|TAAAAGTTG|TCATAGTTTC|AGTAGGTCAT|2460
AGGGAGATGA|GTTTGTATGC|TGTAATATGC|AGCGTTTAAA|GTTAGTGGGT|TTTGTGATTT|2520
TTGTATTGAA|TATTGCTGTC|TGTTACAAAG|TCAGTTAAAG|GTACGTTTAA|ATATTAAAGT|2580
TATTCTATCT|TGGAGATAAA|ATCTGTATGT|GCAATTCACC|GGTATTACCA|GTTTATTATG|2640
TAAACAGAG|ATTTGGCATG|ACATGTTCTG|TATGTTTCAG|GGAAAAATGT|CTTTAATGCT|2700
TTTTCAAGAA|CTAACACAGT|TATTCCTATA|CTGGATTTTA|GGTCTCTGAA|GAAGTCTGG|2760
TGTTTAGGAA|TAAGATGTG|CATGAAGCCT|AAAATACCAA|GAAAGCTTAT|ACTGAATTTA|2820
AGCAAGAGAA|TAAAGGAGAA|AAGAGAAGAA|TCTGAGAATT|GGGAGGCGAT|AGATTCTTAT|2880
TAAATCACA|AAATTTGTTG|TAAATTAGAG|GGGAGAAATT|TAAATTAAG|TATAAAAAGG|2940
CAGAATTAGT|ATAGAGTACA|TTCATTAAAC|ATTTTGTGCA|GGATTATTTT|CCGTAATAAC|3000
GTAGTGAGCA|CTCTCATATA|CTAATTAGTG|TACATTAAAC|TTTGATATAA|ACAGAAATCT|3060
AATATATTTT|AATGAATTCA|AGCAATATAC|ACTTGACCAA|GAAATTTGAA|TTTCAAAATG|3120
TTCGTGCGGG|TTATATACCA|GATGAGTACA|GTGAGTAGTT|TATGATACAC|CAGACTGGGT|3180
TATTGCAAG|TTATATATCA|CCAAAAGCTG|TATGACTGGA|TGTTCTGGTT|ACCTGGTTTA|3240
CAAAATTATC|AGAGTAGTAA|AAGTTTGATA|TATATGAGGA|TATTAATACT|ACACTAAGTA|3300
TCATTTGATT|CGATTAGAA|AGTACTTTGA|TATCTCTCAG|TGCTTCAGTG|CTATCATTGT|3360
GAGCAATTGT|CTTTATATAC|GGTACTGTAG|CCATACTAGG|CCTGTCTGTG|GCATTCTCTA|3420
GATGTTTCTT|TTTTACACAA|TAAATTCCTT|ATATCAGCTT|G
  
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A121 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
 Unigene number: Hs.79136
 Protein Accession #: NP_036451
 Signal sequence: 1-21
 Pfam domain: Zip[591-743]
 Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745
 Cellular Localization: plasma membrane

70
 75
 80

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|1|11|21|31|41|51|
|MARKLSVILI|LTFALSVTNP|LHELKAAAFP|QTTEKISPWN|ESGINVDLAI|STRQYHLQQL|60
FYRYGENNSL|SVEGFRKLLQ|NIGIDKIKRI|HIHHDHHDHS|DHEHSDHER|HSDHEHSDH|120
EHHSDDHDS|HNHNAAGSKN|KRKALCPDHD|SDSSGKDPNR|SQKGARHPE|HAGRRNVKD|180
SVSASEVTST|VYNTVSEGTH|FLETIETPRP|GKLFPPKDVSS|STPPSVTSKS|RVSRLAGRKT|240
NESVSEPRKQ|FMYSRNTNEN|PQECFNASKL|LTSHGMIQV|PLNATEFNYL|CPAIIINQIDA|300
RSLCIHTSEK|KAETPPKTYT|LQIAWVGFI|AISIISFLSL|LGVLVPLMN|RVFFKFLLSF|360
LVALVGTLS|GDAFLHLLPH|SHASHHHSHS|HEEPAMEMKR|GPLFSLHSSQ|NIEESAYFDS|420
TWKGLTALGG|LYFMFLVEHV|LTLIKQFKDK|KKKNQKKPEN|DDVFEIKKQL|SKYESQLSTN|480
EEKVDTDDRT|EGYLIRADSQE|PSHFDSQQPA|VLEEEVEMIA|HAHPQEVYNE|YVPRGCKNKC|540
HSHFHDITLGQ|SDDLIIHHHDH|YHHILHHHHH|QNHHPHSHSQ|RYSREELKDA|GVATLAWMVI|600
MGDLGHNFSQ|GLATGAAPTE|GLSSGLSTSV|AVFCHLPHE|LGDFAVLLKA|GMTVKQAVLY|660
NALSAMLAYL|GMATGIFIGH|YAENVSMWIF|ALTAGLFMYV|ALVDMVPEML|HNDASDHGCS|720
  
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RWGYFFLQNA GMLLGFGIML LISIFEHKIV FRINF

A122 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
CCGCAGAGGA GCCTCGGCCA GGCTAGCCAG GCGCGCCCCA GCCCTCCCCC AGGCCGCGAG 60
CGCCCCCTGCC GCGGTGCCTG GCCTCCCCTC CCAGACTGCA GGGACAGCAC CCGGTAACATG 120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
GGGTCCGSCC GCGCGCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCGAGA 240
ATGCTCTGCG CTTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
GGGAACGCGG CCAGTGCAGG GCATCACGGG TTGTAGCAT CGGCACGTCA GCCTGGGGTC 360
TGTCACATATG GAACTAAACT GGCTGTGTC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
TGTAAGACTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
AGATGCTTTC CAGGATACAC CGGAAAACCC TGCACTCAAG ATGTGAATGA GTGTGGAATG 540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
TCAGGACTCC GCCTGGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT 780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840
AAATGTCAACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
GGGTCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCTCT AGAGCACCCTG GTACCATCAA AGACAGAATC 1080
AAGAAAGTTG TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAATTAA AAATGTTACC 1140
CCAGAACCCA CAGGACTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA 1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
AGCCTCGCAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAAT CCGCCTGATT 1380
CTGGTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT 1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
TGGAATCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCCTGGCA 1560
GGTCAACAAG AAGACATTGG CCGATTGAAA CTTCTCCTAC CTGACCTGCA ACCCCAAAGC 1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCGGAGACA AAGTCGGGAA ACTTCGAGTG 1680
TTTGTGAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
TGGAAGACAG GGAATAATCA GTTGATCAA GGAACCTGAT CTACCCAAAG CATCATTTT 1800
GAAGCAGAAC GTGGCAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTGCTGTGTT 1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTGT ATGTCAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
TCTTGATATA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCCCTCCT 2160
CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220
TAGAAAAAAA AGCACAGAGA AATGTTTAACT TGTTTGACTC TTATGATACT TCTTGGAAC 2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340
TGATATATTA AATCTTTGT AATAATAATA TCCAAATCAT CAAAAAATA AAAAAAAA

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A123 Protein sequence:

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Protein Accession #: NP_056322.2
 Signal sequence: 1-21
 Transmembrane domains: none found
 MAM domain: 402-546
 EGF domain: 80-259
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRSKGV 60
CEATCEPGCK FGECVGPNNK RCFPGYTGKT CSQDVNECGM KPRPCQHRV NTHGSYKFC 120
LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPS SGLRLAPNGR DCLDIDECAS 180
GKVICPYNRR CVNTFGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNQ 240
GSPFKCKQKG YKNGNLRCSA IPENSVEVL RAPGTIKDRI KKLAKHNSM KKKAKIKNVT 300
PEPTRTPPK VNLQPFNYEE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER 360
SLRGDVFPPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHIGD WKQDREDDFD 420
WNPADRDNAI GFYMAVPALA GHKIDIGRLK LLLPDLQFQS NFCLLFYDRL AGDKVKGLRV 480
FVKNNSNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERKGKGTG EIAVDGVLLV 540
SGLCPDLSLS VDD

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A124 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Nucleic Acid Accession #: NM_001719

Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

```

5      1      11      21      31      41      51
|      |      |      |      |      |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCCGGTGC GGCCTGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCTGGGCG CTCTGGGCAC 180
CCCTGTTCTT GCTGCGCTCC GGCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
10 GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTGCCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
GCCAGGGCTT CTCCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
GCCTGCAAGA TAGCCATTTC CTCACGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
15 TTGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCGGGATC TACAAGGACT 660
ACATCCGGGA AGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCCT TGGGCTCGG 780
20 AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC 840
GGCACAACCT GGGCCTGACG CTCTCGGTGG AGACGTGGA TGGGAGAGC ATCAACCCCA 900
AGTTGGCGGG CTGATTGGG CGGCACGGGC CCCAGAACA CGAGCCCTTC ATGGTGGCTT 960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA 1020
GCCAGAACCG CTCGAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
AGAACAGCAG CAGCGACCG AGGCAGGCCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
25 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCGGCC TACTACTGTG 1200
AGGGGGAGTG TGCCTTCCCT CTGAACCTCT ACATGAACGC CACCAACCAC GCCATCGTGC 1260
AGACGCTGGT CCACTTCATC AACCCGGAAC CGGTGCCCAA GCCCTGCTGT GCGCCACGC 1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
30 TTGGGGCCAA GTTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCCCTTTG TGAGACCTTC CCCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
TCCTACAAGC TGTCACGGCA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
GCCGGGCCAG GTCATTGGCT GGGAAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
35 TTATGAGCGC CTACCAGCCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
GGGCACATTG GTGCTGTGTC GAAAGGAAAA TTGACCGGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAACCG AATGAATG

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40 A125 Protein sequence:
Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
Unigene number: Hs.170195
Probeset Accession #: BE616633
Protein Accession #: NP_001710.1
Signal sequence: 1-30
Pfam domains: TGFb_propeptide [37-281]
Transmembrane domains: none found
Cellular Localization: secreted

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50      1      11      21      31      41      51
|      |      |      |      |      |
MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRRLRSQE RREMQREILS 60
ILGLPHRRRP HLQKHNAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
55 LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRYKYD 180
IRERFDNETF RISVYQLQE HLGRESLFL LDRSLWASE EGWLVDITA TSNHWVNP 240
HNLGLQLSVE TLDQSLNPK LAGLGRHGP QNKQPFMVA FKADEVHFRS IRSTGSKQRS 300
QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAYCE 360
GECAFLNSY MNAIHAIVQ TLVHFIPET VPKPCCAPTQ LNAISVLYFD DSSNVILKXY 420
60 RNMVVRACGC H

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A126 DNA SEQUENCE
Gene name: integrin, beta 8
Unigene number: Hs.52620
Probeset Accession #: AA479726
Nucleic Acid Accession #: NM_002214
Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

```

70      1      11      21      31      41      51
|      |      |      |      |      |
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TCCCTTCGAC CTCGCGGGCG TACCCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
75 TAGGGTGGTT TCCCCCCCAG CTTGGGGCTT TGTGGGGT TGATTGTGTT TGGCTCTTCG 300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCCTTTCTT 360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT 420
TGGCCGTCGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCGGTGCG GAGCCGGGAG 480
GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGGCC GCTTACCTGC ACCGCTTGCT 540
80 CCGAGCCCGG GGGTCCGCTT GCTAGGCTTG CGGAAAACGT CTAAGCGACA CTCGCCCGCG 600
GGCCCGGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGCGCG 660
GGGGCGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTGTACG GCTGCATTTC 720
TCTGCCTGCA AAACGACCGG CGAGGTCCCG CCTCGTTCCT CTGGGACGCC TGGGTGTTTT 780

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5 CACTTGTCTT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840
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 TTTCAGGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTTAATA AGCAAAGGCT 960
 GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAAAAGAAA 1020
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080
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 50 TTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720
 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAGCT 3780
 GAATGTTAA

A127 Protein sequence:

55 Gene name: Integrin, beta 8
 Unigene number: Hs.52620
 Probeset Accession #: AA479726
 Protein Accession #: NP_002205.1
 60 Signal sequence: 1-39
 Transmembrane domains: 682-704
 EGF domain: 552-584
 INB domain: 54-469
 Cellular Localization: plasma membrane

65
 70 1 MCGSALAFFT 11 AAFVCLQNDR 21 RGPASFLWAA 31 WVFSLVLGLG 41 QGEDNRCASS 51 NAASCARCLA 60
 LGPECGWCVQ EDFISGGSRG ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120
 GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSRKMAFF 180
 SRDFRLGFGS YVDKTVSPYI SIHPIRIHNQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA 240
 VHRQKISGNI DTPEGGFDM LQAAVCESHI GWRKEAKRLI LVMTDQTSHL ALDSKLAGIV 300
 75 VPDNGNCHLK NNIVYKSTTM EHPSLGQLSE KLIDNNINVI FAVQKQFHW YKDLLPLLP 360
 TIAGEIESKA ANLNINLVVEA YOKLISEVKV QVENQVQGIY FNITAIKCPDG SRKPGMEGCR 420
 NVTSDNEVLF NVTVTMKKCD VTGKKNYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK 480
 CVDETFLDSK CFQCDENKCH FDEDQFSSES CKSHKDQPV C SGRGVCVCGK CSCHKIKLKG 540
 VYGKYCEKDD FSCPYHHGNL CAGHGECEAG RCQCFSGWEG DRCQCPASAA QHCVNKSGQV 600
 80 CSGRGTCVCG RCECTDPSI GRFCEHCPTC YTACKENWNC MQCLHPHNLS QAILDQCKTS 660
 CALMEQQHYV DQTECFSSP SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNSNKIKSSS 720
 DYRVASASKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF

A128 DNA SEQUENCE

Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942
 Probeset Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5

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    GTTTTACTGA CGTTCAAGAT ATTCCTTGTC ATCATTGTGC TTCAATGTCG TCTGGTAACA 180
    TCCCTGGGAAG AAGATACTGA TAATTCAGT TTGTCAACAC CACCTGCTAA ATTATCTGTT 240
    GTCAGTTTTG CCCCCTCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
15  AGCTTACTCC CTTCAAAACGA AACAGAAAAA ACTAAATCA CTATAGTAAA AACCTTCAAT 360
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    GAGCTCAACA AAACCTGACA AACCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
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    ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
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    GGGAACTGTC CTACACTGCT ATTGTTGCTA CATGTATCGA GCCTTGATTG CTCCTAGTTA 4380
    TATACAGGGT CTATCTGCTT TCCTACCTAC ATCTGCTTGA GCAGTGCCCTC AAGTACATCC 4440
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    ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560

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CTGACTTGTC TTGCAATAT TTCTTTTCTG ATTTATTTAA TTTTCTTGTA TTTATATGTT 4620
 AAAATCAAAA ATGTTAAAAA CAATGAAATA AATTGTCAGT TAAGA

A129 Protein sequence

Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

1 11 21 31 41 51
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 MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSP PAKLSVVSFA 60
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 GEIMFYQDKE STVPQNHIT NGTLTGVLISL SELKRSELNK TLQTLSETYF IMCATAEAQS 180
 TLNCTFTIKL NNTMNACAAI AALERVKIRP MEHCCCSVRI PCPSSPEELG KLQCDLQDPI 240
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 PQPSAPIASS PAIDMPPQSE TISSPMPQTH VSGTPPPVKA SFSPTVSAP ANVNTTSAPP 360
 VQTDIVNTSS ISDLENQVLQ MEKALSLGSL EPNLAGEMIN QVSRLHSP DMLAPLAQRL 420
 LKVVDDIGLQ LNFSTNTISL TSPSLALAVI RVNASSFNNT TFVAQDPANL QVSLETQAPE 480
 NSIGTITLPS SLMNNLPAHD MELASRVQFN FFETPALFQD PSLENLSLIS YVSSSVANL 540
 TVRNLTRNVT VTLKHINPSQ DELTVRCVFV DLGRNGGRGG WSDNGCSVKD RRLNETICTC 600
 SHLTSGVLL DLSTSVLPA QMALTFTITY IGCGLSSIFL SVTLVTYIAF EKIRRDYPSK 660
 ILIQLCAALL LLNLVFLDLS WIALYKMQGL CISVAVFLHY FLLVSVFTWMG LEAFHMYLAL 720
 VKVFNTYIRK YILKFCIVGW GVPVVVTII LTISPDPNYL GSYGKFPNGS PDDFCWNNN 780
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 ITWGFADFV GPVNVTFMVL FAIFNTLQGF FIFIFYCVAK ENVRKQWRRY LCCGKLRLAE 900
 NSDWSKTATN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SGNNGMASTER 960
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A130 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 ProbeSet Accession #: AA460530
 Nucleic Acid Accession #: NM_003667
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 TCAGGAACGC GCGCTCTGGC GCTGCAGACG CCCGCTGAGT TGCAGAAGCC CACGAGCGGG 120
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 10 AATGTTTTCA AAGGTTGAGA ACCTGAAAAT GTGAGATTGA GTATATCAGA GCAGTAATTA 3000
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A131 Protein sequence

15 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Protein Accession #: NP_003658.1
 Signal sequence: 1-22
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
 20 Cellular Localization: plasma membrane

25 1 11 21 31 41 51
 | | | | | |
 MDTSRLGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSVFTSY IDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVL 120
 LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180
 AFRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLLETLD 240
 30 LNNYNLDEFP TAIRTLNLSK ELGFHSNNIR SIPEKAFVGN PSLITIHFYD NPIQFVGRSA 300
 FQHLPELRTL TLNGASQITE FPDLTGTANL ESLTLTGAQI SSSLPTVCNQ LPNLQVL DLS 360
 YNLELDLPSF SVQCKLQKID LRHNEIYEIK VDTFQQLSL RSLNLAWNKI AIHPNAFST 420
 LPSLIKLDLS SNLLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPYAYQCC 480
 AFGVCENAYK ISNQWNKGDN SSMDDLHKKD AGMFAQQDER DLEDFLDFFE EDLKALHSVQ 540
 35 CSPSPGPFPK CEHLDDGLI RIGVNTIAVL ALTCLNVLTS TVFRSPLYIS PIKLLIGVIA 600
 AVNMLTGVS AVLAGVDAFT FGSFARHGAW WENGVGCHVI GFSLIFASES SVFLLTLAAL 660
 ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMMAVPL LGGSKYGASP LCLPLPFGE 720
 STMGYMAVALI LLNSLCFLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LLFTNCILNC 780
 VFAFLSFSFL INLTFISPEV IKFILLVVVP LPACLNPLLY ILFNPFPKED LVSLRKQTYV 840
 40 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900
 VAFVFC

A132 DNA SEQUENCE

45 Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Probeset Accession #: U25128
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 | | | | | |
 GGCCGGTGGC CCGGCCCGGA CCACCCAGC TCGCGTCTGT TACTGGCCAC AAGTTTGCTC 60
 TGGGCCAGCC AAGTTGGCAA CTTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120
 55 TCTTCTTACA GCCGTTCCGG GCATGGCCGG GCTGGGGGCG TCGCTCCACG TCTGGGGTTG 180
 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATTA 240
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
 AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTGTGTT 360
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGC CCTCCTTATA TTATGACTT 420
 60 CAACCATAAA GGAATGTGCT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCCT CGCTTCTGCG AGCCAGATAT 540
 CAGCATAGGA AAGCAAGAA TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCAT GGTTACTTCA GACGATTGCA 660
 TTGCACTAGG AACTATATCC ACATGCACTT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720
 65 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
 AATAATGCAG GATGACCCAG AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCACAATA 840
 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG 900
 GATCTCTGGT GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTTCT TTTCGGACAC 960
 70 CAAATACCTG TGGGGCTTCA TCTGTATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC 1020
 ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TCCGAGGTGC TGGGAACCTA GTGCTGGAGA 1080
 CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200
 CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCITGGTCC TAGTCTTTGG 1260
 AGTGCAATTAC ATCGTGTTCT TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320
 75 CGCATGTCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TCTTTGTGTT CTATCATCTA 1380
 CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440
 CTCCGTGGAG TGGAAAGGGA CACCGCCATG TGGCAGCCCG AGATGCGGCT CAGTGCTCAC 1500
 CACCGTGACG CACAGACCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560
 TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACCTTACC 1620
 80 TGCTTATGTC TGGAGTAAC TCGCTGAGCA CTGCTGCGCA CAGCTTTTCC ACGAGGAGAC 1680
 CAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740
 GGAATCTAAC CAGACACTG AAGGATGCCA AGGAGAACT GAGGATGTTT TCTGAATGGA 1800
 CATTTGTGGC TGACTTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860
 ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT 1920
 TTTTAGGCTC CATGAATTGG CTCTGTGAAA TACTAACGAC ATGAAAATGC AAGTGTCAT 1980

5 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 2040
 GCTCTGTGAT TGTTCATTTT TTCTGTCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100
 GCTGTAGCTT TCTCTCATAT ATATCACCCCT AAATATAATG AAGATCTTTT AGTGTGTATC 2160
 ATTTTCCTTT TAGAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220
 ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280
 GATCTAAGAA CAAGTACTTG CTGGAAAATT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAAG AATATTTCAC 2400
 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460
 10 TTCTTTGTAA ACCATGTCAT GTGGAAGAT TTCCTCAGTT AGTGAGCTTG TGTCTGCAAA 2520
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTTCTTG 2580
 TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAAAAATTT GTTTTAAAAA 2640
 T

A133 PROTEIN SEQUENCE

15 Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Protein Accession #: NP_005039.1
 Signal sequence: 1-25
 20 Pfam domain: 7tm_2 [141-420]
 Transmembrane domains: 177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51
 | | | | |
 MAGLGASLHV WGLWMLGSL LARAQLSDG TITIEEQIVL VLKAKVQCEL NITAOEQEGE 60
 GNCFPENDGL ICFPRGTVGK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA 120
 NYSDCLRLFLQ PDISIGKQEF FERLYVMYTV GYSISFGLA VAILIIGYFR RLHCTRYNIH 180
 30 MHLEFVSFMLR ATSIFFVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240
 VPMFIYFLATN YYWILVEGLY LHNLIFFVAFF SDTKYLWGF I LIGWGFPAF VAAWAVARAT 300
 LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK 360
 LAKSTLVVLV VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFVVS ILYCYCNGEV 420
 QAEVKMKWSR WNLSDVDNKRTP PCGSRRCGS VLTVTHTSTS SQSQVAASR MVLISGKAAK 480
 35 IASRQPDSDHI TLPGYVWSNS EQDCLPHSFH BETKEDSGRQ GDDILMEKPS RPMESNPDE 540
 GCQGETEDVL

A134 DNA sequence

40 Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 | | | | |
 ATGCTGTCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
 GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCAGC 120
 GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC 180
 50 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240
 CCGCGGCGCG CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCTT 300
 CGCCTGCGTC CTGAGCGTTC CCGGGGAGG GTCCGGTTCG CAGTGAACCC TCCAGAGGCT 360
 TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCATC AGCGAGTGCA 420
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
 55 GCTCCTGGAC CTAGGGCCCG GCGTCGTGCG CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC 540
 CCGCGCGGAA AGCGCCGCGG GACAGTCAGT GACGAGGCCG GGGGGTCCGC GGGGCCACGA 600
 CTTCTCGGAG ACCGTCTGCG GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660
 TGTGGGGGCG TCGCCGCTCG TCCGCTCTCT CATCTGGAA CGCCGCTTCG CTCCTGCAGC 720
 TGCTGCTGGC TCGCTGCTGT GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780
 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840
 60 GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGOGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGCGGCTGG CGAGCCTGGC 960
 CGGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020
 GGAGACGGCG AGGGTGCGCC CCCACCCGTG AGGGCCTGGC AGCGGTGCTC CCCTGAAGGC 1080
 TCCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCCG TGCCAGACGC 1140
 65 CGCGGATTCC CATCTCTCC ACGCGGCGGC CCCTCTCCCC TGCAAGCGCC CGCCTTGCCC 1200
 ATCTACGTGC CGTTCTCAT TGTGGGCTCC GTGTTGTGCG CCTTTATCAT CTTGGGGTCC 1260
 CTGGTGGCAG CCTGTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCCGA 1320
 GCCCCAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCAGTGTC CAGCACCTCC 1380
 70 CGGGGTCGTG CCTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCACTTCC 1440
 GGGGCCCCGG CGCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCCGGA AGGGACCATG 1500
 AACAACTGTG ATGTCAACAT GCCCACGAAT TTCTCTGTGC TGAACGTGCA GCAGGCCACC 1560
 CAGATGTGTC CACATCAAGG GCAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGCAG 1620
 CACGACTCTG TGCCCATGCA AGCTGTGCCA CCTTTCATGG ACGGCCTGCA GCCTGGCTAC 1680
 75 AGGCAGATTC AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
 ACTGTATAAC CGAGAGTCAC TGGTGGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAAGTCC GCACATGTCG GTGGTATTTA TGGCACGATT CTTTGGATG 1860
 GCTTCATTTC CCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920
 CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCCTC AGCTGGAGAT GACTGTGATG 1980
 80 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
 AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100
 TTGTTGTTGA TGCACAGAGA TCAAAATGCC TGGTATCTCC CTTTACTTGG GACTTTTTTT 2160
 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCCAGGC TGGAGTGCAG 2220
 TGGTGCATC TCGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCAACA CTCCTGCCTC 2280
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTT 2340

TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400
 TCTGCCCTGTC TCAGCCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCCAGCC 2460
 TGAGCCCTTTT TTTTCTTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520
 ATTCTAAAAG GAAACCTGTT TGAACCTCTG GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
 5 GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640
 GGGCCTATTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTCTTACA 2700
 TTAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAAAACCATT CATCCCCTTC 2820
 10 TTGATTGATT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCCTTTT 2880
 TATATTGAAA TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940
 TGGTTATGGT TTGGCGTTTC CTTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCTC 3000
 GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060
 AAAAAATTTT TTTCTCTTAGT TATAAAAATT CAAAGAAATG TGTTACAAAG ATACTTAGTA 3120
 15 TAGTCTCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTTT 3180
 GCAGATCATA AGGCTTTTTT TACTCTTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240
 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCCCTT CTTCTCCAC ACTGTTCTTG 3300
 ATTTCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAATATAT 3360
 CAAATTCAG TGAATTATT TGTGTGTTCT TTACTTATAT AAAAAAAGAT AACTTTAAGG 3420
 20 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAATCGCT 3480
 GTATGGTATG GTCTTCTACA CATTATATGC TATAGATATC TATCGATCAT CTTTCTATTC 3540
 TGTTTTATGA CTGAATAATG TAAACCCAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
 TTTTAAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
 TGAAAAAATA AAAAAAATA AAAAAAATA

A135 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 30 Transmembrane domains: 402-424
 Cellular Localization: not determined

1 11 21 31 41 51
 35 | | | | |
 MLSGFLMSPS TQHRAQYTPG GKKLPEWASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
 GEAEGKNRGE PPAPIRAQQQ PRPPAGQAP GTAAGGAQDP RLRPRGRSGR VRLPVKPPEA 120
 SGRQPRGSD CIPRFPSASA THKAVPKGTG PPAEDGDGLG AFGPRARRRR LLGVAAEGSG 180
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAFVRVP CGALAARPSF HPGTFLRSCS 240
 40 CCWLRCWRRG RGPSGEYCHG WLDAQGVWRI GFQCPERFDG GDAITCCGSC ALRYCCSSAE 300
 ARLDQGGCND DRQQGAGEPG RADKDGPRRL GRASCLRGTD GDGEGAPPV RAWQRCSPGE 360
 SPKGRQLLRA PFGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPLIVGS VFVAFIILGS 420
 LVAACCCRLC RPKQDPQQR APGGRNLMET IPMIPASST RGSSSRQSSS AASSSSSANS 480
 45 GARAPPTRSQ TNCCLPEGTM NNVVYVNMPTN FSVLNCQQAT QIVPHQGGYL HPPYVGYTVQ 540
 HDSVPMTAVP PFMDGLQPGY RQIQSFPFHT NSEQKMPYAV TV

A136 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 50 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 55 | | | | |
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAAG AGAGAGTGGG 60
 GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
 CAGCAAAGGT ACACACACCT GGTGCAATT CAAACCAAAG AAGAGATTGA GTACCTAAAC 180
 60 TCCATATTGA GCTATTACAC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACATGTG 240
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAAGTG GGCTCCAGGT 300
 GAACCCACAA ATAGGCCAAA AGATGAGGAC TGGCTGGAGA TCTACATCAA GAGAGAAAAA 360
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
 GCTGCTGTGA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
 65 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGAATCAAGT GTGAGCAAAT TGTGAAGTGT 540
 ACAGCCCTGG AATCCCTCTG GCATGGAAGC CTGGTTTGCA GTCAACCACT GGGAACTTTC 600
 AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 ACCATGCAGT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTTGGA 780
 70 AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTGGA ACTAATGGGA 840
 GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
 CCTGCTGGAG AGTTACCTTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
 TTTGAGGGAG CAGCCAGGTG TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAAATCCA 1080
 75 GTTTGTGAAG CATTCTGAGT CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
 CTTCTAGTGT CTTCTGGCAG TTTCCGTAT GGGTCCAGCT GTGAGTCTC CTGTGAGCAG 1200
 GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAAAC 1260
 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
 GTGAGGTGTG CTCATTCCCC TATTGGAGAA TTCACCTACA AGTCTCTTG TGCCCTTCAG 1380
 80 TGTGAGGAGG GATTTGAAAT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
 TGGACAGAAG AGGTTCCTTC CTGCCAAGTG GTAAATGTT CAAGCCTGGC AGTTCGGGGA 1500
 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGCA CTGTGTGCAA GTTCGCTGTG 1560
 CCTGAAGGAT GGACGGTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCTTT GGTAGCTGGA 1680
 CTTTCTGCTG CTGCACTCTC CCTCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740

TGCTTACGGA AAGCAAAGAA ATTTGTTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

A137 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)
Unigene number: Hs.89546
Probeset Accession #: M24736
Protein Accession #: NP_000441
Signal sequence: 1-22
Transmembrane domains: 555-573
C-lectin domain: 23-139
Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QORYTHLVAI QNKKEIEYLN 60
SILSYSPSYW WIGIRKVN NV WVVVGTKQKL TEEAKNWAPG EFNNRQKDED CVEIYIKREK 120
DVGWMWDERC SKKKLALCYT AACTNTSCSG HGECVETINN YTCKCDPFGS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
ECDAVTNPAN GFVECFQNPQ SFPWNTTCTF DCEEGFELMG AQSLQCTSSG NWDNEKPTCK 300
AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEFGM LQGPAQVECT TQGQWTQQIP 360
VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN 420
EKPTCEAVRC DAVHQPPKGL VRCASHPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
WTEEVPSQVQ VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLLWLRL CLRKAKKFVP ASSCQSLESD 600
GSYQKPSYIL

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A138 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Nucleic Acid Accession #: AA487468
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTTGGGTCT CTGCTCTCTA CTCGTCACAG TTTCTTCCAA CCTTGCCATT 120
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
ATGGTTATTG ATCACTGGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
CAAAATGAAG AAATAACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
GACCCCTTCT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
TATGAGCCTC GGGATTATAC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTCA 600
GAAGAAAAAC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAAT 660
TACTATTATA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

```

A139 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Protein Accession #: none found
Signal sequence: 1-23
Transmembrane domains: none found
Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLRGWGD DITWVQTYEE GLFYAQKSKK 60
PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIIMNL MHETTCKNLS PDGQYVPRIM 120
FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

```

A140 DNA SEQUENCE

Gene name: TMPSRSS3a
Unigene number: Hs.298241
Probeset Accession #: AI538613
Nucleic Acid Accession #: AB038157
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
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ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTATGCCCC GTGTGAGCCA 60
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACTGTGGC CTACTATCTC TTCCGTGGTG 120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCCGATGTC 180
AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240

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TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTTGC ACCAGATGCA 300
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 5 TCAGGGAAGT ACAGATGTCT CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAGA CCATGTGCTC CGATGACTGG 600
 AAGGTCACCT ACGCAATGT TGCCTGTGCC CAACTGGGT TCCCAAGCTA TGTGAGTTCA 660
 10 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCTCTCG GCCACGTGGT TACCTTGCA GGCACAGCCT GTGGTCATAG AAGGGGCTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCCT GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTA TGACTTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
 15 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTGG TGGAGAAGAT TGTCTACCAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATGCCCC TTATGAAGCT GGCCGGGCCA 1140
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTTGCCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAGA TGTGCTGGAC GTGAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 TCCCTGTGTC TGAACCAAGC GGCCTGCCCT TTGATTCCA ACAAGATCTG CAACCAACAG 1320
 20 GACGTGTACG GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACCA CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA 1620
 25 TCCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCTTG GAGCTCTGAG 1680
 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCTTCCA TCTGATTCCA GCACAACCTT 1740
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
 TTGCCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCAACC CAACTAATT 1920
 30 TTGTATTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGTCTC AAACCCCTGA 1980
 CCTCAAATGA TGTGCTGCT TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
 ACBCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160
 ACGAGATAAG CAGTTATGTG ACCTCAGCTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
 35 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCAGTT TTCTCTCTA GGGACCAGAA 2280
 CCAACCCACC CCTTCTACT TCCAAGACTT ATTTTCACAT GTGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGGCTTAT TTTCTGATG TCTTGTAGC ATTTGTGCT TGACGTATTA 2400
 TTGTCCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAAAAA

A141 Protein sequence:

Gene name: TMPRSS3a
 Unigene number: Hs.298241
 ProbeSet Accession #: AI538613
 Protein Accession #: BAB20077
 45 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_SPc domain: 216-444
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLPLKFFP IIVIGIILI 60
 55 LALAIGLGIH FDCSGKYRRC SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GQNAVLQVF 120
 TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 VTALHHSYVY REGCASGHV VTLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQFQGYH 240
 LCGGSVITPL WIITAHCVMY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGA GDASPVLNHA 360
 60 AVPLISNKIC NHRDVGII SPSMLCAGYL TGGVDSQCGD SGGPLVCQER RLWLKLVGATS 420
 FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT

A142 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 65 ProbeSet Accession #: AA314779
 Nucleic Acid Accession #: none found
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CCAAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
 75 CTGAGATCCT TGCCTAGACT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
 CGGCTGCTCC TATTGCTGAG CTGCCCTGGC AAAACAGGAG TCCTGGGTGA TATCATCATG 180
 AGACCCAGCT GTGCTCTGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTAAGTTCAGG 240
 AAGCTGAGGA ACTGGTCTGA TGCCGAGCTC GAGTGTCACT CTACGGAAA CGGAGCCAC 300
 CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
 80 CAGAGAAGCC AGCCGATATG GATTTGCCCTG CACGACCCAC AGAAGAGGCA GCAGTGGCAG 420
 TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480
 AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTTAA CTTGGAGCAG CAACGAATGC 540
 AACAAAGGCC AACACTTCCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600
 AACTCTTGCA CCAGCCCCGT CCTCTTCCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660
 TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GCCTTTTTTA 720

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GGCTTAGAGA CAGAAACTTT AGCATTGGGC CCAGTAGTGG CTTCTAGCTC TAAATGTTTG 780
CCCCGCCATC CTTTTCACCA GTATCCTTCT TCCCTCCTCC CCTGTCTCTG GCTGTCTCGA 840
GCAGTCTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900
AAAGATTTGA AGACAGAAGG AAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
ACACCCCTCT GCCCTCTCTC CATTGCCTGC ACCCCACCCC AGCCACTCAA CTCCTGCTTG 1020
TTTTTCCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTG ATGTGGGCCA 1080
TACATTCTTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA
  
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A143 Protein sequence:

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Protein Accession #: none found
 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

```

1      11      21      31      41      51
MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWFYHKSN CYGYFRKLNR WSDAELEQCS 60
YGNQAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLRSWSG 120
KSMGGNKHCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP
  
```

A144 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

```

1      11      21      31      41      51
GCGGAACACC GCGCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
TCCCTCGTGG ACCTCTGCGG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGC CGCG 120
CCTCCGAGCC GTCCCGGGCG GTCTTCAGGG AGGCTGAAAGT GACCTTGGAG GCGGGAGGCG 180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
AAAGAAGGCT ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAA GGCAAGGGTC 420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
ACAGCATCAC GTGGCCCGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GACCCCATG AACATCTCCA 660
TCATCGTGAC CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
AGGACCCACA CGACCTCATG TTCACAATT CACCGGAGCAG AGGCACCATC AGCGTCATCT 900
CCAGTGGCCT GGACCGGGAA AAGTCCCTTG AGTACACACT GACCATCCAG GCCACAGACA 960
TGGATGGGGA CGGCTCCGAC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
ACAATGCTCC CATGTTTGAC CCCAGAAAGT ACGAGGCCCA TGTGCCTGAG AATGCAGTGG 1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGAGCG CCCCAACTCA CCAGCGTGGC 1140
GTGCCACCTA CCTTCACTC GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
AGCACACCCT GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACCT 1320
CCACAGCCAC CATAGTGTGC CACGTGGAGG ATGTGAATGA GGCACTGTG TTTGTCCCAC 1380
CCTCCAAAGT CGTTGAGTGC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
CTGCAGAAGA CCTTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCTG AGAGACCCAG 1500
CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTAC AGCTGTGGGC ACCCTCGACC 1560
GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTG GCCATGGAGA 1620
ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
ACCATGGCCC AGTCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAGC CCTGTGCGCC 1740
ACGTGCTGAA CATCACGAC AAGGACCTGT CTCCCCACAC CTCCCCCTTC CAGGCCAGC 1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920
ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
ATGTGAAAC CTGCCCTGGA CCCTGGAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGT GGTGAGAAAG AAGCGGAAGA 2100
TCAAGGAGCAT CTCCTACTC CCAGAAGATG ACACCCGTGA CAACGCTCTT TACTATGGCG 2160
AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
AGGCCAGGCC GGAGGTGTTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
TGTACCGTCC TAGGCGAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
AGGCGGTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTGGTG TTCGACTATG 2400
AGGCGAGCGG TCCGAGGCC GCGTCCCTGA GCTCCCTCAC CTCCTCCGCC TCCGACCAAG 2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGCTT CAAGAAGCTG GCAGACATGT 2520
ACGGTGGCGG GGAGGACGAC TAGGCGGCCCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC 2580
CACAGAGCAT CTCGAAGGGG TCTCAGTTCC CCTTCAGCT GAGGACTTCG GAGCTTGTC 2640
GGAAGTGGCC GTAGCAACTT GCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
TCTTAGCTT TTCAGGATGG AGGAATGTGG GCAGTTGAC TTCAGCACTG AAAACCTCTC 2760
CACCTGGGCC AGGGTGGCCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820
TGCTCAACCC TGTGCTCTGG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTCTCT 2880
CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940
  
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TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAGA GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCATT CTGGTTTCCA GACCCCAATG CCTCCCATTG GGATGGATCT CTGCGTTTTT 3060
 ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CCTGTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACATCGTG TATATGTACT AGAAGTTTTT TATTAAAGAA A

A145 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675

Cellular localization: plasma membrane

1 11 21 31 41 51
 MGLPRGPLAS LLLQLVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPPSKR ILRRHKRDWV VAPISVPENG 120
 KGFFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK 180
 YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGLVP GTSVMQVTAT 240
 DEDDAIYTYN GVVAYSISQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMGDGSGST TAVAVVEILD ANDNAPMFDP QKYEAVHPEN AVGHEVQRLT VTDLDAPNSP 360
 AWRTATYIMG GDDGDHFTTT THPESNQGL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPFSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMDP DSGQVTAAGT LDREDEQFVR NNIYEVMLA DMNGSPPTTG TGTLTLTLID 540
 VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPHSTSPFQ AQLTDDSDIY WTAEVNNEEGD 600
 TVVLSLKKFL KDPTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660
 GAVLALLFL LLLLLLVRKK RKIKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDITLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

A146 DNA SEQUENCE:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGAATTCCTT TTTTCTTTT TTTGAGATGG AGTTTCACTC TTGTTGGCCA GGCTGGAGTG 60
 CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCCTCCCG GGTTCAGCG ATTCTCCTGC 120
 CTGAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT 180
 CTTTCTTATT TAGTAGAGAT GGGGTTTAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240
 ACCTCAGGTG ATCCACTTGC CTGGCCCTCC CAAAGTGCTA GGATTACAGC CGTGAAACTG 300
 TGCTCGCTG ATTCTTTTTT TGTGTTGGA TTTTGAAGC AGGGTCTCCC TTGGTCGCCC 360
 AGGCTGGAGT GCAGTGGTGC GATCTTGGCT CACTATAACC TCCACCTCCT GGTTCAGAGT 420
 GATCCTCCCA CTTTAGCTCT CTGAGTAGCT GTGATTACAG GCGTGACCCA CCACACCCGG 480
 CTAATTTTTG TATTTTTTAT AGAGACAGGG TTTCACCATG TTGGCCAGGC TGTCTCTCAA 540
 CTCCTGGACT CAAGGGATCC GCCTGCCTCC ACTTCCCAAA GTCCCGAGAT TACAGGTGTG 600
 AGTCACCATG CCGTACCTTA TAATTTCTAA GTCAATTTTT CTGGTCCATT TCTTCCTTAG 660
 GGTCTCACA ACGAATCTGC ATTAGGCGGT ACAATAATCC TTAACCTCAT GATTACAAAA 720
 AGGAAGATGA AGTGATTCAT GATTAGAAA GGGGAAGTAG TAAGCCCACT GCACACTCCT 780
 GGTATGATG CCTAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAAA 840
 TTTGGTTTAA ATTAATTATC TAAATATCTA AAAACATTTT TGGATACATT GTTGATGTGA 900
 ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCCAG 960
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 AACTAAGCTT GAATAAAATT TCTGCTGATA CTACAGATAA CTCGGGAAGT GTTAACCAAA 1140
 TTATGATGAT GGCAACAAC CCAGAGGACT GGTGAGTTT GTTGCTCAAA CTAGAGAAAA 1200
 ACAGTGTTC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTCTGTAC AGTCAAGCAA 1260
 TTGAAGCGCT TCCCCAGAT AAATAGGCC AAAATGAGAG TTTTGCTAGA ATTCAAGTGA 1320
 GATTGCTGA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAAATGG 1380
 CCAGAGCAAA CTGCAAGAAA TTTGCTTTTG TTCTATATATC TTTTGACAAA TTTGAACTGT 1440
 CACAAGGTAA TGTCAAAAAA AGTAAACAAC TTCTTCAAAA AGCTGTAGAA CGTGGAGCAG 1500
 TACCACTAGA AATGCTGGA ATTGCCCTGC GGAATTTTAA CCTCCAAAAA AAGCAGCTGC 1560
 TTTCAGAGGA GAAAAAGAA AATTATCAG CATCTACGGT ATTAACCTGC CAAGAATCAT 1620
 TTTCCGGTTC ACTTGGGCAT TTACAGAATA GGAACAACAG TTGTGATTCC AGAGGACAGA 1680
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 AACCAGTGG AAATGATTCC TGTGAATTAA GAAATTTTAA GTCTGTTCAA AATAGTCATT 1980
 TCAAGGAACC TCTGTTGTCA GATGAAAAGA GTTCTGAAGT TATTATTACT GATTCAATTA 2040
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 AAGAACCAGA GGTTCACAG AGTAACCAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT 2160
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 AGTCAACACC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTTGT AAGACACCAA 2340

GCAGCAATAC CTTGGATGAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGAATGACT 2400
 TTCCACCTGC TTGTTCAGTTG TCAACACCTT ATGGCCAACC TGCCTGTTTC CAGCAGCAAC 2460
 AGCATCAAAT ACTTGGCCAT CCACCTTCAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA 2520
 5 ATGAATGCAT TTCGGTTAAA GGAAGAATTT ATTCATATT AAAGCAGATA GGAAGTGGAG 2580
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 15 GTGATGTTTG GTCTTCTAGGA TGTATTTTGT ACTATATGAC TTACGGGAAA ACACCATTTT 3180
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 CTATCCAGT TAACCAATG GCCAAGGGA CCACGAAGA AATGAAATAT GTTCTGGGCC 3420
 20 AACTTGTGTTG TCTGAATTCT CTAACCTCCA TTTGAAAGC TGCTAAACT TTATATGAAC 3480
 ACTATAGTGG TGTGAAAGT CATAATTCTT CATCTCCAA GACTTTTGAA AAAAAAGGG 3540
 GAAAAAATG ATTTGCAATT ATTGTAATG TCAGATAGGA GGTATAAAAT ATATTGGACT 3600
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 ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAAGAAA ACTGTAAAA TAGCAACCAC 3720
 25 TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGAATCTAC 3780
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAACTTG 3840
 TAAATAAAGT TTTGTGGCTA AAATGA

A147 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 35 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51
 | | | | |
 MNKVRDIKNN FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLKLEKNS 60
 VPLSDALLNK LIGRYSAIE ALPPDKYQON ESFARIQVRF AELKATQEPD DARDYFQMAR 120
 ANCKKFAFVH ISFAQFELSQ GNVKKSQQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180
 45 EEEKKNLSAS TVLTAQESFS GSLGHLQNRN NSCDSRGQTT KARFLYGENM PPQDAEIGYR 240
 NSLRQTNKTK QSCPFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPGSKP 300
 SGNDSCELRN LKSVQNSHFH EPLVSEKSS ELIITDSITL KNKTESLLA KLEETKEYQE 360
 PEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHTTFE QPVFSVSKQS 420
 PPISTSKWFD PKSICKTPSS NTLDDVMSCF RTPVVKNDFF PACQLSTPYG QPACFQQQOH 480
 50 QILATPLQNL QVLASSANE CISVKGRIYS ILKQIGSGGS SKVFQVINEK KQIYAIKYVN 540
 LEEADNQLTD SYRNEIAYLN KLQQHSDKII RLYDYEITDQ YIYVMMECGN IDLNSWLKKK 600
 KSIDPWERKS YWNMLEAVH TIHQHGIVHS DLKPANFLIV DGMLKLIDFG IANQMOPDIT 660
 SVVKDSQVGT WNYMPPEAIK DMSSSRENGK SKSKISPKSD VWSLGCILYV MTYKTPFQ 720
 IINQISKLHA IIDPNHEIEF PDIPEKDLQD VLKCCCLKRDP KQRISIPELL AHPYVQIQTH 780
 55 PVNQMAKGTT EEMKYVLGQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRGK 840
 K

A148 DNA SEQUENCE

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 Probeset Accession #: NM_012152
 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 70 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTT TCTGCCTGTT TATTTTCTT 180
 TCTAATTCTC TGGTCATCGC GGCAGTGATC AAAACAGAA AATTTCAATT CCCCTTCTAC 240
 TACCTGTTGG CTAATTTTAC GTCTGCCGAT TTCTTCGCTG GAATGCGCTA TGTATTCTG 300
 ATGTTTAAAC CAGGCCCACT TTCAAAACT TTGACTGTCA ACCCGTGGTT TCTCCGTGAG 360
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT GCCTGGGAG 420
 75 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480
 CTGCTCATTT TGCTTGTCTG GGCCATGCCC ATTTTATATG GGGCGTCCC CACTGGGC 540
 TGGAAATTGC TCTGCAACAT CTCTGCCTGC TCTTCCCTGG CCCCATTATA CAGCAGAGT 600
 TACCTTGTTT TCTGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGTGATC 660
 CTGCGGATCT ACGGTGACGT CAAGAGGAAA ACCAACGTCT TGTCTCCGCA TACAAGTGGG 720
 80 TCCATCAGCC GCCGGAGGAG ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
 GCGTTTGTGG TATGCTGGAC CCCGGGCTGT GTGGTTCTGC TCCTCGACGG CCTGAACTGC 840
 AGGCAGTGTG GCGTGCAGCA TGTGAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900
 GTCGTGAACC CCATCATCTA CTCCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960
 ATGATCTGCT GCTTCTCTCA GGAGAACCAC GAGAGGCGTC CCTCTGCGAT CCCCTCCACA 1020
 GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080

GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGCCACCCA GGTGATGACT 1140
GTCTTAGG

5

A149 Protein sequence:

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
Unigene number: Hs.258583
Probeset Accession #: NM_012152
Protein Accession #: NP_036284
Signal sequence: none found
Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295
Cellular Localization: plasma membrane

10

15

1	11	21	31	41	51	
MNECHYDKHM	DFFYNRSNTD	TVDDWTGTKL	VIVLCVGTFF	CLFIFFSNLS	VIAAVIKNRK	60
FHFPPFYLLA	NLAAADFFAG	IAYVFLMFNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
LVIAVERHMS	IMRMRVHSNL	TKKRVTLIL	LVWAIAlFMS	AVPTLGWNCL	CNISACSSLA	180
PIYSRSYLVF	WTVSNLMAFL	IMVVVYLRIY	VYVKRKINVL	SPHTSGSISR	RRTPMKLMKT	240
VMTVLGAFVV	CWTPGLVLL	LDGLNCRQCG	VQHVKRWFLL	LALLNSVVP	IIYSYKDEDM	300
YGTMKMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK	STS	

20

25

ProstateA150 DNA SEQUENCE

Gene name: ESTs
Unigene number: Hs.293616
Probeset Accession #: AW043782
Nucleic Acid Accession #: none found
Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

30

35

1	11	21	31	41	51	
AGCAACGACG	CGGGGACGCG	GGAGCGGCGG	CGCGCCATG	TGGCTGCTGG	GGCCGCTGTG	60
CCTGCTGCTG	AGCAGCGCCG	CGGAGAGCCA	GCTGCTCCCC	GGGAACAACT	TCACCAATGA	120
GTGCAACATA	CCAGGCAACT	TCATGTGCAG	CAATGGACGG	TGCATCCCGG	GCGCCTGGCA	180
GTGTGACGGG	CTGCCTGACT	GCTTCGACAA	GAGTGATGAG	AAGGAGTGCC	CCAAGGCTAA	240
GTGGAATATG	GGCCCAACCT	TCTTCCCTCG	TGCCAGCGCG	ATCCATTGCA	TCATTGGTCC	300
CTTCCGGTGC	AATGGGTTTG	AGGACTGTCC	CGATGGCAGC	GATGAAGAGA	ACTGCACAGC	360
AAACCTCTCG	CTTTGCTCCA	CGCCCCGCTA	CCACTGCAAG	AACGGCCTCT	GTATTGACAA	420
GAGCTTCATC	TGCGATGGAC	AGAATAACTG	TCAAGACAAC	AGTGATGAGG	AAAGCTGTGA	480
AAGTTCTCAA	GAACCCGGCA	GTGGGCAGGT	GTTTGTGACT	TCAGAGAACC	AACTTGTGTA	540
TTACCCGAGC	ATCACCTATG	CCATCATCGG	CAGCTCCGTC	ATTTTTGTGC	TGGTGGTGGC	600
CCTGTGGGCA	CTGGTCTTGC	ACCACCAGCG	GAAGCGGAAC	AACCTCATGA	CGCTGCCCCG	660
GCACCGGCTG	CAGCACCCCT	TGCTGTCTGC	CGCCTGGTG	GTCTTGGAAC	ACCCCAACCA	720
CTGCAACGTC	ACCTACAACG	TCAATAATGG	CATCCAGTAT	GTGGCCAGCC	AGGCGGAGCA	780
GAATGCGTCG	GAAGTAGGCT	CCCCACCCCT	CTACTCCGAG	GCCTTGCTGG	ACCAGAGGCC	840
TGCGTGGTAT	GACCTTCTTC	CACCGCCCTA	CTCTTCTGAC	ACGGAATCTC	TGAACCAAGC	900
CGACCTGCCC	CCCTACCGCT	CCCGTCCCGG	GAGTGCCAAC	AGTGCCAGCT	CCCAGGCAGC	960
CAGCAGCCTC	CTGAGCGTGG	AAGACACCAG	CCACAGCCCG	GGGACGCTCG	GCCCCCAGGA	1020
GGGCACTGCT	GAGCCCAGGG	ACTCTGAGCC	CAGCCAGGGC	ACTGAAGAAG	TATAAGTCCC	1080
AGTTATTCCA	AACTCCATAT	GGGTTAATCT	GCTCTGACTT	GTGCAATTC	TAACATTTG	1140
TGCTCATGGG	AAGCTCTTTA	AGCACTGTGA	AGGATGTCTC	AAGTTACAGT	TTGGGATATT	1200
AACTATCTCT	GCATTCCTCT	CCTCCCCCAG	ACTTCAGAGA	TGTTTTTCTG	GCGTCTCAGT	1260
TGACATGATC	TGTTGTGCGT	CTTTTCTGTC	AGGTCACTCT	TCCCTTGGGA	CCCGAGATCA	1320
CACCTTCATT	TTTCACATTA	TTCTGTTTCT	GTGGGAGAGA	CAGCATATAA	AACAGTATTG	1380
AAATAGGCTG	GGAGAGAGCA	ATGTTTCTGT	GCTATATTGG	ATGCTCAGAA	GTGCAGGAGA	1440
CGCTGGACCC	AATTCTCTCT	GCTGGGTAGT	TACCTTATAG	CATTTGGGGA	TTGGGTTTAG	1500
ATGATCTAAC	CAGGAGGCCA	TCACTGGATG	GTCAACCCCG	CAAAAAAATT	CCATTTGAGC	1560
ATCAAAACCT	GCTTTGCACA	ATCCTATTGG	ATGCCCCCG	TTCAAGAGAG	TCAGTGGCCA	1620
AAGAAAACCT	TGGACGTGAG	TAACACCCCT	CAGCAGTCGC	AACGTTATTT	TGGTTTGTG	1680
AAGGACTCTG	AAACCATCTA	CCCTGTATAA	ATTCTGGCTT	TAGAAATTTG	CCCAAGAAATG	1740
CTCATTCTGA	GAGCTTTCCT	CAGCAGCATA	TATCATCAGC	CTCATCTTAA	AATAGGCAGG	1800
GAGCCCCCTC	CATGAGTTTA	TCCAAGTTCT	CAGCTCCTAA	AATGCAGGCT	GCCAAGACCC	1860
TACACCTGCC	CTGGCTCTAC	AGCCACTTAC	CTGGTTTCTG	GACTGTCAAC	CTCCAGCTG	1920
ACCTGCCCGT	AGCCAAGGAA	TGAGGACCTA	ACTTGAGTTG	GCCCCAAGTC	TGACCTGGCT	1980
GTATGTCCCT	GTGGCCACCA	CCCAGCCTGT	CTTGCTCATT	CATGCAGCCT	CAACACTGGC	2040
CTCCAAAGTT	CCCTTAACAC	TTGCAAGATC	CTTTTACCT	GTGCAATTGG	ACTTGAGGAC	2100
ACTGGTTTCT	ATCACAGGTG	AGAGCCATGT	TCAATACCTC	CAGCAAGCTC	TCCTGGCTCC	2160
CTGCACTGTG	CAGCCTCCTC	TTCCCAAGGT	CCCAATACCA	GCACCTCTAG	TTAGAGTTAG	2220
GGTCAGGGTC	AGGCCTCTCC	CAACATCCCA	GTAGTTTCTC	CTCTGAGACA	CATGGGCAAG	2280
AGACAATTGG	GAGTCAGAT	TTTCCATTGG	GATCTATTTT	AAATCTTTTA	GAAATGCATT	2340
TGAAACAGTG	TGTTTGTGTT	TTCCCTTCTA	GTTAAGGGAC	TATTTATATG	TGTATAGGAA	2400
AGCTGTCTCT	TTTTTTGTGTT	TTCTTTTAAC	AAGGTCACAA	GAAAGATGCA	AAAGGAGATC	2460
ACACCTTTCG	CCCGCTGAGC	CCCGTGATAA	CAAGTCACTC	CAGACTAACC	TGTGTGCCAG	2520
ACATTTGTGC	ATTGTTGTCAC	TTTGAGGTTA	TTATTTATCA	AGTTCTTGAA	GGAAGCAGAA	2580
AGAGGGACTC	CTCTCTCCCT	CCGTGTATAG	TCTCTATGTT	TGTGCTAGTT	TTTCTTTTCT	2640
TTCTCTGTGT	CCAGTCAGCC	ACAGGGCCCG	CCTCCCTGCA	GGAATAAGGG	GTAAACAGTT	2700
AGGTGTTTGT	TGGCAAGAAA	CCACACTGAC	TGATGAGGGG	TAAATGGGAA	CCAGGTAGAG	2760
CCACTCCGGG	CAGCTGTAC	CCATTGAGAA	CTTCTTTCCG	CAGCTGAAGA	AATGTTTCAGT	2820

AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTGAG 2880
 TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTTACAGAA 2940
 AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA 3000
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAAGAA CTTTTGATGA CAGCCAGAAAT GTGTTAGAAC TCTGGCTGAA 3120
 CATTTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCTTCTTC 3180
 TTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATCTTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTGTAGT 3300
 AGATAAGGGA TGCTACTATA TGCTTTTATA AAACAAACAG GGACATTTT ATTATAGATT 3360
 TGATTTTATT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG 3540
 AAAATAGTCT CATCTCTTTT TTCTCAAAAT GAGATCCGTG TTTTATTTTA GCATTAAAT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720
 GAAAGTTGT GTGTGCTGTC TTTTGTGTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780
 TTATACCTTC TAATAAATTT GCAGTTTCAT TCTTTCTGTT TGTGCAAAWG GWMCTAMARM 3840
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCACTTCGGG 3900
 TGGGGCGCG GGGCCACGT AGGTACGGCG ACCACGGGG CCCAAACGGG ACCCCAGAAG 3960
 GAAACCTG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCGCCGG 4020
 GGAAACCGCA GAGTGTGCG TAAACACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
 GGACTCAACC AGSAGGACCC AAGGGAACCC GATAGAGTAC G

A151 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MWLLGPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFDKSD 60
 EKECPKAKSK CGPTFFPCAS GIHCCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNLGLCIDKSF ICDGQNNQCD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180
 VIFVLVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240
 YVASQAEQNA SEVSGSPSYS EALLDQRPFAW YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEV

A152 DNA SEQUENCE

Gene name: Transmembrane protease, serine 2 (TMPRSS2)
 Unigene number: Hs.105807
 Probeset Accession #: T48536
 Nucleic Acid Accession #: NM_005656.1
 Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GTCATATGTA ACATTCCAGA TACCTATCAT TACTCGATGC TGTGATAAAC AGCAAGATGG 60
 CTTTGAACCTC AGGGTCAACCA CCAGCTATTG GACCTTACTA TGAAAAACCAT GGATACCAAC 120
 CGGAAACCCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG 180
 CTCAGTACTA CCCGTCCCCC GTGCCCCAGT ACGCCCCGAG GGTCTGACG CAGGCTTCCA 240
 ACCCCGTCGT CTGCACGCAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAAGACTA 300
 AGAAAGCACT GTGCATCAC TTAGCCCTGG GGACCTTCCT CGTGGGAGCT GCGCTGGCCG 360
 CTGGCCTACT CTGGAAGTTC ATGGGCAGCA AGTGCTCCAA CTCTGGGATA GAGTGGGACT 420
 CCTCAGGTAC CTGCATCAAC CCCTCTAACT GGTGTGATGG CGTGTACAC TGCCCCGGCG 480
 GGGAGGACGA GAATCGGTGT GTTCGCCTCT ACGGACCAAA CTTCATCCTT CAGATGTACT 540
 CATCTCAGAG GAAGTCTTGG CACCCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600
 GGGCGGCTG CAGGGACATG GGCTATAAGA ATAATTTTTA CTCTAGCCAA GGAATAGTGG 660
 ATGACAGCGG ATCCACCAGC TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT 720
 ATAAAAAATC TATCCACAGT GATGCCCTGT CTTCAAAGAG AGTGGTTTCT TTACGCTGTT 780
 TAGCCTGCGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG 840
 CGTCCCGGG GGCCTGGCCC TGGCAGGTCA GCCTGCAGT CCAGAACGTC CACGTGTGCG 900
 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCGCG CCACTGCGTG GAAAAACCTC 960
 TTAACAATCC ATGGCATTGG ACGGCATTTG CGGGGATTTT GAGACAATCT TTCAATGTCT 1020
 ATGGAGCCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA 1080
 AGAACAAATGA CATTCGCTG ATGAAGCTGC AGAAGCCTCT GACTTCAAC GACCTAGTGA 1140
 AACCACTGTG TCTGCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT 1200
 CCGGTGGGG GGCACCCGAG GAGAAAGGGA AGACCTCAGA AGTGTGAAC GGTGCCAAG 1260
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAAC CTGATCACAC 1320
 CAGCATGAT CTGTGCCCGG TTCCTGCAGG GGAACGTCGA TTCTTGCCAG GGTGACAGT 1380
 GAGGGCCTCT GGTCACTTCG AACACAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440
 GTTCTGGCTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTTCAGG 1500
 ACTGGATTTA TCGACAATGT AAGGCAACG GCTAATCCAC ATGGTCTTCG TCCTTGACGT 1560
 CGTTTACAA GAAACAATG GGGCTGGTTT TGCTTCCCG TGCATGATT ACTCTTAGAG 1620
 ATGATTGAGA GGTCACTTCA TTTTATTAA ACAGTGAAC TGTCTGGCTT TGGCACTCTC 1680
 TGCCATACTG TGCAGGCTGC AGTGGCTCCC CTGCCAGGCC TGCTCTCCCT AACCCCTTGT 1740

CCGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGGAAGAGG 1800
 GTTGGAGGCT GCCCCATTG AGATCTTCCT GCTGAGTCCT TTCCAGGGGC CAATTTTGA 1860
 TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920
 GGAAGAGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTTGGTAGTG 1980
 TCCCAGCCT ACTTACAAAG GGGATTTTGC TGATGGGTTC TTAGAGCCTT AGCAGCCCTG 2040
 GATGGTGGCC AGAAATAAAG GGACCAGCCC TTCATGGGTG GTGACGTGGT AGTCACTTGT 2100
 AAGGGGAACA GAAACATTTT TGTTCTTATG GGGTGAGAAAT ATAGACAGTG CCCTTGGTGC 2160
 GAGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220
 CATTGGGTGG GGCTCCTGGG AGGGAGACTC AGCCTTCCTC CTCATCCTCC CTGACCCTGC 2280
 TCCTAGCACC CTGAGAGTG AATGCCCTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340
 ATGTCGGCCT CTTCAGGCCT GATAGTCATT GAAATGAG GTCCATGGGG GAAATCAAGG 2400
 ATGCTCAGTT TAAGGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
 CTGAGTTCAA AGCCATCTT

A153 Protein sequence:

Gene name: Transmembrane protease, serine 2 (TMPRSS2)
 Unigene number: Hs.105807
 Probeset Accession #: T48536
 Protein Accession #: NP_005647.1
 Signal sequence: none found
 Transmembrane domains: 85-107
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYFSPVP QYAPRVLTQA 60
 SNPVVCTQPK SPSGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120
 DSSGTCINPS NWCDGVSHCP GGEDENRCVR LYGPNFILQM YSSQRKSWHP VCQDDWNENY 180
 GRAACRDMGY KNFYSQGI VDDSGSTSM KLNTSAGNVD IYKLYHSDA CSSKAVVSLR 240
 CLACGVNLNS SRQSRIVGGE SALPGAWPWQ VSLHVQNVHV CGGSIITPEW IVTAAHCVKE 300
 PLNNPWHWTA FAGILRQSFY FYGAGYQVQK VISHPNYDSK TKNNIDIALMK LQKPLTFNDL 360
 VKPVCPLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLETQRC NSRYVYDNL 420
 TPAMICAGFL QGNVDSQCGD SGGPLVTSNN NIWWLIGDTS WSGGCAKAYR PGVYGNVMVF 480
 TDWIYRQMK NG

A154 DNA SEQUENCE

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
 Unigene number: Hs.129179
 Probeset Accession #: A1694767
 Nucleic Acid Accession #: A1694767
 Coding sequence: 130-1086 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CAGAGAGGCT GTATTTTCACT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60
 GGGGTACAC ATTCTTCCA TACGGTTGAG CCTCTACCTG CTTGGTCTG GTACACAGTTC 120
 AGCTTCTTCA TGATGGTGA TCCCAATGGC AATGAATCCA GTGCTACATA CTTTCACTCA 180
 ATAGGCTCC CTGGTTTAGA AGAGGCTCAG TTCTGGTTGG CCTTCCATT GTGCTCCCTC 240
 TACCTTATTG CTGTGCTAGG TAACTTGACA ATCATCTACA TTGTGCGGAC TGAGCACAGC 300
 CTGCATGAG CCATGTATAT ATTCTTTGC ATGCTTTCAG GCATTGACAT CCTCATCTCC 360
 ACCCTATCCA TGCCCAAAAT GCTGGCCATC TTCTGGTTCA ATTCCACTAC CATCCAGTTT 420
 GATGCTTGTC TGCTACAGAT GTTTGCCATC CACTCCTTAT CTGGCATGGA ATCCACAGTG 480
 CTGCTGGCCA TGCTTTTGA CCGCTATGTG GCCATCTGTG ACCCACTGCG CCATGCCACA 540
 GTACTTACGT TGCTCTGTGT CACCAAAATT GGTGTGGCTG CTGTGGTGGC GGGGGCTGCA 600
 CTGATGGCAC CCCTTCTGTG CTTTCATCAAG CAGCTGCCCT TCTGCCGCTC CAATATCCTT 660
 TCCATTCCT ACTGCCATCA CCAAGATGTC ATGAAGCTGG CCTGTGATGA TATCCGGGTC 720
 AATGTCGTCT ATGGCCTTAT CGTCATCATC TCCGCCATTG GCCTGGACTC ACTTCTCATC 780
 TCCTTCTCAT ATCTGCTTAT TCTTAAGACT GTGTTGGGCT TGACACGTGA AGCCAGGCC 840
 AAGGCATTG GCACCTTGGT CTCTCATGTG TGTGCTGTGT TCATATTCTA TGTACCTTTC 900
 ATTGGATTGT CCATGGTGCA TCGCTTAGC AAGCGGCGTG ACTCTCCACT GCCCGTCATC 960
 TTGGCCAATA TCTATCTGCT GGTTCCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020
 ACAAGGAGA TTGCAGAGCG CATCCTTCGA CTTTCCATG TGGCCACACA CGCTTCAGAG 1080
 CCCTAGGTGT CAGTGATCAA ACTTCTTTTC CATTGAGAGT CCTCTGATTC AGATTTTAAT 1140
 GTTAACATT TGGAGAGCAG TATTCAGAAA AAAAATTTC TTAATAAAAA TACAATCAG 1200
 ATCCTTCAAA TATGAACTG GTTGGGGAAT CTCCATTTT TCAATATTAT TTTCTTCTTT 1260
 GTTTTCTGC TACATATAAT TATTAATACC CTGACTAGGT TGTGGTTGGA GGGTTATTAC 1320
 TTTTCATTTT ACCATGCACT CCAATCTAA ACTGCTTCTA CTGATGGTTT ACAGATTCT 1380
 GAGATAAGAA TGGTACATCT AGAGAACATT TGCCAAAGGC CTAAGCACAG CAAAGGAAAA 1440
 TAAACACAGA ATATAATAAA ATGAGATAAT CTAGCTTAAA ACTATAACTT CCTCTCAGA 1500
 ACTCCCAACC ACATTGGATC TCAGAAAAAT ACTGTCTTCA AAATGACTTC TACAGAGAAG 1560
 AAATAATTTT TCCTCTGAGC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620
 AGAGTACATT TACCTACGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT 1680
 ATGAGACCTG TTTTCTCTAT TTAATTTTCT TATCAACCTT TTAATTAGGC AAAGATATTA 1740
 TTAGTACCTT CATGTAGCC ATGGGAAAA TGAATTTTCT TGGGGATCAG TGAATTAAT 1800
 GGGGTCATAC AAGTATAAAA ATTAATAAAA AAAGACTTCA TGCCCAATCT CATATGATGT 1860
 GGAAGAACTG TTAAGAGAC CAACAGGGTA GTGGGTAGA GATTTCAGA GTCTTACATT 1920
 TTCTARAGGA GGTATTTAAT TTCTTCTCAC TCATCCAGTG TTGATTTAG GAATTTCTGT 1980
 GCAACAGAAC TCATGGCTTT AATCCCACTA GCTATTGCTT ATTGTCTTGG TCCAATTGCC 2040
 AATTACCTGT GTCFTGGAAG AAGTGATTTT TAGGTTTACC ATTATGGAAG ATTCCTATTC 2100
 AGAAAGTCTG CATAGGGCTT ATAGCAAGTT ATTTATTTT AAAAGTTCCA TAGGTGTTTC 2160
 TGATAGGAC TGAGGTATTG GAGCCACAG TTATGATGGG AAGTATGGAA TGGCAGGTGT 2220
 TGAAGATAAC ATTGGCCTTT TGAGTGTGAC TCGTAGCTGG AAAGTGAGGG AATCTCAGG 2280

ACCATGCTTT ATTTGGGGCT TTGTGCAGTA TGGAACAGGG ACTTTGAGAC CGGGAAAGCA 2340
 ATCTGACTTA GGCATGGGAA TCAGGCATT TTGCTTCTGA GGGGCTATTA CCAAGGGTTA 2400
 ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAAACTC AAATTACATA 2460
 TACTAAAACA TGTGATCATA TATGTGGTAA GTTTCATTTT CTTTTTCAAT CCTCAGGTTT 2520
 CCTGATATGG ATTCCTATNA CATGCTTTCA TCCCTTTTG TAATGGATAT CATATTTGGA 2580
 AATGCTTATT TAATACTTGT ATTTGCTGCT GGACTGTAAG CCCATGAGGG CACTGTTTAT 2640
 TATTGAATGT CATCTCTGTT CATCATTGAC TGCTCTTTGC TCATCATTGA ATCCCCAGC 2700
 AAAGTGCCTA GAACATAATA GTGCTTATGC TTGACACCGG TTATTTTTC TCAAACCTGA 2760
 TTCCTTCTGT GCTGAACACA TAGCCAGGCA ATTTTCCAGC CTTCTTTGAG TTGGGTATTA 2820
 TTAAATTTTA GCCATTACTT CCAATGTGAG TGGAAAGTAC ATGTGCAATT TTTATACCTG 2880
 GCTCATAAAA CCTCCCATG TGCAGCCTTT CATGTTGACA TTAATGTGA CTTGGGAAGC 2940
 TATGTGTTAC ACAGAGTTAA TTAACNGAA AGGCCTGGNA ATTTTTTGN ANNAAACTG 3000
 TGGCCNNGAG GCCCNCAACC CTTTTNNNA ATTTGGCAAN NTCCCACTT GTANTTTGGT 3060
 AAGGAGGCCA GTTGATTAAG TGAAAAATAA AGTACTATTG TGTC

A155 PROTEIN SEQUENCE

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
 Unigene number: Hs.129179
 Protein Accession #: not available
 Signal sequence: none found
 Pfam domain: 7tm_1 [43-293]
 Transmembrane domains: 29-51, 57-79, 82-104, 203-225, 239-261, 273-295
 Cellular Localization: not determined

1 11 21 31 41 51
 | | | | |
 MVDPNNGNESS ATYFILIGLP GLEEAQFWLA FPLCSLYLIA VLGNLTIIYI VRTEHSLHEP 60
 MYIFLCMLSG IDILISTSSM PKMLAIFWFN STTIQFDACL LQMFALHSLS GMESTVLLAM 120
 AFDRYVAICH PLRHATVLTPL PRVTKIGVAA VVRGAALMAP LPVFIKQLPF CRSNILSHSY 180
 CLHQDVMKLA CDDIRNVNVY GLIVIISAIG LDSLLISFSY LLILKTVLGL TREAQAKAFG 240
 TCVSHVCAVF IFYVPFIFLS MVHRFSKR RD SPLPVILANI YLLVFPVLNP IVYGVKTKEI 300
 RQRILRLFHV ATHASEP

A156 DNA SEQUENCE

Gene name: vasoactive intestinal peptide receptor 1
 Unigene number: Hs.198726
 Probeset Accession #: X77777
 Nucleic Acid Accession #: NM_004624.1
 Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)

TCGGAGCCTG CGGAGGGTGG TGGTGGTGGT GGTGGTGGCC CTCGCCCGCC TCACTCATGC 60
 CTCCTCCTCC TCTGCTCTCG CTCAGGCGCC TCGGTGGCGG TTGGTGGCGG GTTACGCGGC 120
 TGGTGGTCCG GCGCGGCGGG GCTCGCTCTC GGGGAGGCGG GGGCGGATCT CGCGGCGCAG 180
 GCGGCGGCGG CCGAGGTGGG GTGCGCGCGG GGAGGCGGCT CGAGCTTCGT GCTGCGCGCT 240
 CGCTCTTGGG CTCCTCGCTG CAGGAGGAGT GTGACTATGT GCAGATGATC GAGGTGCAGC 300
 ACAAGCAGTG CCTGGAGGAG GCCCAGCTGG AGAATGAGAC AATAGGCTGC AGCAAGATGT 360
 GGGACAACCT CACTGCTGG CCAGCCACCC CTCGGGGCCA GGTAGTTGTC TTGGCTGTGC 420
 CCTCATCTT CAAGCTCTTC TCCTCCATTC AAGGCCGCAA TGTAAGCCGC AGCTGCACCG 480
 AGCAAGGCTG GACGCACCTG GAGCCTGGCC CGTACCCCAT TGCCGTGGT TTGGATGACA 540
 AGGCAGCGAG TTTGGATGAG CAGCAGACCA TGTCTACCG TTCTGTGAAG ACCGGCTACA 600
 CCATTGGCTA CGGCTGTGCC CTCGCCACCC TTCTGGTGGC CACAGCTATC CTGAGCCTGT 660
 TCAGGAAGCT CCACTGCACG CGGAACCTACA TCACACATGCA CCTCTTCATA TCCTTCATCC 720
 TGAGGCGTGC CGCTGTCTTC ATCAAAGACT TGGCCCTCTT CGACAGCGGG GAGTCGGACC 780
 AGTGCTCCGA GGGCTCGGTG GGCTGTAAGG CAGCCATGGT CTTTTTCCAA TATTGTGTCA 840
 TGGCTAACTT CTCTGGCTG CTGGTGGAGG GCCTCTACCT GTACACCCCTG CTTGCCGTCT 900
 CCTTCTTCTC TGAGCGGAAG TACTTCTGGG GGTACATACT CATCGGCTGG GGGGTACCCA 960
 GCACATTAC CATGGTGTGG ACCATCGCCA GGATCCATT TGAGGATTAT GGTCTGTCTCA 1020
 GGTGCTGGGA CACCATCAAC TCCTCACTGT GGTGGATCAT AAAGGGCCCC ATCCTCACCT 1080
 CCATCTTGGT AAATTCATC CTGTTTATTT GCATCATCCG AATCCTGCTT CAGAACTGC 1140
 GGCCCCCAGA TATCAGGAAG AGTGACAGCA GTCCATACTC AAGGCTAGCC AGGTCCACAC 1200
 TCCTGCTGAT CCCCCTGTTT GGAGTACACT ACATCATGTT CGCCTTCTTT CCGGACAATT 1260
 TTAAGCCTGA AGTGAAGATG GTCTTTGAGC TCGTCGTGGG GTCTTTCCAG GGTTTTGTGG 1320
 TGGCTATCCT CTACTGCTTC CTCATAGGTG AGGTGCAGGC GGAGCTGAGG CGGAAGTGGC 1380
 GCGGCTGGCA CCTGCAGGGC GTCTTGGGCT GGAACCCCAA ATACCGGCAC CCGTCGGGAG 1440
 GCAGCAACGG CGCCACGTGC AGCACGCGG TTTCCATGCT GACCCGCGTC AGCCAGGTG 1500
 CCGCGCGCTC CTCAGCTTC CAAGCCGAAG TCTCCCTGGT CTGACCACCA GGATCCAGC 1560
 CCAAGCGGCC CCTCCCGCCC CTTCCCACTC GCAGCAGAGC CCGGGGACAG AGGCCTGCCC 1620
 GGGCGCGCCA GCCCGGCCCC TGGGCTCGGA GGCTGCCCCC GGCCCCCTGG TCTCTGGTCC 1680
 GGACACTCCT AGAGAAGCGCA GCCCTAGAGC CTGCCTGGAG CGTTTCTAGC AAGTGAGAGA 1740
 GATGGGAGCT CCTCTCTGG AGGATGCAGG TGGAACTCAG TCATTAGACT CCTCTCCAA 1800
 AGGCCCCCTA CGCCAAATCAA GGGCAAAAAG TCTACATACT TTATCCTGTA CTCTGCCCCC 1860
 TGCTGGCTCT TCTGCCCAAT TGGAGGAAAG CAACCGGTGG ATCCTCAAAC AACACTGGT 1920
 TGACCTGAGG GCAGAAAGGT TCTGCCCGGG AAGGTACACA GCACCAACAC CACGGTAGTG 1980
 CCTGAAATTT CACCATTGCT GTCAAGTTCC TTTGGGTAA GCATTACCAC TCAGGCATT 2040
 GACTGAAGAT GCAGCTCACT ACCCTATTCT CTCTTTACGC TTAGTTATCA GCTTTTAAA 2100
 GTGGGTATT CTGGAGTTT TGTGGGAGA GCACACCTAT CTTAGTGGTT CCCACCGAA 2160
 GTGGACTGGC CCCTGGGTCA GTCTGGTGGG AGGACGGTGC AACCCAAGGA CTGAGGGACT 2220
 CTGAAGCTC TGGGAAATGA GAAGGCAGCC ACCAGCGAAT GCTAGGTCTC GGACTAAGCC 2280
 TACCTGCTCT CCAAGTCTCA GTGGCTTCAT CTGTCAAGTG GGAATCAAGA GACTGCCCTC CTTGTCCACC 2340
 TTCTTATCTC TCTGTGCTGT GGAAGCAACA GGAATCAAGA GACTGCCCTC CTTGTCCACC 2400
 CACCTATGTG CCAACTGTTG TAACTAGGCT CAGAGATGTG CACCTAGGG CTCTGCACGA 2460

AAGCAGATCC TCACCCCTGCT ACACATACAG GATTTGAAC T CAGATCTGTC TGATAGGAAT 2520
 GTGAAAGCAC GGACTCTTAC TGCTAACTTT TGTGTATCGT A ACCAGCCAG ATCTCTTGG 2580
 TTATTTGTTT ACCACTTGTG TTATTAATGC CATTATCCCT GAATTCCTCT TGCCACCCCA 2640
 CCCTCCCTGG AGTGTGGCTG AGGAGGCTC CATCTCATGT ATCATCTGGA TAGGAGCCTG 2700
 CTGGTCACAG CCTCTCTGTG CTGCCCTTCA CCCCAGTGGC CACTCAGCTT CCTACCCACA 2760
 CCTCTGCCAG AAGATCCCTT CAGGACTGCA ACAGGCTTGT GCAACAATAA ATGTTGGCTT 2820
 GGAAAAA AAAA

A157 Protein sequence:

Gene name: vasoactive intestinal peptide receptor 1
 Unigene number: Hs.198726
 Probeset Accession #: X77777
 Protein Accession #: JC2195
 Signal sequence: none found
 Transmembrane domains: 181-202, 214-236, 255-277, 290-311, 332-354, 377-399, 408-430
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MPPFPLLSLR RLGGGWSAVT RLVVAAAGAR SRGGRGGRG AGGGGRGGVA RRRRLRLRAA 60
 RSLLGSSSLQE ECDYVQMIEV QHKQCLEEAQ LENETIGCSK MWDNLTCPWA TPRGQVVVLA 120
 CPLIFKLFSS IQGRNVSRSR TDEGWHLEP GPYPACGLD DKAASLDEQQ TMFYGSVKTG 180
 YTIYGLSLA TLVATALLS LFRKLHCTRN YIHMHLFISF ILRAAAVFIK DLALFDSGES 240
 DQCEGSGVGC KAAMVFFQYC VMANFFWLLV EGLYLYTLA VSFFSERKYF WGYILIGWGV 300
 PSTFTMWVTI ARIHFEDYGL LRCWDITNSS LWWIIGPIL TSILVNFIIF ICIIRILLQK 360
 LRPPDIRKSD SSPYSRLARS TLLLIPLFGV HYIMFAFFPD NFKPEVKMVF ELVVGSEFQGF 420
 VVAILYCFLN GEVQALRRK WRRWHLQGV L GWNPKYRHPS GGSNGATCST QVSMILTRVSP 480
 GARRSSSFQA EVSLV

A158 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Nucleic Acid Accession #: AL133619
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCGGAC CCCGGGCTCT 60
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCGGCA GAGCCCGCAG 120
 CTGAGGAGCA GCGACCGGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCTCTG 180
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCATGAGG AGATCGAGCA TCTGAAGCGG 240
 GAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCTCCCA GGCACACTCA 300
 ACCTGCGCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA 360
 GGGGGAACAC AGGACGGGGA GCCCTCCAG ACTGTCTTG CCCACTGGC TGCACTGGCC 420
 CCTGTATGCC AACCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGTACCTCT 480
 AGCCGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCAG TGCTGCTCTC GGAAGCCCA 540
 GGGCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGGT GCTCCCAAGA CCTCCCTCCT 600
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG 660
 CCTCAGATTG CTGCTGTGGC CAGGCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCCTGT TTCTTGGCCA CTGTGTCGAAG 840
 GCATCTCCCC ATCTGTACAG CGGCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900
 GCTCACTTCC CATATCTTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGGA 960
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCCT GGGCTCTCCC TTCCAGGGA 1020
 GACATGGAGA AGGGGGTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080
 CTGTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CTGTCAGTGC TGGGGACGCT 1140
 GACAGGACAC GGAAGAGGC CATGCTTTCC CTGCGGACCT GCTGTTCCAT GTGTCCCAAG 1200
 CCCTCCTGCT TTCCAGATGG CCCCTCAGGA AACCACTTT CCAGGGCTC TGCTCCCTTG 1260
 GGCCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320
 AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGG 1380
 GGCGGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440
 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGG 1500
 TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCAGA AGGCGGACCT GGAAGAGGAG 1560
 CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTGGGG TACAAGGGCA GGCAGAAAG 1620
 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAGGGC 1680
 AGGCAGATGG GGGCGGGGGC ACACCCCA ATGATCCTGC CCCTCCCTT CCGAAAGCCC 1740
 ACCCACTTA GGCAGTGCAG AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCCTGCAG 1800
 ACCCAAGAGC TGGCGCACT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860
 CCGGAGGAAG CTAGCTTTCC CAGGAGCCAA GAAGCCACGC ATTTCCCAA GGTCTCCACC 1920
 AAGAGCCTCT CCAAGAAATG CTTGAGCCCA CTTGTGGCG AGCGTGCCAT CTGCGCCGCA 1980
 CTGAAGCAGA CCCCAGAA CAACCTTTGCC GAGAGGCAGA AGAGGCTGCA GGCATGCGAG 2040
 AAACGGCGCC TGCATCGCTC AGTGCTTTGA

A159 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Protein Accession #: T43457
 Signal sequence: none found
 Transmembrane domains: 303-322
 Cellular Localization: not determined

	1	11	21	31	41	51	
5	MSGAGVAAAGT	RPPSSPTPGS	RRRRQRPSVG	VQSLRPQSPQ	LRQSDPQKRN	LDLEKSLQFL	60
	QQQHSEMLAK	LHEEIEHLKR	ENKGEPARGP	RPALPPQAH	TLPLPQHRNT	AINSSSTRLGS	120
	GGTQDGEPLQ	TVLAHLAALA	PVCQPSGYRF	WGTWTDAA	SRGWTMLCSQ	AQHVLLSGSP	180
	GPEVIAGRQV	ATGCSPLDPP	PSRAEMGRNP	WDSFPCPARSL	PQIAAVARPR	ISSPMALSPH	240
10	MLGAQGIWTH	SIQGSPLAIW	AATMGTKGGS	RVLFPCHLSK	ALPHPDSSGPH	PAQDPGLWSQ	300
	AHFPLSLGLG	LTSGGHLTGG	WSQPGNIAAG	AVPRALPSQ	DMEKGVGGP	FPSRCGNSSE	360
	LFWAKCGFSR	QPPQCSAGDA	DRTREEAMLS	LGTCCSMCPK	PSCFPDGPSP	NHLSRASAPL	420
	GARWVCINGV	WVEPGGPPSA	RLKEGSSRTH	RPGGKRGRLA	GGADTVRSP	ADSLSMSSSQ	480
	SVKSIANSAN	SQKARPPQG	SFNKQDSKAD	VSQKADLEEE	PLHNSKLDK	VPGVQQQARK	540
15	EKAEASNAGA	ACMGNSQHQG	RQMAGAHPP	MILPLPLRKP	TTLRQCEVLI	RELWNTNLLQ	600
	TQELRHLKSL	LEGSQRQAAA	PEEASFPRDQ	EATHFPKVST	KSLSKKCLSP	PVAERAILPA	660
	LKQTPKNFA	ERQKRLQAMQ	KRRLHRSVL				

A160 DNA SEQUENCE

Gene name: LIV-1 protein, estrogen regulated

Unigene number: Hs.79136

Probeset Accession #: U41060

Nucleic Acid Accession #: NM_012319.2

Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
30	CTCGTGCCGA	ATTGCGGCAG	AGACCGCGTG	TTCGCGCCTG	GTAGAGATTT	CTCGAAGACA	60
	CCAGTGGGCC	CGTGTGGAAC	CAAACTCTGC	CGCGTGGCCG	GGCCGTGGGA	CAACGAGGCC	120
	GCGGAGACGA	AGGCGCAATG	GCGAGGAAGT	TATCTGTAAT	CTTGATCTCT	ACCTTTGCC	180
	TCTCTGTAC	AAATCCCCTT	CATGAACATA	AAGCAGCTGC	TTTCCCCCAG	ACCACTGAGA	240
	AAATTAGTCC	GAATTGGGAA	TCTGGCATT	ATGTTGACTT	GGCAATTTCC	ACACGGCAAT	300
	ATCATCTACA	ACAGCTTTTC	TACCGCTATG	GAGAAAATAA	TTCTTTGTCA	GTTGAAGGGT	360
35	TCAGAAAATT	ACTTCAAAAT	ATAGGCATAG	ATAAGATTAA	AAGAATCCAT	ATACACCATG	420
	ACCACGACCA	TCATCTCAGC	CACGAGCATC	ACTCAGACCA	TGAGCGTCAC	TCGACCATG	480
	AGCATCACTC	AGACCACGAG	CATCACTCTG	ACCATGATCA	TCATCTCTAC	CATAATCATG	540
	CTGCTTCTGG	TAAAATAAAG	CGAAAAGCTC	TTTGCCCAAG	CCATGACTCA	GATAGTTCAG	600
	GTAAGAATCT	TAGAAACAGC	CAGGGGAAAG	GAGCTCACC	ACCAGAACAT	GCCAGTGGTA	660
40	GAAGGAATGT	CAAGGACAGT	GTTAGTGCTA	GTGAAGTGAC	CTCAACTGTG	TACAACACTG	720
	TCTCTGAAGG	AACTCACTTT	CTAGAGACAA	TAGAGACTCC	AAGACCTGGA	AAACTCTTCC	780
	CCAAAGATGT	AAGCAGCTCC	ACTCCACCCA	GTGTCACATC	AAAGAGCCGG	GTGAGCCGGC	840
	TGGCTGGTAG	GAAAACAAAT	GAATCTGTGA	GTGAGCCCGC	AAAAGGCTTT	ATGTATTCCA	900
	GAAACACAAA	TGAAAATCCT	CAGGAGTGTT	TCAATGCATC	AAAGCTACTG	ACATCTCATG	960
45	GCATGGGCAT	CCAGGTTCCG	CTGAATGCAA	CAGAGTTCAA	CTATCTCTGT	CCAGCCATCA	1020
	TCAACCAAAAT	TGATGCTAGA	TCTTGTCTGA	TTCATACAAG	TGAAAAGAAG	GCTGAAATCC	1080
	CTCCAAAGAC	CTATTCAATG	CAAAATAGCCT	GGGTTGGTGG	TTTTATAGCC	ATTTCCATCA	1140
	TCAGTTCTCT	GTCTCTGCTG	GGGGTTATCT	TAGTGCCCTC	CATGAATCGG	GTGTTTTTCA	1200
	AATTTCTCCT	GAGTTTCTCT	GTGGCACTGG	CCGTTGGGAC	TTTGAGTGGT	GATGCTTTTT	1260
50	TACACCTTCT	TCCACATTC	CATGCAAGTC	ACCACCATAG	TCATAGCCAT	GAAGAACCAG	1320
	CAATGGAAT	GAAAAGAGGA	CCACTTTTCA	GTCACTGTGC	TTCTCAAAAC	ATAGAAGAAA	1380
	GTGCTTATTT	TGATTTCCAG	TGGAAGGGTC	TAACAGCTCT	AGGAGGCTCG	TATTTATGTT	1440
	TTCTTGTGTA	ACATGTCCTC	ACATTGATCA	AACAATTTAA	AGATAAGAAG	AAAAAGAATC	1500
	AGAAGAAACC	TGAAAATGAT	GATGATGTGG	AGATTAAAG	GCAGTTGTCC	AGGTATGAAT	1560
55	CTCAACTTTT	AACAAATGAG	GAGAAAGTAG	ATACAGATGA	TCGAACTGAA	GGCTATTTAC	1620
	GAGCAGACTC	ACAAGAGCCC	TCCCCTTTTG	ATTCTCAGCA	GCCTGCAGTC	TTGGAAGAAG	1680
	AAGAGGTCAT	GATAGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GTACCCAGAG	1740
	GGTGCAAGAA	TAAATGCCAT	TCACATTTCC	ACGATACACT	CGGCCAGTCA	GACGATCTCA	1800
	TTCAACACCA	TCATGACTAC	CATCATATTC	TCCATCATCA	CCACCACCAA	AACCACCATC	1860
60	CTCAGCAGTA	CAGCCAGCGC	TACTCTCGGG	AGGAGCTGAA	AGATGCCGGC	GTCCGCACTT	1920
	TGGCTTGGAT	GGTGATAATG	GGTGATGGCC	TGCACAAATT	CAGCGATGGC	CTAGCAATTG	1980
	GTGCTGCTTT	TACTGAAGGC	TTATCAAGTG	GTTTAAAGTAC	TTCTGTGTCT	GTGTTCTGTC	2040
	ATGAGTTGCC	TCATGAATTA	GGTGACTTTG	CTGTTCTACT	AAAGGCTGGC	ATGACCGTTA	2100
	AGCAGGCTGT	CCTTTATAAT	GCATTGTCTG	CCATGCTGGC	GTATCTTGGA	ATGGCAACAG	2160
65	GAATTTTCT	TGGTCTTAT	GCTGAAAATG	TTTCTATGTG	GATATTGGA	CTTACTGCTG	2220
	GCTTATTCAT	GTATGTTGCT	CTGGTTGATA	TGGTACCTGA	AATGCTGCAC	AATGATGCTA	2280
	GTGACCATGG	ATGTAGCCGC	TGGGGGTATT	TCCTTTTACA	GAATGCTGGG	ATGCTTTTGG	2340
	GTTTGGGAAT	TATGTTACTT	ATTTCCATAT	TTGAACATAA	AATCGTGTTC	CGTATAAAT	2400
	TCATGTTAAG	GTTTAAATGC	TAGAGTAGCT	TAAAAAGTTG	TCATAGTTTC	AGTAGGTCAT	2460
70	AGGGAGATGA	GTTTGTATGC	TGTACTATGC	AGCGTTTAAA	GTTAGTGGGT	TTTGTGATTT	2520
	TTGTATTGAA	TATTGCTGTC	TGTTACAAAG	TCAGTTTAAAG	GTACGTTTTC	ATATTTAAGT	2580
	TATTTCTATC	TGGAGATAAA	ATCTGTATGT	GCAATTCACC	GGTATTACCA	GTTTATTATG	2640
	TAAACAAGAG	ATTTGGCATG	ACATGTTCTG	TATGTTTCAG	GGAAAATGT	CTTTAATGCT	2700
75	TTTTCAAGAA	CTAACACAGT	TATTCCTATA	CTGGATTTTA	GGTCTCTGAA	GAAGTCTGG	2760
	TGTTTAGGAA	TAAAGATGTG	CATGAAGCCT	AAAATACCAA	GAAAGCTTAT	ACTGAATTTA	2820
	AGCAAGAGAA	TAAAGAGAG	AAGAGAGAG	TCTGAGAATT	GGGGAGGCAT	AGATTCTTAT	2880
	AAAAATCACA	AAATTTGTTG	TAAATTAGAG	GGGAGAAATT	TAGAATTAA	TATAAAAGG	2940
	CAGAATTAGT	ATAGAGTACA	TTCAATTAAC	ATTTTGTGTC	GGATTATTTT	CCGTAATAAC	3000
	GTAGTGAGCA	CTCTCATATA	CTAATTAGTG	TACATTTAAT	TTGTATTAAT	ACAGAAATCT	3060
80	AAATATATTT	AATGAATTTA	AGCAATATAC	ACTTGACCAA	GAAATTTGGA	TTTCAAAATG	3120
	TTCTGTCGGG	TTATATACCA	GATGAGTACA	GTGAGTAGTT	TATGTATCAC	CAGACTGGGT	3180
	TATTGCAAG	TTATATATCA	CCAAAAGCTG	TATGACTGGA	TGTTCTGGTT	ACCTGGTTTA	3240
	CAAAATTATC	AGAGTAGTAA	AACTTTGATA	TATATGAGGA	TATTAAAACT	ACACTAAGTA	3300
	TCATTTGATT	CGATTTCAG	AGTACTTTGA	TATCTCTCAG	TGCTTCAGTG	CTATCATTTG	3360

GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCGTG GCATTCTCTA 3420
GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

A161 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
Unigene number: Hs.79136
Protein Accession #: NP_036451
Signal sequence: 1-21
Pfam domain: Zip[591-743]
Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745
Cellular Localization: plasma membrane

1	11	21	31	41	51	
MARKLSVILI	LTFALSVTNP	LHELKAAAPP	QTTEKISPNN	ESGINVDLAI	STRQYHLQQL	60
FYRYGENNSL	SVEGFRKLLQ	NIGIDKIKRI	HIHHDHDHHS	DHEHHSDBER	HSDHEHSDH	120
EHHSDDHSHS	HHNHAASGKN	KRKALCPDHD	SDSSGKDPNN	SQKGGAHRPE	HASGRRNVKD	180
SVSASEVTST	VYNTVSEGT	FLETIETPRP	GKLFPPKDVSS	STPPSVTSKS	RVSRLAGRKT	240
NESVSEPRKG	FMYSRNTKGN	PQECFNASKL	LTSHGMGIQV	PLNATEFNYL	CPAIIINQIDA	300
RSCLIHSTSEK	KAEIPPKTYS	LQIAWVGFI	AISIISFLSL	LGVILVPLMN	RVFFKFLLSF	360
LVALAVGTLG	GDAFLHLLPH	SHASHHSHS	HEEPAMEMKR	GPLFSLSSQ	NIEESAYFDS	420
TWKGLTALGG	LYPMFLVEHV	LTLIKQFKDK	KKKNQKKPEN	DDDVEIKKQL	SKYESQLSTN	480
EEKVDTDDRT	EGYLRADSQE	PSHFDSQPPA	VLEEEVEMIA	HAHPQEVYNE	YVPRGCKNKC	540
HSHFHDTLGG	SDDLIIHHHD	YHHILHHHHH	QNHHPHSHSQ	RYSRRELKDA	GVATLAWMVI	600
MGDGLHNFSD	GLAIGAAFTG	GLSSGLSTSV	AVFCHPELPE	LGDFAVLLKA	GMTVKQAVLY	660
NALSAMLAYL	GMATGIFIGH	YAENVSMWIF	ALTAGLFMYV	ALVDMVPEML	HNDASDHGCS	720
RWGYFFLQNA	GMLLGFGIML	LISIFEHKIV	PRINF			

A162 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.87223
Probeset Accession #: AA250737
Nucleic Acid Accession #: NM_001203
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
CGCGGGGGCGC	GGAGTCGGCG	GGGCGCTCGCG	GGACGCGGGC	AGTGCGGAGA	CCGCGGCGCT	60
GAGGACGCGG	GAGCGGGGAG	CGCAGCGCGG	GGGTGGAGTT	CAGCCTACTC	TTTCTTAGAT	120
GTGAAAGGAA	AGGAAGATCA	TTTCATGCCT	TGTTGATAAA	GTTTCAGACT	TCTGCTGATT	180
CATAACCAT	TGGCTCTGAG	CTATGACAAG	AGAGGAAACA	AAAAGTTAAA	CTTACAAGCC	240
TGCCATAAGT	GAGAAGCAAA	CTTCCTTGAT	AACATGCTTT	TGCGAAGTGC	AGGAAAATTA	300
AATGTGGGCA	CCAAAGAAAG	GGATGGTGAG	AGTACAGCCC	CCACCCCGCG	TCCAAAGGTC	360
TTGCGTTGTA	AATGCCACCA	CCATTGTCCA	GAAGACTCAG	TCAACAATAT	TTGCAGCACA	420
GACGATATAT	GTTTCACGAT	GATAGAAGAG	GATGACTCTG	GGTTGCGTGT	GGTCACTTCT	480
GGTTGCGTAG	GACTAGAAGG	CTCAGATTTT	CAGTGTCTGG	ACACTCCCAT	TCCTCATCAA	540
AGAAGATCAA	TTGAATGCTG	CACAGAAAGG	AACGAATGTA	ATAAAGACCT	ACACCCTACA	600
CTGCCTCCAT	TGAAAAACAG	AGATTTTGT	GATGGACCTA	TACACCACAG	GGCTTTACTT	660
ATATCTGTGA	CTGCTGTGAG	TTTGCTCTTG	GTCCTTATCA	TATTATTTTG	TTACTTCCGG	720
TATAAAAGAC	AAGAAACAG	ACCTCGATAC	AGCATTGGGT	TAGAACAGGA	TGAAACTTAC	780
ATTCTCTCTG	GAGAATCCCT	GAGAGACTTA	ATTGAGCAGT	CTCAGAGCTC	AGGAAGTGGA	840
TCAGCGCTCC	CTCTGCTGGT	CCAAGGACT	ATAGCTAAGC	AGATTTCAGT	GGTGAAACAG	900
ATTGGAAGAG	GTGCTATGG	GGAAGTTTGG	ATGGGAAAGT	GGCGTGCGCA	AAAGGTAGCT	960
GTGAAAGTGT	TCTTCACCAC	AGAGGAAGCC	AGCTGGTTCA	GAGAGACAGA	AATATATCAG	1020
ACAGTGTGTA	TGAGGCATGA	AAACATTTTG	GGTTTCATTG	CTGCAGATAT	CAAAGGGACA	1080
GGGTCTGGGA	CCCAATTTGA	CCTAATCACA	GACTATCATG	AAAATGGTTC	CCTTTATGAT	1140
TATCTGAAGT	CCACCACCTT	AGACGCTAAA	TCAATGCTGA	AGTTAGCCTA	CTCTTCTGTC	1200
AGTGGCTTAT	GTCAATTACA	CACAGAAATC	TTTAGTACTC	AAGGCACACC	AGCAATTGCC	1260
CATCGAGATC	TGAAAAGTAA	AAACATTCTG	GTGAAGAAAA	ATGGAACCTG	CTGTATTGCT	1320
GACCTGGGCC	TGGCTGTTAA	ATTTATTAGT	GATACAAATG	AAGTTGACAT	ACCACCTAAC	1380
ACTCGAGTTG	GCACCAACAG	CTATATGCCT	CCAGAAGTGT	TGGACGAGAG	CTTGAACAGA	1440
AATCACTTCC	AGTCTTACAT	CATGGCTGAC	ATGTATAGTT	TTGGCCTCAT	CCTTTGGGAG	1500
GTGTCTAGGA	GATGTGTATC	AGGAGGTATA	GTGAAGAAGT	ACCAGCTTCC	TTATCATGAC	1560
CTAGTGCCCA	GTGACCCCTC	TTATGAGGAC	ATGAGGGAGA	TTGTGTGCAT	CAAGAAGTTA	1620
CGCCCTCAT	TCCCAACCGG	GTGGAGCAGT	GATGAGTGTC	TAAGGCAGAT	GGGAAAACCT	1680
ATGACAGAAT	GCTGGGCTCA	CAATCCTGCA	TCAAGGCTGA	CAGCCCTGCG	GGTTAAGAAA	1740
ACACTTGCCA	AAATGTCAGA	GTCCAGGAC	ATTAACTCT	GATAGGAGAG	GAAAAGTAAG	1800
CATCTCTGCA	GAAAGCCAA	AGGTACTCTT	CTGTTTGTGG	GCAGAGCAAA	AGACATCAAA	1860
TAAGCATCAA	CAGTACAAGC	CTTGAACATC	GTCCTGCTTC	CCAGTGGGTT	CAGACCTCAC	1920
CTTTGAGGGA	GCGACCTGGG	CAAAGACAGA	GAAGCTCCCA	GAAGGAGAGA	TTGATCCGTG	1980
TCTGTTTGTA	GGCGGAGAAA	CCGTTGGGTA	ACTTGTTCAC	GATATGATGC	AT	

A163 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.72472 / Hs.87223
Probeset Accession #: AA250737 / U89326
Protein Accession #: NP_001194
Signal sequence: 1-13
Transmembrane domains: 128-144
PFAM domains: activin_receptor [30-111], protein kinase [204-491]
Cellular Localization: plasma membrane

	1	11	21	31	41	51			
5	MLLR	SAGKLN	VGTKKEDGES	TAPT	PRPKVL	RCKCHHHCPE	DSVNNICSTD	GYCFTMIEED	60
	DSGL	PVVTSG	CLGLESGDFQ	CRDT	PIPHQR	RSIECCTERN	ECNKDLHPTL	PPLKNRDFVD	120
	GPIH	HRALLI	SVTVCSLLLV	LIIL	FCYFRY	KRQETRPRYS	IGLEQDETYI	PPGESLRDLI	180
	EQSQ	SSSGSGS	GLPLLVRTI	AKQI	QMVKQI	GKGRYGEVWM	GKWRGEKVAV	KVFFTTEAS	240
	WFRE	TEIYQT	VLMRHNILG	FIAADI	KGTG	SWTQLYLITD	YHENGSLYDY	LKSTTLDAKS	300
10	MLKL	AYSSVS	GLCHLHTEIF	STQK	PAIAH	RDLSKNILV	KKNGTCCCIAD	LGLAVKFISD	360
	TNEVD	IPPNP	RVGTRKYMPP	EVLD	ESLNRN	HFQSYIMADM	YSFGLILWEV	ARRCVSGGIV	420
	EEYQL	PHYHDL	VPBDPSYEDM	REIV	CIKKLR	PSFPNRWSSD	ECLRQMGKLM	TECWAHPAS	480
	RLTAL	RVKKT	LAKMSESQDI	KL					

A164 DNA sequence

15	Gene name:	ESTs
	Unigene number:	Hs.157601
	Probeset Accession #:	W07459
	Nucleic Acid Accession #:	AC005383
20	Coding Sequence:	328-2751 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51		
25	GACAGT	GTTC	GCGGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGCGTAGAAG	TGAAGTACTT	60
	TTTTATT	TGCG	AGACCTGGGC	CGATGCCGCT	TTAAAAACG	CGAGGGGCTC	TATGCACCTC	120
	CCTGGCGGTA	GTTCCTCCGA	CCTCAGCCGG	GTCGGGTCTG	GCCGCCCTCT	CCCAGGAGAG		180
	ACAAACAGGT	GTCCCACTG	GCAGCCGCGC	CCCGGGCGCC	CCTCCTGTGA	TCCCGTAGCG		240
	CCCCCTGGCC	CGAGCCGCGC	CCGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG		300
	TCGCCGCTCT	CCTTCCGTTA	TATCAACATG	CCCCCTTCC	TGTTGCTGGA	GGCCGTCTGT		360
30	GTTTTCTCTGT	TTTCCAGAGT	GCCCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAGCAA		420
	GAAACCATCG	GGAAGATTTC	AGCTGCCAGC	AAAATGATGT	GGTGCTCGGC	TGCAGTGGAC		480
	ATCATGTTTC	TGTTAGATGG	GTCTAACAGC	GTCGGGAAAG	GGAGCTTTGA	AAGGTCCAAG		540
	CACTTTGCCA	TCACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA		600
	GCATTCAGT	TCAGTTCCAC	TCCTCATCTG	GAATTCCTCT	TGGATTCTT	TTCAACCCAA		660
35	CAGGAAGTGA	AGGCAAGAAT	CAAGAGGATG	GTTTTCAAAG	GAGGGCGCAC	GGAGACGGAA		720
	CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCTCTGAG	GCAGAAATGC	TTCTGTGCCC		780
	CAGATCCTCA	TCATCGTCA	TGATGGGAAG	TCCCAGGGGG	ATGTGGCACT	GCCATCCAAG		840
	CAGCTGAAGG	AAAGGGGTGT	CACGTGTGTT	GCTGTGGGGG	TCAGGTTTCC	CAGGTGGGAG		900
40	GAGCTGCATC	CACCTGGCCG	CGAGCCTAGA	GGGCAGCACG	TGCTGTGTCG	TGAGCAGGTG		960
	GAGGATGCCA	CCAACGGCCT	CTTCAGACCC	CTCAGCAGCT	CGGCCATCTG	CTCCAGCGCC		1020
	ACGCCAGACT	GCAGGGTCTG	GGCTCACCCC	TGTGAGCACA	GGACGCTGGA	GATGGTCCGG		1080
	GAGTTCTGCTG	GCAATGCCCG	ATGCTGGAGA	GGATCGCGGC	GGACCTTTGC	GGTGTCTGGT		1140
	GCACACTGTC	CCTTCTACAG	CTGGAAGAGA	GTGTTCTTAA	CCCACCTGTC	CACCTGCTAC		1200
	AGGACCACCT	GCCCAGGGCC	CTGTGACTCG	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT		1260
45	CCAGAAGGAC	TGGACGGCTA	CCAGTGCCCTC	TGCCCGCTGG	CCTTGGAGG	GGAGGCTAAC		1320
	TGTGCCCTGA	AGCTGAGCCT	GGAATGCAGG	GTCGACCTCC	TCTTCTCTGT	GGACAGCTCT		1380
	GCGGGCACCA	CTCTGGACGG	CTTCTGCGG	GCCAAAGTCT	TCGTGAAGCG	GTGTTGTGCG		1440
	GCGGTGCTGA	GCGAGGACTC	TGCGGCCCGA	GTGGGTGTGG	CCACATACAG	CAGGGAGCTG		1500
	CTGGTGGCGG	TGCTGTGGGT	GGAGTACCAG	GATGTGCTTG	ACCTGGTCTG	GAGCCTCGAT		1560
50	GGCATTCCTC	TCCCTGGTGG	CCCCACCTTG	ACGGGCAGTG	CCTTGCAGCA	GGCGGCAGAG		1620
	CGTGGCTTCG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAGT	GGTGGTTTTG		1680
	CTCACTGAGT	CACACTCCGA	GGATGAGGTT	GCGGGCCGAG	CGCGTACAGC	AAGGGCGCGA		1740
	GAGCTGTCTC	TGCTGGGTGT	AGGCAGTGAG	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA		1800
	GGCAGCCCAA	AGCATGTATG	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT		1860
55	GAGCTGCAGG	GGAAGCTGTG	CAGCCGGCAG	CGGCCAGGGT	GCCCGACACA	AGCCCTGGAC		1920
	CTCGTCTTCA	TGTTGGACAC	CTCTGCCTCA	GTAGGGCCCG	AGAATTTTGC	TCAGATGCAG		1980
	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGACGTGAC	ACAGGTCCGC		2040
	CTGGTGGTGT	ATGGCAGCCA	GGTGCAACT	GCCCTCGGGC	TGGACACCAA	ACCCACCCGG		2100
60	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC		2160
	ACCGCCCTGC	TGCACATCTA	TGACAAAGTG	ATGACCGTCC	AGAGGGGTGC	CCGGCCTGGT		2220
	GTCCCCAAG	CTGTGGTGGT	GCTCACAGGC	GGGAGAGGCG	CAGAGGATGC	AGCCGTTTCT		2280
	GCCCCAGAAG	TGAGGAACAA	TGGCATCTCT	GTCTTGGTCT	TGGGCGTGGG	GCCTGTCTTA		2340
	AGTGAGGGTC	TGCGGAGGCT	TGCAGGTCCC	CGGGATTCCC	TGATCCACGT	GGCAGCTTAC		2400
65	GCCGACCTGC	GGTACCACCA	GGACGTGCTC	ATTGAGTGGC	TGTGTGGAGA	AGCCAAGCAG		2460
	CCAGTCAACC	TCTGCAAAAC	CAGCCCGTGC	ATGAATGAGG	GCAGCTGCGT	CCTGCAGAAT		2520
	GGGAGCTACC	GCTGCAAGTG	TGGGATGGC	TGGGAGGGCC	CCCACTGCGA	GAACCGTGAG		2580
	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	GGATGGATT	TTGAGACGCC	CCTGAGGCAC		2640
	ATGGCTCCCG	TGCAGGAGGG	CAGCAGCCGT	ACCCCTCCCA	GCAACTACAG	AGAAGGCCTG		2700
70	GGCATCTGAA	TGGTGCTTAC	CTTCTGGAAT	GTCTGTGCCC	CAGGTCCTTA	GAATGTCTGC		2760
	TTCCCGCCGT	GGCCAGGACC	ACTATTCTCA	CTGAGGGAGG	AGGATGTCCC	AACTGCAGCC		2820
	ATGCTGCTTA	GAGACAAGAA	AGCAGCTGAT	GTCAACCCCA	AACGATGTTG	TTGAAAAGTT		2880
	TTGATGTGTA	AGTAAATACC	CACCTTCTGT	ACCTGCTGTG	CCTTGTGTAG	GCTATGTCAT		2940
	CTGCCACCTT	TCCCTTGAGG	ATAAACAAAG	GGTCTGTAAG	ACTTAAATTT	AGCGGCCTGA		3000
75	CGTTCCTTTG	CACACAATCA	ATGCTCGCCA	GAATGTTGTT	GACACAGTAA	TGCCAGCAG		3060
	AGGCCCTTAC	TAGAGCATCC	TTTGACGGGC	GAAGGCCACG	GCCTTTCAG	ATGGAAGCA		3120
	GCAGCTTTTC	CACCTTCCCA	GAGACATTCT	GGATGCATTT	GCATTGAGTC	TGAAAGGGGG		3180
	CTTGAGGGAC	GTTTGTGACT	TCTTGGCGAC	TGCCCTTTGT	GTGTGGAAGA	GACTTGGAAA		3240
	GGTCTCAGAC	TGAATGTGAC	CAATTAACCA	GCTTGGTTGA	TGATGGGGGA	GGGGCTGAGT		3300
80	TGTGCATGGG	CCCAGTCTG	GAGGGCCACG	TAAATCGT	CTGAGTCTGT	AGCAGTGTCC		3360
	ACCTTGAAGG	TCTTC						

A165 Protein sequence

Gene name:
 Unigene number:
 Protein Accession #:
 Signal sequence:
 Transmembrane domains:
 VGM domains:
 EGF domains:
 Cellular Localization:

ESTs
 Hs.157601
 none found
 1-17
 none found
 49-223; 341-518; 529-706
 298-333; 715-748
 secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
MPFFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
15 SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
FAVGVRFPFRW EELHALASEP RQGHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCV RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD 300
20 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVFKRFV RAVLSBDSRA RVGVATYSRE LLVAVPVGEY QDVFDLVWSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LTTESHSEDE VAGPARHARA RELLLLGVS 480
EAVRAELEEI TGSFKHVMVY SDPQDLFNQI PELQGLCSR QRPQCRTQAL DLVFMLD TSA 540
SVGPENFAQM QSFVRSCALQ FEVNPDVTV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
25 APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLRNNGI 660
SVLVVGVGPV LSEGLRRLAR PRDSLHVAAYADLRYHQDV LIEWLCEGAK QPVNLCKPSP 720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP

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A166 DNA sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
 Unigene number: Hs.37744
 Probeset Accession #: AA011176
 Nucleic Acid Accession #: AF272890
 Coding Sequence: 87-1520 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
TGCTACCCGCG GCCCGGGCTT CTGGGGTGTG CCCCACCCAC GCGCCAGCCC TGCCACACCC 60
40 CCCGCCCCCG GCCTCCGCGC CTGCGGATGG GCGCGGGGGT GCTCGTCTCT GCGCGCTCCG 120
AGCCCGGTAA CCTGTGCTCG GCGGCACCGC TCCCGGACGG GCGCGCCACC GCGCGCGGCG 180
TGCTGGTGCC CGGTCGCGCG CCGGCCTCGT TGCTGCTCTC GCGCAGCGAA AGCCCCGAGC 240
CGCTGTCTCA GCAGTGGACA GCGGGCATGG GTCTGCTGAT GCGGCTCATC GTGCTGCTCA 300
TCGTGGCGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCCGCGG CTGCAGACGC 360
TCACCAACCT CTTTCATCAT TCCCTGGCCA GCGCCGACCT GGTTCATGGG CTGCTGCTGG 420
45 TGCGGTTGCG GCGGCACCAT CTGGTGTGGG GCGGCTGGGA GTACGGCTCC TTCTTCTGCG 480
AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540
TTGCCCTGGA CCGCTACCTC GCCATCACCT CGCCCTTCCG CTACCGAGAG CTGCTGACGC 600
GCGCGCGGGC GCGGGGCTCT GTGTGCACCG TGTGGGCCAT CTCGGCCCTG GTGTCTCTCC 660
TGCCCATCCT CATGCACTGG TGGCGGGCGG AGAGCGACGA GCGCGCGCGC TGCTACAAAG 720
50 ACCCAAGTGT CTGCGACTTC GTCACCAACC GGGCCTACGC CATCGCCTCG TCCGTAGTCT 780
CCTTCTACGT GCCCTGTGTC ATCATGGCCT TCGTGTACCT GCGGGTGTTC CGCGAGGCCC 840
AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCCGTTT CCTCGCGGCG CCAGCGCGGC 900
CGCCCTCGCC CTCGCCCTCG CCCGTCGCCG GCGCCGCGCC GCGCCCGGGA CCCCCGCGCC 960
CGCGCGCGCG GCGCGCCACC GCCCGCTGG CCAACGGGCG TGCGGGTAAG CGGCGGCCCT 1020
55 GCGCGCTCGT GGCCTACGCG GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG 1080
TCTTACGCTG TGTGCTGGTG CCTTCTTCC TGGCCAACGT GGTGAAGGCC TTCCACCGCG 1140
AGCTGGTGCC CAGCCGCTCT TTCGTCCTCT TCAACTGGCT GGGCTACGCC AACTCGGCCT 1200
TCAACCCCAT CATCTACTCG CGCAGCCCG ACTTCCGCAA GGCCTTCCAG GGACTGCTCT 1260
60 GCTGCGCGCG CAGGGCTGCC GCGCGCGGCC ACGCGACCCA CGGAGACCGG CCGCGCGCCT 1320
CGGGCTGTCT GGCCCGGGCC GAGCCCGCGC CATCGCCCGG GCGCGCCTCG GACGACGACG 1380
ACGACGATGT CGTCGGGGCC ACGCCGCGCG CGCGCCTGCT GGAGCCCTGG GCGCGCTGCA 1440
ACGCGCGGGC GCGCGCGGAC AGCGACTCGA GCCTGGACGA GCGGTGCGCG CCGGCTTCG 1500
CCTCGGAATC CAAGGTGTAG GCGCCGCGCG GGGCGCGGGA CTCCGGGCAC GGCTTCCCAG 1560
65 GGAACGAGG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAACCTGA AGCCACCAAT 1620
CCTCGTCTGA ATCATCCGAG GCAAAGAGAA AAGCCACGGA CCGTGCACA AAAAGGAAAG 1680
TTTGGGAAGG GATGGGAGAG TGGCTTGTCT ATGTTCCTTG TTG

```

A167 Protein sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
 Unigene number: Hs.37744
 Protein Accession #: AA011176
 Signal sequence: none found
 Transmembrane domains: 62-84, 95-117, 135-157, 177-198, 226-248
 Pfam domain: 7tm_1 [75-377]
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MGAGVLVLGA SEPGNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQWWTAG 60
80 MGLLMALIVL LIVAGNVLVI VAIKTPRLQ TLTNLFIMSL ASADLVMGLL VVPFGATIVV 120

```

WGRWEYGSFF CELWTSVDVL CVTASIELTC VIALDRYLAI TSPFRYQSLI TRARARGLVC 180
 TWVAISALVS FLPILMHWR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM 240
 AFVYLRVFRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPF RFAAAAATAP 300
 LANGRAGKRR PSRLVALREQ KALKTLGIIM GVFTLCWLPF FLANVVKAFH RELVDPDRLEFV 360
 FFWNLGYANS AFNPPIYCRS PDRKAFQGL LCCARRAARR RHATHGDRPR ASGCLARPGP 420
 PPSPGAASDD DDDDVVGATP PARLLEPWAG CNGGAAADSD SSLDEPCRPG FASESKV

A168 DNA sequence

Gene name: CEGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Nucleic Acid Accession #: AJ400877
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GGGCTCCGCG CACACCTCCC CGCGCCGCGG CCGCCACCGC CCGCACTCCG CCGCCTCTGC 60
 CCGCAACCGC TGAGCCATCC ATGGGGGTCG CGGGCCGCAA CCGTCCCGGG GCGGCCTGGG 120
 CGGTGCTGCT GCTGCTGCTG CTGCTGCCGC CACTGCTGCT GCTGGCGGGG GCGTCCCGC 180
 CCGGTCCGGG CCGTGCCGCG GGGCCGCAAG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCTTACAAG TGCTCTTGCA 300
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC 360
 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGTT 420
 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG 480
 AGAACAAATG CCGCTGCCAG CATACCTGTG TCAACGTCAT GGGGAGCTAT GAGTGTGCTG 540
 GCAGGAGAGG GTTTTTCTCT AGTGACAATC AGCACACCTG CATTCACCGC TCGGAAGAGG 600
 GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660
 GCAGCGTCGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720
 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780
 GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840
 AGCGAGAGGA CACTGTCTTG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900
 ATAAACGGGT GAACCGCGG CTGCTCATGG AAACGTGTGC TGTCAACAAAT GGAGGCTGTG 960
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 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT 1080
 GTGATCATTG CTGCAAAAAC ATCGTGGGCA GTTTTGACTG CGGTGCAAG AAAGGATTTA 1140
 AATTATTAAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT 1200
 GTGACCAAGC CTGCATCAAC CACCTTGCCA CATTTGCTTG TGCTTGCAAC CGAGGGTACA 1260
 CCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGAGGCT 1320
 GTGAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CCTGGGTACA 1380
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 CACCCCGTGT GTCCCTGCAC TGGCGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT 1500
 GTCACTCTGG CATTCACCTC TCTTCAGATG TCACCACCAT CAGGACAAGT GTAACCTTTA 1560
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 TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACCTCAGAA 1860
 AGGCGTCCA TTTCACTTCC TTTCACTTCC AGCTCTCAGG CATGAACCTC CAGTGGGCTA 1920
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 CAGAAAACCA ATGTGTGAGT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAAGCT 2040
 GCATTTTATG TGGTACATTT GAATCCCAAA ACTGAGGAAG ACAAATGACT TGTGAACCAT 2100
 GCCCAAGACC AGGAAATTTCT GGGGCCCTGA AGACCCAGCA AGCTTGAAT ATGTCTGAAT 2160
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 GTGCCCTGGG CAGTTCACAG CCTGAAGCTG GTCGAACTTC CTGCTTCCCC TGTGGAGGAG 2280
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 CATACCAGCC TGAATTTGGA AAAAATAATT GTGTTTCTTG CCCAGGAAAT ACTACGACTG 2460
 ACTTTGATGG CTCCACAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520
 GAGATTTTCA TGGTACATTT GAATCCCAAA ACTACCCAGG CAATTACCCA GCCAACACCG 2580
 AGTGTACGTG GACCATCAAC CCACCCCCCA AGCGCCGCAT CCTGATCGTG GTCCCTGAGA 2640
 TCTTCCCTGC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTCTTCAT 2700
 CCAATTCTGT GACAACATAT GAAACCTGCC AGACCTACGA ACGCCCCATC GCCTTCACCT 2760
 CCAGGTCAAA GAAGCTGTGG ATTCAATTCA AGTCCAATGA AGGGAACAGC GCTAGAGGTT 2820
 TCCAGGTCCC ATACGTGACA TATGATGAGG ACTACCGGA ACTCATTGAA GACATAGTTC 2880
 GAGATGGCAG GCTCTATGCA TCTGAGAACC ATCAGGAAAT ACTTAAGGAT AAGAACTTA 2940
 TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAAGTAC ACAGCCCAGG 3000
 AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT 3060
 TTTTGAGACC TTACAAATGA CTCAGCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG 3120
 GGTGCTGGG ACAGAGCTGT CTTCTTCTG CATGTGAGCA CAGTCGGGTA TTGCTGCCTC 3180
 CCGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGGTAAATT 3240
 GAACCTTGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300
 CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGGCTGGCT GAGCTGAGCT 3360
 TTGCTGAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTAATCTTCC TCAAGGAGTC 3420
 TGTAGTGGAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTCAGC TTCCTCTAGC 3480
 CCGGCCCTCT CTAAGGGAGC CCTCTGCAC CTGTGTCAGG CTCTGACAG GCAGAACAGG 3540
 CAAGAGGGGA GGGAGGAGA CCCCTGCAGG CTCCCTCCAC CCACCTTGAG ACCTGGGAGG 3600
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACCTG 3660
 AGTTCTAAGC AGTGCTCGTG AAAAAAAGAA GCAGAAAGAA TTAGAAATAA ATAAAACTA 3720
 AGCACTTCTG GAGACAT

A169 Protein sequence

Gene name: CEGP1
 Unigene number: Hs.222399

Probeset Accession #: AA256485
 Protein Accession #: CAB92285
 Signal sequence: 1-31
 Transmembrane domains: none
 PFAM domains: EGF-like_domains [49-84,132-167,177-213,286-321,407-442] CUB_domain [809-918]
 Cellular Localization: may be secreted

10 1 11 21 31 41 51
 | | | | | |
 MGVAGRNRPG AANAVLLLLL LLPPLLLLAG AVFPGRGAA GPQEDVDECA QGLDDCHADA 60
 LCQNTPTS YK CSCKPGYQGE GRQCEDIDEC GNELNNGCVH DCLNIPGN YR CTCFDGFM LA 120
 HDGHNCLD VD ECLENNNGCQ HTCVNVMGSY ECCCKEGFFL SDNQHTCIHR SEEGLS CMNK 180
 15 DHGCSHICKE APRGSVACEC RPFGE LAKNQ RDCILTCNHG NGGCQHSCDD TADGPECSCH 240
 PQYKMH TDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGC DR TCKDT 300
 STGVHC SCFV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFLLTDEK 360
 SCQDVDECSL DR TCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCQQVCVN 420
 TVGSYECQCH PGYKLHWK K DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480
 20 SSVDTTIRTS VTFKLNEGKC SLKNAELFPE GLR PALPEKH SSVKESFR YV NLTCSSGKQV 540
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600
 FHLQLSGMNL DVAKKPPRTS ERQAESCQVG QGHAENQCVS CRAGTY YDGA RERCILCPNG 660
 TFQNEEQMT CEPCPRPONS GALKTP EAWN MSECGGLCQP GEYSADGFAP CQLCALGT FQ 720
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCS PGHFY NTTTHRCIRC PVGT YQPEFG 780
 25 KNNCVSCPGN TTTDFDGS TN ITQCKNRRCG GELGDF TGYI ESPNYPGNYP ANTECTWTIN 840
 PPPKRRLIV VPEIFLP IED DCGDYLVMRK TSSNSNVTTY ETCQTYERPI AFTSRSKKLW 900
 IQFKSNEGNS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960
 LAHPQNYFKY TAQESREMF P RSFIRLLRSK VSRFLRPYK

A170 DNA sequence

Gene name: DEME-6 protein (KIAA0452)
 Unigene number: Hs.125783
 Probeset Accession #: AL039402
 Nucleic Acid Accession #: AF007170
 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

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 AAGGAGGCGG CCTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CATGAGGCC 60
 CTGGACCACT CACTGACCGC CCTGGACCTC TTCCTCACCA ACCAGTTCTC AGAAGCACTC 120
 40 AGCTACCTCA AGCCACAGAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
 CTGGAGATGC AGGCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCAACATG 240
 ATGAAGGAGG CACAGATGCT GTGT CAGAGG CACCGGAGGA AGTCTTCTGT AACAGATTCC 300
 TTCAGCAGCC TGGTGAAACCG CCCACGCTG GGC CAATTCA CTGAAGAAGA AATCCACGCT 360
 GAGGTCTGCT ATGCAGATG C CTGCTGCAG CGAGCAGCCC TGACTTCTCT GCAGGACGAG 420
 45 AACATGTTGA GCTTCATCAA AGGCGGCATC AAAGTTCGAA ACAGCTACCA GACCTACAAG 480
 GAGCTGGACA GCCTTGT TCA GTCCCTCAAA TACTGCAAGG GTGAGAACCA CCGCACTTT 540
 GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT CCTTCTCTACT 600
 AGGATCTCGA GGCTGTTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660
 CAGCTGGAGG AGGGACGCTC AGGGCACAGC TTCGCTCTG TGCTCTGTGT CATGCTCCTG 720
 50 CTGTGCTACC ACACCTTCTC CACTTTCGTG CTCGGTACTG GGAACGTCAA CATCGAGGAG 780
 GCCGAGAAGC TCTTGAAGCC CTACCTGAAC CGGTACCCCTA AGGGTGCCAT CTTCTCTGTT 840
 TTTGCAGGGA GGATTGAAGT CATTAAAGGC AACATTGATG CAGCCATCCG GCGTTTCGAG 900
 GAGTGCTGTG AGGCCAGCA GCACTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960
 55 ATGTGGTGCT TCACCTACAA GGGCCAGTGG AAGATGTCTT ACTTCTACGC CGACCTGCTC 1020
 AGCAAGGAGA ACTGCTGTGC CAAGGCCACC TACATTTACA TGAAGGCCGC CTACCTCAGC 1080
 ATGTTTGGA AGGAGGACCA CAAGCCGTTT GGGGACGACG AAGTGGAAAT ATTTCGAGCT 1140
 GTGCCAGGCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200
 CGGAAGTCCC GGCCTACTT CTCCTCCAAC CCTATCTGCG TGCCAGTGCC TGCTCTGGAA 1260
 60 ATGATGTACA TCTGGAAACG CTACGCCGTG ATTGGGAAGC AGCCGAAACT CACGGATGGG 1320
 ATACTTGAGA TTATCACTAA GGCTGAAGAG ATGCTGGAGA AAGGCCCAGA GAACGAGTAC 1380
 TCAGTGGATG ACGAGTGCTT GGTGAAATTG TTGAAAGGCC TGTGTCTGAA ATACCTGGGC 1440
 CGTGTCACAG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAAAA GAAGATTAAA 1500
 TATGACCACT ACTTGATCCC AAACGCCCTG CTGGAGCTGG CCTGTCTGCT TATGGAGCAA 1560
 65 GACAGAAACG AAGAGGCCAT CAAACTTTTG GAATCTGCCA AGCAAAACTA CAAGAATTAC 1620
 TCCATGGAGT CAAGGACACA CTTTGAATC CAGGCAGCCA CACTCCAAGC CAAGTCTTCC 1680
 CTAGAGAACA GCAGCAGATC CATGGTCTCA TCAGTGTCTT TGTAGCTTTG TGCAGCAGTT 1740
 CCGGGCTGGA AGACAGAGAC AGCTGGACAG AGCTCCTGAA AACATTTCAA AATACCCCT 1800
 CCCCTGCCCC TGCCCTGCC T TGGGGTCCA CCGGCACTCC AGTTGGATGG CACAACATAG 1860
 70 TGTATCCGTG CAGAAGCCGA GCTGGCATT TCAACAGTGT AGCCAAGGGC CTTTGCCAG 1920
 GGCAGAGCAG GTGGAGCCCT CTGCCTGCCC TATCACACAT ACGGGTACTT GCTTTTCACT 1980
 GTGATGTTTA AGAGAATGTA TGAACAGTTT ACATTTTCCT TAGAAATACA TTGATGGGAT 2040
 CACAGTTGGC TTTAAAAACC AACACAATC AACCACTGT AAGTCTTTGT CTTACCTAT 2100
 TATCATCTG AGGTAAATCT CTTTATATGA TGA TGCCAAA GGGCAAATG CTTTCAAAT 2160
 75 TCAGCAAGTT CTCAGCTTGT GTGACGGAAG GTCCTTCAGA GGACCTGAGG AATGCCTGGG 2220
 AGAGGCTAAG CCTCAGGCTT CAATGCTTCT GGGGTGAGG ATGAGGATGT ACACAGACAC 2280
 CCACTACCTT ACTACTCACA CTCCTTTTGT AAATTTTCAA TTTAAAAATC 2340
 AAGCAGCTCT TTTTGTAGT ATAAAATCTG AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400
 AGTAGAAAAT GCCAGGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460
 80 AAATTTGGGG GGCAGGAGGA GGTTCCTAGA ATCCAGCTG TATCTTTGCT GTATGCCAAA 2520
 CTGAAACCA TGGGAATAAT TTATGAAACA TAAAAATCTT CTGTACTTCA CTCCAAGGTA 2580
 CATTGCTTA CTGACAGCAT TTTTGTTAAA ACTGTTATTC TTGAAAAAAA AAAAAAAA 2640
 AA

A171 Protein sequence

Gene name: DEME-6 protein (KIAA0452)
 Unigene number: Hs.125783
 Probeset Accession #: AL039402
 Protein Accession #: AAC39582
 Signal sequence: none
 Transmembrane domains: 210-226
 Cellular Localization: plasma membrane

1 11 21 31 41 51
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 MTALDLFLTN QFSEALSYYLK PRTKESMYHS LTYATILEMQ AMMTFDPQDI LLAGNMMKEA 60
 QMLCQRHRRK SSVTDSFSSL VNRPTLGQFT EEEIHAEVCY AECLLQRAAL TFLQDENMVS 120
 FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHFEGGV KLGVGAFNLT LSMLPTRLIR 180
 LLEFVGFSGN KDYGLLQLEE GASGHSFRSV LCVMLLLCYH TFLTFLVLTG NVNIEEAEKL 240
 LKPYLNRYPK GAIFLFFAGR IEVIKGNIDA AIRRFEECC E AQQHWKQFHH MCYWELMWCF 300
 TYKGQWKMSY FYADLLSKEN CWSKATYIYM KAAVLSMFGK EDHKPFQDDE VELFRAVPGL 360
 KKKIAGKSLP TEKFAIRKSR RYFSSNPISL PVPALMMYI WNGYAVIGKQ PKLTDGILEI 420
 ITKAEEMLEK GPENEYVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDHY 480
 LIPNALLELA LLLMEQDRNE EAIKLLLESAK QNYKNYSMES RTHFRQAAT LQAKSSLENS 540
 SRSMVSSVSL

A172 DNA sequence

Gene name: EST
 Unigene number: Hs.200102
 Probeset Accession #: AL117406
 Nucleic Acid Accession #: none found
 Coding sequence: 1-4044 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 ATGACTAGGA AGAGGACATA CTGGGTGCC AACTCTTCTG GTGGCCTCGT GAATCGTGCC 60
 ATCGACATAG GCGATGACAT GGTTTCAGGA CTTATTTATA AAACCTATAC TCTCCAAGAT 120
 GGCCCTCTGA GTACAGCAAG GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCACCG 180
 TGGGGGAAGT ATGATGCTGC CTTGAGAACC ATGATTCCCT TCCGTCCCAA GCCGAGGTTT 240
 CCTGCCCCCT AGCCCTCTGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC 300
 ACCCCGCTCA TGATCCCAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCTTCACTG 360
 TCAGTCCATG ATGCTTCAGA CAAAATGTC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA 420
 GTCTCAAGGC GAGGGATTGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA 480
 ACAAGGTTGA TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATTGCCAG TGTACTCGGG 540
 CCAATATTGA TTATACCAAA GATCCTGGAA TATTCAGAAG AGCAGTTGGG GAATGTTGTC 600
 CATGGAGTGG GACTCTGCTT TGCCCTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTTC 660
 TCCTCCAGTT GGATCATCAA CCAACGCACA GCCATCAGGT TCCGAGCAGC TGTTTCTCTC 720
 TTTGCCTTTG AGAAGCTCAT CCAATTTAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC 780
 ATCAGCTTCT TCACCGGTGA TGTAAGTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA 840
 GTACTGATCA CCTGCGCATC GCTGGTCATC TGCAGCATTT CTTCTACTT CATATTGGA 900
 TACTGTGAT TATTGTCCAT CTTATGCTAT CTCCTGGTTT TCCCACTGGC GGTATTATG 960
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 GTGACCACTG AAGTTCTCAC TTGCATTAA CTGATTAAAA TGTACACATG GGAGAAACCA 1080
 TTTGCAAAAA TCATTGAAGT TATGGAAGT CTGACTTTCT GCTCCAAAC TGGTGATGGC 1140
 ATGGCCTTCA GCATGTGGC CTCCTTGAAT CTCCTTCGGC TGTGAGTGT CTTTGTGCTT 1200
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 GAGCTGGAGA GGAACGGGCA TGCTTCTGAG GGGATGACCA GGCTTAGAGA TGCCCTCGGG 1440
 CCAGAGGAAG AAGGGAACAG CCTGGGCCCA GAGTTGCACA AGATCAACCT GGTGGTGTCC 1500
 AAGGGGATGA TGTTAGGGGT CTGGGCAAC ACGGGGAGTG GTAAGAGCAG CCGTTTGTCA 1560
 GCCATCTCTG AGGAGATGCA CTTGCTCGAG GGCTCGGTGG GGGTGCAGGG AAGCCTGGCC 1620
 TATGTCCCGC AGCAGGCCCTG GATCGTCAGC GGAACATCA GGGAGAACAT CCTCATGGGA 1680
 GGCGCATATG ACAAGGCCCG ATACCTCCAG GTGCTCCACT GCTGCTCCCT GAATCGGGAC 1740
 CTGGAACCTT TGCCCTTTGG AGACATGACA GAGATTGGAG AGCGGGGCTT CAACCTCTCT 1800
 GGGGGGAGAG AACAGAGGAT CAGCCTGGCC CGCGCCGTCT ATTCCGACCG TCAGATCTAC 1860
 CTGCTGGACG ACCCCTGTCT TGCTGTGGAC GCCACGTGG GGAAGCAGT TTTTGAGGAG 1920
 TGCATTAAGA AGACACTCAG GGGGAAGACG GTCGTCTTGG TGACCCACCA GCTGCAGTAC 1980
 TTAGAATTTT GTGGCCAGAT CATTTTGTTG GAAATGGGGA AAATCTGTGA AAATGGAAC 2040
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 TACATCCAGG CAGCTGGAGG TTACATGGTC TCTTGATATA TTTTCTTCT CGTGGTGTCT 2340
 ATCGTCTTCT TAACGATCTT CAGCTTCTGG TGGCTGAGCT ACTGTTTGA GCAGGGCTCG 2400
 GGGACCAATA GCAGCCGAGA GAGCAATGGA ACCATGGCAG ACCTGGGCAA CATTGCAGAG 2460
 AATCCTCAAC TGTCCTTCTA CCAGCTGGTG TACGGGCTCA ACGCCCTGCT CCTCATCTGT 2520
 GTGGGGGTCT GCTCCTCAGG GATTTTCACC AAAGTCACGA GGAAGGCATC CACGGCCCTG 2580
 CACAAACAGC TCTTCAACAA GGTTTTCCGC TGCCCCATGA GTTTCTTTGA CACCATCCCA 2640
 ATAGGCCGGC TTTTGAACAG CTTGCGAGGG GACTTGGAAC AGCTGGACCA GCTCTTGCCC 2700
 ATCTTTTCAG AGCAGTCTCT GGTCTCTGTC TTAATGGTGA TCGCCGTCTT GTTGATTGTC 2760
 AGTGTGCTGT CTCCATATAT CCGTGTAAAT GGAGCCATAA TCATGGTTAT TTGCTTCATT 2820
 TATTATATAT TGTTCAGAA GGCCATCGGT GTGTTCAAGA GACTGGAGAA CTATAGCCGG 2880
 TCTCCTTAT TCTCCACAT CCTCAATTCT CTGCAAGGCC TGAGCTCCAT CCATGTCTAT 2940
 GGAAGAACTG AAGACTTCTAT CAGCCAGTTT AAGAGGCTGA CTGATGCGCA GAATAACTAC 3000
 CTGCTGTTGT TTCTATCTTC CACACGATGG ATGGCATTGA GGCTGGAGAT CATGACCAAC 3060
 CTTGTGACCT TGGCTGTGTC CCTGTTCGTG GCTTTTGGCA TTCTCTCCAC CCCCTACTCC 3120

TTAAAGTCA TGGCTGTCAA CATCGTGCTG CAGCTGGCGT CCAGCTTCCA GGCCACTGCC 3180
 CGGATTGGCT TGGAGACAGA GGCACAGTTC ACGGCTGTAG AGAGGATACT GCAGTACATG 3240
 AAGATGTGTG TCTCGGAAGC TCCTTTACAC ATGGAAGGCA CAAGTGTGCC CCAGGGGTGG 3300
 CCACAGCATG GGGAAATCAT ATTTCCAGGAT TATCACATGA AATACAGAGA CAACACACCC 3360
 ACCGTGCTTC ACGGCATCAA CCTGACCATC CGCGGCCACG AAGTGGTGGG CATCGTGGGA 3420
 AGGACGGGCT CTGGGAAGTC CTCTTGGGC ATGGCTCTCT TCCGCCTGGT GGAGCCCATG 3480
 GCAGGCCGGA TTCTCATTTA CGGCGTGGAC ATTTGCAGCA TCGGCCTGGA GGAATTGCGG 3540
 TCCAAGCTCT CAGTGATCCC TCAAGATCCA GTGCTGCTCT CAGGAACCAT CAGATTCAAC 3600
 CTAGATCCCT TTGACCGTCA CACTGACCAG CAGATCTGGG ATGCTTGGGA GAGGACATTC 3660
 CTGACCAAGG CCATCTCAAA GTTCCCAAAA AAGCTGCATA CAGATGTGGT GGAACACGGT 3720
 GGAAACTTCT CTGTGGGGGA GAGGCAGCTG CTCTGCATTG CCAGGGCTGT GCTTCGCAAC 3780
 TCCAAGATCA TCCTTATCGA TGAAGCCACA GCCTCCATTG ACATGGAGAC AGACACCCCTG 3840
 ATCCAGCGCA CAATPCGPTA AGCCTTCCAG GGCTGCACCG TGCTCGTCAT TGCCACCCGT 3900
 GTCAACCATG TGCTGAAGT TGAACCATC CTGGTTATGG GCAATGGGAA GGTGGTAGAA 3960
 TTTGATCGGC CGGAGGTACT GCGGAAGAAG CCTGGGTCAT TGTTCGCAGC CCTCATGGCC 4020
 ACAGCCACTT CTCTACTGAG ATAAGGAGAT GTGGAGACTT CATGGAGGCT GGCAGCTGAG 4080
 CTCAGAGGTT CACACAGGTG CAGCTTCGAG GCCCAGAGTC TGCGACCTTC TTGTTTGGAG 4140
 ATGAGAACTT CTCCTGGAAG CAGGGGTAAA TGTAGGGGGG GTGGGGATTG CTGGATGGAA 4200
 ACCCTGGAAT AGGCTACTTG ATGGCTCTCA AGACCTTAGA ACCCCAGAAC CATCTAAGAC 4260
 ATGGGATTCA GTGATCATGT GTTCTCTCTT TTAACCTTACA TGCTGAATAA TTTTATAATA 4320
 AGGTAAAAGC TTATAGTTTT CTGATCTGTG TTAGAAGTGY TGCAATGCT GTACTGACTT 4380
 TGTAAATAT AAAACTAAGG AAAACTCAAA AAAAAA AAAA

A173 Protein sequence

Gene name: EST
 Unigene number: Hs.200102
 Probeset Accession #: AL117406
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 169-185, 199-215, 275-291, 304-320, 387-403, 770-786, 829-845, 907-923, 927-943, 1018-1034
 PFAM domains: ABC_transporter [502-673], ABC_membrane_region [163-432, 771-1060]
 ATP-binding_domains [508-516, 1139-1147]
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | | |
 MTRKRTYVWP NSSGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQERNP EAPGRAAVPP 60
 WGKYDAALRT MIPFRPKPRF PAPQPLDNAG LFSYLTVSWL TPLMIQSLRS RLDENTIPPL 120
 SVHDASDKNV QRLHRLWEEE VSRRGIEKAS VLLVMLRFQR TRLIFDALLG ICFCIASVLG 180
 PILIIPKILE YSEBQLGNV HGVGLCFALF LSECVKSLSF SSSWIINQRT AIRFRAAVSS 240
 FAPEKLIQFK SVIHITSGEA ISFFTGDVNY LFEGVCYGPL VLITCASLVI CSISSYFIIG 300
 YTAFAIALCY LLVFLAVFM TRMAVKAQHH TSEVSDQIRI VTSEVLTICIK LIKMYTWEKP 360
 FAKIIEGMES LTFCKPGDG MAFSMLASLN LLRLSVFFVP IAVKGLTNSK SAVMRFKKFF 420
 LQESPVFYVQ TLQDPSKALV FEEATLSWQQ TCGIVNGAL ELERNHASE GMTRPRDALG 480
 PEEEGNSLGP ELHKINLVVS KGMMLGVCGN TGSGKSSLLS AILEEMHLE GSVGVQGSLS 540
 YVPQQAIVS GNIRENLMG GAYDKARYLQ VLNCCSLNRD LELLFPDGMT EIGERGLNLS 600
 GGQQRISLA RAVYSDRIY LLDDPLSAVD AHVGKHIFEE CIKKTLRGKT VVLVTHQLQY 660
 LEFCGQIILL ENKICENG T HSELMQKKGK YAQLIQMHK EATSDMLQDT AKIAEKPKVE 720
 SQALATSLEE SLGNNAVPEH QLTQEEEMEE GSLSWRVYHH YIQAAAGGYM SCIIFFVVL 780
 IVFLTIFSFV WLSWLEQGS GTNSSRESNG TMADLGNLAD NPQLSFYQLV YGLNALLLIC 840
 VGVCSGIFT KVTRKASTAL HNKLFNKVFR CPMSFFDTIP IGRLLNCFAG DLEQLDQLLP 900
 IFSEQFLVLS LMVIAVLLIV SVLSPYILLM GAIIMVICFI YMMFKAIG VFKRLNYSR 960
 SPLFSLILNS LQGLSSIHVY GKTEDFISQF KRLTDAQNNY LLLFLSSTRW MALRLEIMTN 1020
 LVTLAVLFV AFGISSTPYS FKVMANIVL QLASSFQATA RIGLETEAQF TAVERILQYM 1080
 KMCVSEAPLH MEGTSCPGW PQHGEIIFQD YHMKYRDNTF TVLHGINLTI RGEHVVGIVG 1140
 RTSGKSSLG MALFRLVEFM AGRILIDGVD ICSIGLEDLR SKLSVIPQDP VLLSGTIRFN 1200
 LDPFDRHTDQ QLFDALERT LTKAISFPK KLHTDVVENG GNFSVGERQL LCIAARVLRN 1260
 SKIILIDEAT ASIDMETDTL IQRTIREAFQ GCTVLVIAHR VTTVLNCDHI LVMGNKGKVE 1320
 FDRPEVLRKK PGSLEAALMA TATSSLR

A174 DNA sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | | |
 ATGCTGTCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCAGG 60
 GGAAGAAGAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCGAG 120
 GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC 180
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240
 CCGCGGCGCG CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCTT 300
 CGCCTGCGTC CTGGACGTTT CCGGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360
 TCCGACGAGC AGCCCGGGGG GCCTTCTGAC TGCAATCCGA GATTTCATC AGCGAGTGCA 420
 ACTCATAAGC CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
 GCTCCTGGAG CTAGGGCCCG GCGTCGTCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC 540
 CCGCGCGGAA AGCGCGCGCG GACAGTCAGT GACGAGGCCG GGGGGTCCGC GGGGCCACGA 600
 CTTCTCGGAG ACCGTCTGCG GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660
 TGTGGGGCGC TCGCGCTCGT TCCGTCTCCT CATCTGGGAA CGCGGCTTCG CTCTGCAGC 720
 TGCTGCTGCG TCGCGTCTGT GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780

5 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840
 GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960
 CGGGCGGACA AAGACGGGCC CGGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020
 GGAGACGGCG AGGGTGCGCC CCCACCGTG AGGGCTGGC AGCGGTGCTC CCTTGAAGGC 1080
 TCCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCCG TGCCAGACGC 1140
 CGCGGATTCC CATCTTCTCC ACGCGGCGGC CCTCTCCCC TGCAGCGGCC CGCCTTGCCC 1200
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 10 CTGGTGGCAG CTGTGTGCTG CAGATGTCTC CGGCCAAGC AGGATCCCCA GCAGAGCCGA 1320
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 CGGGGGTCTG CTTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440
 GGGGCCCGGG CGCCCCAAC AAGGTACAG ACCAAGTGT GCTTGCCGGA AGGGACCATG 1500
 AACAACTGTG ATGTCAACAT GCCCAGAAAT TTCTCTGTGC TGAAGTGTCA GCAGGCCACC 1560
 15 CAGATTGTGC CACATCAAGG CAGATATCTG CATCCCCCAT ACGTGGGGTA CACGGTGCAG 1620
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 20 GCTTCATTTG CCCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920
 CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980
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 AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100
 TTGTTGTTGA TCGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160
 25 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGTCTCTG TTGCCCAGGC TGGAGTGCAG 2220
 TGGTGCATC TCGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCCACA CTCTGCCTC 2280
 AGCCTCCAC TCAGGCTGGG TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTT 2340
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGTGCTCTC ACTCTCCTGA CCTCAAGCAA 2400
 TCTGCCTGTC TCAGCCTCCC AAGTGTCTGG GATTACAGGC GTGAGCCACC GCCCCAGGCC 2460
 30 TGAGCCTTTT TTTTTTCTA ATGCATCCAA GGTTAAGGGG AAGACGCAAA TAACAGGACT 2520
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 TAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACCTA ATGAAGACAT TTCAGAACTC 2760
 35 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCCCTC 2820
 TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATCTCTTT 2880
 TATATTGAAA TCATAAACTA TCACCCGCTG CTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940
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 40 AAAAAATTTT TTTGCTTAGT TATAAAATG CAAAGAAATG TGTTACAAAG ATACTTAGTA 3120
 TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACAGATAC GATTTACTTT 3180
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 45 CAAATTCAG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAAGAT AACTTTAAGG 3420
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAATCGCT 3480
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 TGTTCATGTA CTGAATAATG TAAACCAAGT GTTGCAATT GGTATCATCA ATGATACTCA 3600
 50 TTTTTTAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
 TGAATAAATA AAAAAAATA AAAAAAATA

A175 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular Localization: not determined

60 1 11 21 31 41 51
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 MLSGFLMSPS TQHRAYQTPG GKKLPEWASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
 65 GEAEGNKRGE PPAWIRAQQQ PRPPFAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPPPEA 120
 SGRQPRGPSD CIPRFPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG 180
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAAPRVVP CGALAARPPSP HPGTPLRSCS 240
 CCWLRCWRRG RGPSGEYCHG WLDAGQVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300
 70 ARLDQGGCDN DRQQAGGEPG RADKDGPRRL GRASCLRGTQ GDGEGAPPFV RAWQRCSPG 360
 SPKGRQLLRA PFGLLRARR RGFPSSPRGG PSPLQRPALP IYVPFLIVGS VFVAFIILGS 420
 LVAACCCRCL RPKQDPQQR APGGRNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS 480
 GARAPPTRSQ TNCCLPEGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGGYL HPPVVGTVQ 540
 HDSVPMTAVP PFMDLQPGY RQIQSPFPHT NSEQKMPAV TV

A176 DNA SEQUENCE

75 Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 80 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GCCCTTGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60

5 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
 CTGGGCGCAG CAGAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC 300
 TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCCGGGCCCC CCTGCCCTGC CTGACGTCC 360
 10 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG 480
 GCGCTCATTG AGCAGCTGTT TGAGGCCCCG GCCCTGAGCC AGCAGGACCG GGGACCTCTG 540
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CCTGGCACTC 600
 AGCCCTTCGA GGTGGGGCGC CCCATCGCAC CCACCCTCTC TGGCTGGAGA CCCCCGGCAG 660
 GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CTTGCCGCCC TTGCCAGATG GGCTCCCCAG 720
 GCCTGCCCCC GGCTGCTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG 780
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCGC CTACTACTGG CCGCTGTCTG 840
 15 TGGACAGTGG GTTACCCCTC CATGAGTTAG CGTCCCCCGG TTTCAGCGG TGCCGCGCTG 900
 GGTCCCATCT TCAGGGAAAG GCACCTGCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960
 AGAGGGCGCG GGGCGGCTCC GACGCGGCTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080
 GTAAGCGGGG GGTGCCCTGC TGGCTGGGGA GCCCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140
 CTGGCCAAAG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200
 20 GGCTGTGATG TGCTTCCCAC AGACCTGGG GTGATGGCTT TCCCCCTCTT GGGCGGACG 1260
 TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA 1320
 GACAGCTCCC AGGCACGTCA TAGGCAAAAGC CTGTTTCCCC CGACTCAGGA TTTCAAAGGC 1380
 CTGGGGTCTT GCTCACCCCTT CTTTGTCTCT ACGCCAGCCG TGTCCCCAGG TTTCAGCTGG 1440
 25 GAGAGGGCAC CTCCCTCAGC CAAGGAAAC GAGAACCCCC AGGATACAGG AGGAGGCTGG 1500
 GGCAGGTCCC CTGGGTGTC ACTCCCTCAG CCCTGCCCA GGGCCACTCC CGCTGGTGCT 1560
 GGAGTACGCA CTGGTGGGG GGCCTGCTC AGCCCCACCT GGAGGGTCCC AGTGTACCA 1620
 GAACCAAGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGG 1680
 TCAGTGTGTG TGGGGCGCAG GGCCTCCGAT CGGGGGTTCAG TGCCTGGGG GCGCAGGGCC 1740
 30 CCCGATGCGG GGTCACTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACCTTGGT 1800
 ACACCTGTCC ACAAGGCACC TGTCTCAGAG GAGGGGGCCT GGCAGGCAGC GTGGCAACTC 1860
 CCTTCCGGAG CGACGCTCCA TGCTAAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCT 1920
 TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980
 GCCCTCCTAC CTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG CCAGGCCTGG 2040
 35 ACCTCTGGG CAGGAAAGGG TGCAGGTCTT GAGGGCTGT GCGCCACAGC CCGACACCC 2100
 AGGTGGAAGT CACGCGCAGT GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGCTCAGCA 2160
 GGTGGGGTTC TGCCCAACAG GGCCTCCCCA CGTCTGCCTT TGAGGGTGGC TGCCATGCC 2220
 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCG 2280
 GGTGACTTCA TCAGGAGACC GCCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340
 40 GAGACAGGCT GGCACCTCCG GAAAACTGC CTTTCAGCCT TGGTGTTCCT TGCAAGGTGA 2400
 AAAGAAATAG GTCTCCACAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCTGGAGAC 2460
 CACGAGGGGA GAATTTAAG GCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520
 GCAGACCTCG CTTGGAGCCT GCCCTAGGAC GCTGGGGCGG TCAGTCTCCG TGCAGGATGT 2580
 GAGCAGCGTC CTTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACACCT 2640
 45 GCGTGACAC CAGTGTGACA CCGGAAATG TCTCAGGATG TTGAATGTG TCCTTGGGG 2700
 CAGAAGTGTG CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA 2760
 TTTTGTGTTG ATCAAGTTGC AAGGAAAGG AACATCTCAG CCGGGCGTGG TGGTTACGC 2820
 50 TTGGAATCCC AGCACTTTCG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCCATCTCT ACAAAAAA AAAAAGAAAG AAAGAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTTT ATATATCTAA 3060
 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

A177 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

60 1 11 21 31 41 51
 | | | | |
 GCGGAACACC GGGCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
 TCCCTCGTGG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCAGCG 120
 65 CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGAGG GCGGGAGGCG 180
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTTCAT GGGCTGCCCT GGGCAAGAGC 240
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAGGGGTC 420
 70 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
 ACAGCATCAC GGGGCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
 AGACAGGCTG GTTGTGTTG AATAAGCCAC TGGACCCGGA GGAGATTGCG AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTA GAGAAATGTT CCTCAGTGGG GGACCCCATC AACATCTCCA 660
 75 TCATCGTGAC CGACCAAGT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
 AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
 CCAGTGGCCT GGACCGGGAA AAAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
 80 ACAATGCTCC CATGTTTGAC CCCAGAAAGT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080
 GCCATGAGGT CAGAGGGCTG ACGGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC 1140
 GTGCGACCTA CCTTATCATG GCGGGTACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CCAGGGCATC CTGACACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
 AGCACACCCT GTACGTTGAA GTGACCAAG AGGCCCTTT TGTGCTGAG CTCCCAACCT 1320
 CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGCTCCAC 1380

5
10
15
20
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30

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CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
CTGCAGAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500
CAGGGTGCGT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560
GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC 1740
ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCACAC CTCCCCTTTC CAGGCCGAGC 1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG 1920
ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
ATGTCGAAAC CTGCGCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
TCTTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160
AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
AGGCCAGGCG GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
TGTACCGTCC TAGGCCAGCC AACCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
AGGGCGCTAA CACAGACCCC ACAGCCCGCG CCTACGACAC CCTCTTGGTG TTCGACTATG 2400
AGGGCAGCGG CTCGACGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520
ACGGTGGCGG GGAGGACGAC TAGGCGGCCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC 2580
CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTCG GAGCTTGTCA 2640
GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTAG AGTGGTGTCT 2700
TCCTTAGCCT TTAGGATGG AGGAATGTGG GCAGTTTAC TTCAGCAGT AAAACCTCTC 2760
CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820
TGCTCAACCC TGTGTCTGTG GCCTGGGCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940
TCAAAACGTT AGAGAAAGTT CTTCAAAGT GCAGCCGAGA GCTGCTGGGC CCATGCGCCG 3000
TCCTGCATT CTGTTTCCA GACCCCAATG CCTCCCATC GGATGGATCT CTGCGTTTTT 3060
ATACTGAGTG TGCCTAGGTT GCCCTTATT TTTTATTTT CCTGTTGCGT TGCTATAGAT 3120
GAAGGGTGAG GACAATCGTG TATATGTACT AGAACTTTTT TATTAAAGAA A

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A178 Protein sequence:

35
40

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Gene name: Cadherin 3, P-cadherin (placental)
Unigene number: Hs.2877
Probeset Accession #: X63629
Protein Accession #: CAA45177
Signal sequence: 1-24
Transmembrane domain: 659-675
Cellular localization: plasma membrane

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45
50
55
60

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1 11 21 31 41 51
MGLPRGPLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEEQEPGQA LGKVFMGCPG 60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
KGFPPQRLNQ LKSNKDRDTH IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREBIK 180
YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSIIHS EPKDPHDLMF THIRSTGTIS VISSGLDREK VPEYTLTIQA 300
TMDGDGDSRT TAVAVVEILD ANDNAPMFD P KYEAHVPE AVGHEVQRLT VTDLDAPNSP 360
AWRATYILIM GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVG EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
DPAGWLAMDP DSGQVTA VGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540
VNDHGPVPEP RQTICNQSP VRHVLNITDK DLSPHSTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKKFL KQDTYDVHLS LSDHGKNEQL TVIRATVDCD HGHVETCPGP WKGGFILLPV 660
GAVLALLFL LVLLLLVRKK RKIKEPLLLP EDDTRDNVVF YGEEGGGEED QDYDITQLHR 720
GLEARPEVVL RNDVAPTII TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF 780
DYESGSGDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEED

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A179 DNA SEQUENCE

60
65

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Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
Unigene number: Hs.258583
Probeset Accession #: NM_012152
Nucleic Acid Accession #: NM_012152
Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

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70
75
80

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1 11 21 31 41 51
CTTCTTTTAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGACTGGACA 120
GGAACAAGAG TTGTGATGTG TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT 180
TCTAATCTCT TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC 240
TACCTGTGTG CTAATTTAGC TGCTGCCGAT TTCTTCGCTG GAATTGCCTA TGTATTCTCT 300
ATGTTTAAAC CAGGCCCAGT TTCAAAAAC TTGACTGTCA ACCGCTGGTT TCTCCGTCAG 360
GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420
AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480
CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTATG GGGCGGTCCC CACACTGGGC 540
TGGAAATTGCC TCTGCAACAT CTCTGCCTGC TCTTCCCTGG CCCCATTFTA CAGCAGGAGT 600
TACCTTGTCT TCTGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGTGTAC 660
CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGCT TGTCTCCGCA TACAAGTGGG 720
TCCATCAGCC GCCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780

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GCGTTTGTGG TATGCTGGAC CCCGGGCTTG GTGGTTCTGC TCCTCGACGG CCTGAACTGC 840
 AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCCCTGC TGTGGGCGCT GCTCAACTCC 900
 GTCGTGAACC CCATCATCTA CTCCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960
 ATGATCTGCT GCTTCTCTCA GGAGAACCAC GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020
 GTCTCAGCA GAGTGCACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080
 GTCTGCAATA AAAGCACTTC CTAAGCTCTG GATGCTCTC GGGCCACCCA GGTGATGACT 1140
 GTCTTAGG

A180 Protein sequence:

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 Probeset Accession #: NM_012152
 Protein Accession #: NP_036284
 Signal sequence: none found
 Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIVLCVGTFF CLFIFFSNSL VIAAVIKNRK 60
 FHFFFYLLA NLAAADFFAG IAYVFLMFNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120
 LVIAVERHMS IMRMVHNSL TKKRVTLLIL LVWAIAlFMG AVPTLGNWCL CNISACSSLA 180
 PIYSRSYLVF WTVSNLMAFL IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT 240
 VMTVLGAFVW CWTPLVLVLL LDGLNCRQCG VQHVKRWFL LALNSVNP IISYKDEDM 300
 YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

A181 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.162859
 Probeset Accession #: AA569531
 Nucleic Acid Accession #: AA569531
 Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGACCTACA GTTACTCATT TTTCAGGCCT GAGTTGATCG TTAATCATCT TAATTATGTT 60
 CATTCTGAAG CCAACAGGAG AACCAAGACC AAAACTTTAT TGTCTCTGCT TTCATTTCCT 120
 GATGAAACCT CTGGACTAAG CACACATCTT CCTTGTATTAT CTCTCTCAA GGAGTGTGGA 180
 GTGCTTCATC TGGACATCCA CGGGAAGAAG GAAGACATGA GAATCACCCA ACAGTCTTCC 240
 CAGCTATACC TGTGGGACAT GGGTGGTTTT ACAATATTTA AGAACCTGTG GATGAGCCTC 300
 ATACCCAGAG GGAACAAACG CTCGCCAAAA AGAGTTACAG AAACCATCCT GAGAGATTTT 360
 AAGCAGAAGC AAAGTTCAAA GATCCAAGAG GAGAGACGAA GAGAGTCTGC AGGACCAAAC 420
 CTCTCTTCAT TCTGTTTGT GGGGAATGCT GGAAGAGGAG ACAGGCCCCA GATTGGGCA 480
 GGAAGTAAAC AGTTTTCAGG CTGAGGCCAA TCTGAGCAGG AACATTCCAA TATTCTTCA 540
 GCTACGTTGT CCCAGCACTT CACTGGTTAA CCTTTTATGT CCACCATTTG TGGATTTCAC 600
 AGCTACTTGT CAATGGTGAA TATTGATCAT CATCATTATC TACTGAGCTG CTACCATATC 660
 CCAGTACTC CTTGCATGTT GTTCATTATT TTCTCAACAC TCAGCATATT TGCAATATGT 720
 TATGTAATAT CCAACTGAAC GAAACTGAAC GCAGAAATGT TTTATTTCTT GCCAAACATC 780
 ACATGAGGAT GAACAATGAA ACCGATTGTA AACAGGATT GTCTGATTCC AACATCTCTG 840
 GGTCTTTTT CACTCTGATA TGCTGCAATT AAAAGCCAT TTCTAAGACT GT

A182 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.162859
 Probeset Accession #: AA569531
 Protein Accession #: none found
 Signal sequence: 1-46
 Transmembrane domains: none found
 Cellular Localization: not determined

1 11 21 31 41 51
 MTYSYSFFRP ELIVNHLNYV HSEANRRTKT KTLSSLSSFL DETSGLSLTHL PCLSLSKCEG 60
 VLHLDIHGKK EDMRITQSS QLYLWDMGGF TIFKNLWMSL IPRGNKRSPK RVTETILRDF 120
 KQKQSSKIQE ERRRESAGPN LSSFVFWGNA GRGDRPQIWA GSKQFSG

A183 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.179809
 Probeset Accession #: N95796
 Nucleic Acid Accession #: XM_050197
 Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 TCACACGTGC CAAGGGGCTG GCTCAGCGGA ACCAGCCTGC ACGCGCTGGC TCCGGGTGAC 60
 AGCCCGCGCG CTCGGCCAGG ATCTGAGTGA TGAGACGTGT CCCCACTGAG GTGCCCCACA 120
 GCAGCAGGTG TTGAGCATGG GCTGAGAAGC TGGACCGGCA CCAAAGGGCT GGCAGAAATG 180
 GGCGCCTGGC TGATTCCTAG GCAGTTGGCG GCAGCAAGGA GGAGAGGCCG CAGCTTCTGG 240
 AGCAGAGCCG AGACGAAGCA GTTCTGGAGT GCCTGAACGG CCCCTGAGC CCTACCCGCC 300

TGGCCCACTA TGCTCCAGAG GCTGTGGGTG AGCCGCCTGC TGCGGCACCG GAAAGCCCAG 360
 CTCTTGCTGG TCAACCTGCT AACCTTTGGC CTGGAGGTGT GTTTGGCCCG AGGCATCACC 420
 TATGTGCCCG CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTTCATGAC CATGGTGTCTG 480
 5 GGCAATTGGT CAGTGTGGG CCTGTCTGT GTCCCGCTCC TAGGCTCAGC CAGTGACCAC 540
 TGGCGTGGAC GCTATGGCCG CGCGCGGCC TFCATCTGGG CACTGTCCTT GGGCATCCTG 600
 CTGAGCCTCT TTCTCATCCC AAGGGCCGGC TGGCTAGCAG GGCTGCTGTG CCCGGATCCC 660
 AGGCCCTGG AGCTGGCACT GCTCATCTG GCGTGGGGC TGCTGGACTT CTGTGGCCAG 720
 GTGTGCTTCA TCCACTGGA GGCCCTGCTC TCTGACCTCT TCCGGGACCC GGACCACTGT 780
 10 CGCCAGGCCT ACTCTGTCTA TGCCCTCATG ATCAGTCTTG GGGGCTGCCT GGGCTACCTC 840
 CTGCCCTGCA TTGACTGGGA CACCAGTGCC CTGGCCCCCT ACCTGGGCAC CCAGGAGGAG 900
 TGCCCTTTTG GCTCTCTCAC CCTCATCTT CTACCTCGG TAGCAGCCAC ACTGCTGGTG 960
 GCTGAGGAGG CAGCGCTGGG CCCCACCGAG CCAGCAGAAG GGCTGTCCGC CCCCTCCTG 1020
 TCGCCCACT GCTGTCCATG CGGGGCCCCG TTGGCTTTCC GGAACCTGGG CGCCCTGCTT 1080
 15 CCCCCTGTC ACCAGCTGTG CTGCGCATG CCCCACACC TCGCGCCGCT CTTCGTGGCT 1140
 GAGCTGTGCA GCTGGATGG ACTCATGACC TTCACGCTGT TTACACGGA TTTCGTGGGC 1200
 GAGGGGCTGT ACCAGGCGT GCCCAGAGCT GAGCCGGGCA CCGAGGCCCG GAGACACTAT 1260
 GATGAAGGCG TTCCGATGGG CAGCCTGGGG CTGTTCTGTC AGTGCGCCAT CTCCCTGGTC 1320
 TTCTCTCTGG TCATGGACCG GCTGGTGCG CGATTGCGCA CTCGAGCAGT CTATTGGGCC 1380
 AGTGTGGCAG CTTTCCCTGT GGCTGCCGGT GCCACATGCC TGTCCACAG TGTGGCCGTG 1440
 20 GTGACAGCTT CAGCCGCCCT CACCGGGTTC ACCTTCTCAG CCCTGCAGAT CCTGCCCTAC 1500
 ACACTGGCCT CCCTCTACCA CCGGAGAGA CAGGTGTTCC TGCCCAAATA CCGAGGGGAC 1560
 ACTGGAGGTG CTAGCAGTGA GGACAGCCTG ATGACCAGCT TCCTGCCAGG CCTTAAGCCT 1620
 GGAGCTCCCT TCCCTAATGG ACACGTGGGT GCTGGAGGCA GTGGCCTGCT CCCACCTCCA 1680
 CCGCGCTCT GCGGGGCCCT TGCTGTGAT GTCTCCGTAC GTGTGGTGGT GGGTGAGCCC 1740
 25 ACCGAGGCCA GGTGGTTC GGGCCGGGCT ATCTGCCTGG ACCTCGCCAT CTGGATAGT 1800
 GCCTTCCTGC TGTCCAGGT GGCCTCATCC CTGTTTATGG GCTCCATGT CCAGCTCAGC 1860
 CAGTCTGTCA TGCCCTATAT GGTGTCTGCC GCAGGCCTGG GTCTGCTCGC CATTTACTTT 1920
 GCTACACAGG TACTATTGA CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAAACTTCC 1980
 30 AGCACATTGG GGTGGAGGGC CTGCTCACT GGGTCCCAGC TCCCCTGCTC TGTAGCCCC 2040
 ATGGGGCTGC CCGGCTGGCC GCCAGTTTCT GTTGTGCCA AAGTAATGTG GCTCTCTGCT 2100
 GCCACCTGT GCTGCTGAGG TGCCTAGCTG CACAGCTGGG GGCTGGGGC TCCCTCTCCT 2160
 CTCTCCCGAG TCTCTAGGGC TGCTGACTG GAGGCCTTCC AAGGGGGTTT CAGTCTGGAC 2220
 TTATACAGG AGGCCAGAA GGCTCCATGC ACTGGAATGC GGGACTCTG CAGGTGGATT 2280
 35 ACCCAGGCTC AGGGTTAACA GCTAGCCTCC TAGTTGAGAC ACACCTAGAG AAGGGTTTTT 2340
 GGGAGCTGAA TAAACTCAGT CACCTGGTTT CCCATCTCTA AGCCCTTAA CCTGCAGCTT 2400
 CGTTAATGT ATGCTCTTGA TGGGAGTTTC TAGGATGAAA CACTCTCCA TGGGATTGA 2460
 ACATATGAAA GTATTTTGTA GGGGAAGAGT CCTGAGGGGC AACACACAAG AACAGGTCC 2520
 CCTCAGCCCC ACAGGCACTG GTCTTTTTTG CTNGANTCCA CCCCCCCCCT CTTTACCCTT 2580
 TT

A184 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.179809
 45 Probeset Accession #: N95796
 Protein Accession #: XP_050197
 Signal sequence: none
 Transmembrane domains: 21-43, 53-75, 90-112, 125-147, 160-182, 199-221, 323-345, 350-372, 379-401
 50 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 55 MVQRLWVSRL LRHRKAQLLL VNLTFGLEV CLAAGITYVP PLLLEVGVVEE KFMTMVLGIG 60
 PVLLGLVCPVL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL 120
 ELALLILGVG LLDFCGQVCF TPLEALLSDL FRDPDHCRA YSVYAFMISL GGCGLYLLPA 180
 IDWTSALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH 240
 CCPCRARLAF RNLGALLPRL HQLCCRMPT LRRLEVAELC SWMALMTFTL FYTDFVGEGL 300
 60 YQGVPAEPG TEARRHYDEG VRMGSLLGLFL QCAISLVFSL VMDRLVQRFQ TRAVYLASVA 360
 AFPVAAGATC LSHSVAVVTA SAALTGTFTS ALQILPYTLA SLVHREKQVF LPKYRGDTGG 420
 ASSEDSLMTS FLPGPKPGAP FPNHVGAGG SGLLPPPPAL CGASACDVSV RVVVGPEPTEA 480
 RVVPGRGICL DLAILDSAFI LSQVAPSLFM GSIVQLSQSV TAYMVSAAGL GLVAIFYFATQ 540
 VVFPKSLDAK YSA

A185 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.11260
 Probeset Accession #: R73640
 70 Nucleic Acid Accession #: AK002126
 Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 75 ATGGTTCGCC GGGGGCTGCT TGCGTGGATT TCCCGGGTGG TGGTTTGTCT GGTGCTCCTC 60
 TGCTGTGCTA TCTCTGTCT GTACATGTTG GCCTGCACCC CAAAAGGTGA CGAGGAGCAG 120
 CTGGCACTGC CCAGGGCCAA CAGCCCCACG GGAAGGAGG GGTACCAGGC CGTCTCTCAG 180
 80 GAGTGGGAGG AGCAGACCG CACTACGTG AGCAGCCTGA AGCGGCAGAT CGCACAGCTC 240
 AAGGAGGAGC TGCAGGAGAG GAGTGAGCAG CTCAGGAATG GGCAGTACCA AGCCAGCGAT 300
 GCTGCTGGCC TGGGTCTGGA CAGGAGCCCC CCAGAGAAAA CCCAGGCCGA CCTCTGGCC 360
 TTCTGCACT CGCAGGTGGA CAAGGCAGAG GTGAATGCTG GCGTCAAGCT GGCCACAGAG 420
 TATGCAGCAG TGCCTTTTGA TAGCTTTACT CTACAGAAGG TGTACCAGCT GGAGACTGGC 480
 CTTACCCGCC ACCCCGAGGA GAAGCCTGTG AGGAAGGACA AGCGGGATGA GTTGGTGGAA 540
 GCCATTGAAT CAGCCTTGGA GACCCTGAAC AATCTGCAG AGAACAGCCC CAATCACCGT 600

CCTTACACGG CCTCTGATTT CATAGAAGGG ATCTACCGAA CAGAAAGGGA CAAAGGGACA 660
 TTGTATGAGC TCACCTTCAA AGGGGACCAC AAACACGAAT TCAAACGGCT CATCTTATTT 720
 CGACCATTTCG GCCCCATCAT GAAAGTGAAA AATGAAAAGC TCAACATGGC CAACACGCTT 780
 ATCAATGTGA TCGTGCCTCT AGCAAAAAGG GTGGACAAGT TCCGGCAGTT CATGCAGAAT 840
 TTCAGGGAGA TGTGCATTGA GCAGGATGGG AGAGTCCATC TCACTGTGTG TTACTTTGGG 900
 AAAGAAGAAA TAAATGAAGT CAAAGGAATA CTTGAAAACA CTTCCAAAGC TGCCAACTTC 960
 AGGAACCTTA CCTTCATCCA GCTGAATGGA GAATTTTCTC GGGGAAAGGG ACTTGATGTT 1020
 GGAGCCCCGT TCTGGAAGGG AAGCAACGTC CTTCTCTTTT TCTGTGATGT GGACATCTAC 1080
 TTCACATCTG AATTCTCTCA TACGTGTAGG CTGAATACAC AGCCAGGGAA GAAGGTATTT 1140
 TATCCAGTTC TTTTCAGTCA GTACAATCCT GGCATAATAT ACGGCCACCA TGATGCAGTC 1200
 CCTCCCTTGG AACAGCAGCT GGTCAATAAG AAGGAAACTG GATTTTGAG AGACTTTGGA 1260
 TTTGGGATGA CGTGTCACTA TCGGTTCAGC TTCATCAATA TAGGTGGGTT TGATCTGGAC 1320
 ATCAAAGGCT GGGCGGAGA GGATGTGCAC CTTTATCGCA AGTATCTCCA CAGCAACCTC 1380
 ATAGTGGTAC GGAGCCCTGT GCGAGGACTC TTCCACCTCT GGCATGAGAA GCGCTGCATG 1440
 GACGAGCTGA CCCCCGAGT GTACAAGATG TGCATGCAGT CCAAGGCCAT GAACGAGGCA 1500
 TCCCACGGCC AGCTGGGCAT GCTGGTGTTC AGGCACGAGA TAGAGGCTCA CCTTCGCAAA 1560
 CAGAAACAGA AGACAAGTAG CAAAAAACA TGA

A186 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.11260
 Probeset Accession #: R73640
 Protein Accession #: NP_060841
 Signal sequence: 1-26
 Transmembrane domains: none found
 Cellular Localization: not determined

1 11 21 31 41 51
 MVRRLGLAWI SRVVVLVLL CCAISVLYML ACTPKGDEEQ LALPRANSPT GKEGYQAVLQ 60
 EWEEQHRNVY SSKLRQIAQL KEELQERSEQ LRNGQYQASD AAGLGLDRSP PEKTDADLLA 120
 FLHSQVDKAE VNAGVKLATE YAAVPFDSFT LQKVYQLETG LTRHPEEKPV RKDKRDELVE 180
 AIESALETLN NPAENSPNHR PYTASDFIEG IYRTERDKGT LYELTFKGDH KHEFKRLILF 240
 RPFPGIMVKV NEKLNMANTL INVIVPLAKR VDKFRQEMQN FREMCIEQDG RVHLTVVYFG 300
 KEBINEVKGI LENTSKAANF RNFTFIQLNG EFSRKGGLDV GARFWKGSNV LFFCDVDIY 360
 FTSEFLNTRC LNTQPGKKVF YPVLFSQYNP GIIYGHDAV PPLEQQLVIK KETGFWRDFG 420
 FGMTQYRSD FINIGGFOLD IKWGGEVDVH LYRKYLSHNL IVVRTFVRGL FHLWHEKRCM 480
 DELTPQYKM CMQSKAMNEA SHGQLGMLVF RHEIEAHLRK QKQKTSKSKT

A187 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGATTCCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
 ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
 TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTTCTGGCTT CTGCAGTCAT CAGTGTTTTA 240
 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300
 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
 CCAGAAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420
 CCAGGTGATA CAGTTTGCCCT TTCTGTGGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTC 480
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540
 AAGGTGACAG CTCTCAGGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCTT TGGACAGGA 660
 GAAAATCTGT AATTGGGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780
 ATAGGAATCA TCACTGTTGT TGGCTGGTTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840
 ATTAGTGTA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTCAAGTG 900
 ACGCTAGCTC TTGGTGTATG GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960
 ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTGGA AACACTGACG 1020
 AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080
 GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATT 1140
 TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
 AGAAACAATA CTCATAATGGG GAAGGGGCTT TAATTGCTCT TGAATGAAG 1260
 ATGGGCTCTG ATGGACTTCA ACAAGACTAC ATCAGAAAAA CTGAATACCC TTTTAGCTCT 1320
 GAGCAAAAGT GGTGCTGTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
 TGTTTTATGA AAGGTGCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAGA GAAGGCACGC 1500
 ATGGGCTCAG CGGACTCAG AGTTCTTGTG TTGGCTTCTG GTCCTGAAC TGGACAGCTG 1560
 ACATTTCTTG GCTTGGTGGG AATCATTTGAT CCACCTAGAA CTGGGTGTGA AGAAGCTGTT 1620
 ACAACACTCA TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATT 1680
 GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCAAAAA CTCCCGAGTC AGCTCAGGA 1740
 GAAGAAATAG ATGCAATGGA TGTTTCAGCAG CTTTCACAAA TAGTACCAAA GGTTCAGTA 1800
 TTTTACAGAG CAGTCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860
 TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920
 ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
 CTAGTGGATG ATGATTTTCA AACATAATG TCTGCAATCG AAGAGGGTAA AGGATTAT 2040

AATAACATTA AAAATTTTCGT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTA 2100
 ATCTCATTGG CTACATTAAAT GAACTTTCTCT AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160
 ATCAATATTA TTATGGATGG ACCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
 GATGTCATTG GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTGATA 2280
 CTTAAATAC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTGT CTTCTGGCGT 2340
 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
 TTTTGTGACA TGTTCAATGC ACTAAGTTC AGATCCCAGA CCAAGTCTGT GTTTGAGATT 2460
 GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTCTCTG GATCCATCAT GGGACAATTA 2520
 CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
 GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
 CTTGAAGTAT GA

A188 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Protein Accession #: AAF27813
 Signal sequence: none found
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
 Cellular Localization: not determined

1 11 21 31 41 51
 | | | | |
 MIPVLTSKKA SELPVSEVAS ILQADLQNGL NKCEVSHHRA FHWNEFDIS EDEPLWKYI 60
 SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVTV AFVQYRSEK SLEELSKLVP 120
 PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRFP EAVDLSIDES SLTGETTPCS 180
 KVTAPQPAAT NGDLASRSNI AFMGLTVRCG KAGGVVIGTG ENSEFGEVFK MMQAEAPKT 240
 PLQKSMDLGL KQLSFYSFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGPLIVTV 300
 TLALGVMRMV KKRAIVKKLE IVETLGCENV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360
 GVGYNQFGEV IVDGDVVHGF YNPAVSRIVE AGCVCNDAVI RNNTLMGKPT EGALIALAMK 420
 MGLDGLQDDY IRKAEYFPSS EQKWMVAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480
 GQTLTLTQQQ RDVYQQEKAR MGSAGLRVLA LASGPELGQL TFLGLVGIIID PPRTGVKEAV 540
 TFLIASGVSI KMITGDSQET AVAIA SRLGL YSKTSQSVSG EEDAMDVQV LSQIVPKVAV 600
 FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGWAMQGTGT DVCKEADMI 660
 LVDDDFQTIM SAIEEGKGIY NNIKNFVRFP LSTSIAALTL ISLATLMNFP NPLNAMQILW 720
 INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
 ELRDNVITPR DTTMTFTCFV FDFMFNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840
 LVYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVABIIK KVERSERKIQ KHVSTSSSF 900
 LEV

A189 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Nucleic Acid Accession #: N62096
 Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ATGGGCTACC AGAGGCAGGA GCCTGTGCATC CCGCCGCGAGA GAGGATTGCC TTATTCAATG 60
 AAGCAAGCTG GGTTCCTTTT GGGAAATATTG CTTTATTCTT GGGTTTCATA TGTACAGAC 120
 TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180
 TTGGTCAATA AACTTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTGTG 240
 TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300
 TTTCAAAGAA TCCAGGAGT TGATCTCGAA AACGTGTTTA TTGGTCGCCA CTTCATTATT 360
 GGACTTTCCA CAGTTACCTT TACTCTGCTT TATCCTTGT ACCGAAATAT AGCAAAGCTT 420
 GGAAAGGTCT CCCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAAAT TGTAATGGCA 480
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAG 540
 CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTTGCCA CCATAACTCC 600
 TTCTTAGTTT ACAGTTCTCT AGAAGAACC ACAGTAGCTA AGTGTCCCG CCTTATCCAT 660
 ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATTCTTTG CTACATGTGG ATACTTGACA 720
 TTTACTGGCT TCACCAAGG GGACTTATTT GAAAATTACT GCAGAAATGA TGACCTGGTA 780
 ACATTGGGAA GATTTTGTTA TGGTGTCACT GTCATTTTGA CATACCCTAT GGAATGCTTT 840
 GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTTCATC GGTTTTCCAC 900
 ATTGTTGTAA CAGTGAATGT CATCACTGTA GCCACGCTTG TGTCATTGCT GATTGATTGC 960
 CTCGGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCTCAT TTTTATCATT 1020
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080
 TCTTGTGTCA TGCTTCCCAT TGGTGTCTGT GTGATGGTTT TTGGATTCGT CATGGCTATT 1140
 ACAAACTACT AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTCC TGACAATTC 1200
 TCTCTACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
 ATTAGTATCT TTCAACTCGA GTAA

A190 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 28-50, 66-88-112-134, 142-164, 217-239, 260-282, 298-320, 327-348, 359-381

Cellular Localization: plasma membrane

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MG YQRQEPVI PPQRGLPYSM KQAGFPLGIL LLEFWVS YVTD FSLVLLIKGG ALSGTD TYQS 60
      LVNKT FGFPG YLLLSVLQFL YPFIAMISYN IIAGDTLSKV FORIPGVDPE NVFIGRHFII 120
      GLSTV TFTLP LSLYRNIAKL GKVSLISTGL TTLILGI VMA RAISLGPHIP KTEDAWVFAK 180
      PNAIQAVGVM SPAFICHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240
10     FTGFTQGDLE ENYCRNDDL VTFGRFCYGV TILTYPMECF VTREVIANVF FGNLSSVFH 300
      IVVTVMVITV ATLVSLIDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360
      SCVMLPIGAV VMVFGFVMAI TNTQDCTHQQ EMFYCFPDNF SLTNTSESHV QQTQLSTLN 420
      ISIFQLE

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A191 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Nucleic Acid Accession #: N62096
 Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

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25     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CCGCCGCAGT TTTCCCTTGT TTTATTGATA 60
      AAAGGAGGGG CCTCTCTGG AACAGATACC TACCACTCTT TGGTCAATAA AACTTTCCGGC 120
      TTTCCAGGGT ATCTGCTCCT CTCTGTCTCT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180
      AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TTCAAAGAAT CCCAGGAGTT 240
      GATCCTGAAA ACGTGTATTAT TGGTCGCCAC TTCAATTATG GACTTTCCAC AGTTACCTTT 300
30     ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT 360
      ACAGGTTTAA CAACTCTGAT TCTTGAATT GTAAATGGCAA GGGCAATTTC ACTGGGTCCA 420
      CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGCGGTC 480
      GGGGTTATGT CTTTTGCATT TATTIGCCAC CATAACTCCT TCTTAGTTTA CAGTTCCTTA 540
      GAAGAACCCA CAGTAGCTAA GTGGTCCGCG CTTATCCATA TGTCCATCGT GATTTCGTGA 600
35     TTTATCTGTA TATTCTTTCG TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660
      GACTTATTTC AAAATTACTG CAGAAATGAT GACCTGGTAA CATTGGAAG ATTTGTTAT 720
      GGTGTCACTG TCAATTTGAC ATACCTTATG GAATGCTTTG TGACAAGAGA GGTAATTGCC 780
      AATGTGTTTT TTGGTGGGAA TCTTTTCATCG GTTTTCCACA TTGTTGTAAC AGTGATGGTC 840
      ATCACTGTAG CCACGCTTGT GTCATTGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC 900
40     AATGGTGTGC TCTGTGCAAC TCCCCTCATT TTTATCATTC CATCAGCCTG TTATCTGAAA 960
      CTGTCTGAAG AACCAAGGAC ACACCTCGAT AAGATTATGT CTTGTGTCAT GCTTCCCATT 1020
      GGTGCTGTGG TGATGGTTTT TGGATTGCTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080
      CATGGGCAGG AAATGTTCTA CTGCTTTCCT GACAATTCTC CTCTCACAAA TACCTCAGAG 1140
45     TCTCATGTTT AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200
      TAA

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A192 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 Signal sequence: 1-26
 Transmembrane domains: 45-61, 92-108, 117-132, 191-207, 274-290, 297-313, 335-351
 Cellular Localization: plasma membrane

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60     1      11      21      31      41      51
      |      |      |      |      |      |
      MG YQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG PPGYLLLSVL QFLYPPFIAMI 60
      SYNIIAGDTL SKVFORIPGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLSIS 120
      TGLTTLILGI VMARAIISLP HIPKTEDAVV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL 180
      EEPTVAKWSR LIHMSIVISV FICIFFATCG YLTFTGFTQG DLFENYCRND DLVTFGRFCY 240
65     GVTVILTYPM ECFVTREVI NVPFGNLSS VFHIVVTVMV ITVATLVSLI IDCLGIVLEL 300
      NGVLCATPLI FIIPSACYLK LSEEPRTSHD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360
      HGQEMFYCFP DNFSLTNTSE SHVQQTQLS TINISIFQLE

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A193 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Nucleic Acid Accession #: N62096
 Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

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75     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CCGCCGCAGG TCAATAAAAC TTTCCGCTTT 60
      CCAGGGTATC TGCTCCTCTC TGTICTTCAG TTTTGTATC TTTTATAGC AATGATAAGT 120
      TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180
      CCGTGAACAC TGTTTATTGG TCGCCACTTC ATTATTGGAC TTTCACAGT TACCTTACT 240
80     CTGCTTTTAT CCTGTGACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300
      GGTTTAACAA CTCTGATTCT TGGAAATGTA ATGGCAAGGG CAATTTCAT GGGTCCACAC 360
      ATACCAAAAA CAGAAGACGC TTGGGTATTG GCAAAGCCCA ATGCCATTCA AGCGGTCCGG 420

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GTTATGTCCTT TTGCATTAT TTGCCACCAT AACTCCTCT TAGTTTACAG TTCTCTAGAA 480
 GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540
 ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
 TTATTTGAAA ATTAAGTCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTATGGT 660
 5 GTCACGTCA TTTTGACATA CCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
 GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCACATG TTGTAAACAGT GATGGTCAATC 780
 ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
 GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTCCAT CAGCCTGTTA TCTGAAACTG 900
 10 TCTGAAGAAC CAAGGACACA CTCCGATAAG ATTATGCTT GTGTCATGCT TCCCATTGGT 960
 GCTGTGTGA TGGTTTTTGG ATTTCGTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
 GGGCAGGAAA TGTCTACTG CTTTCTCTC AATTTCTCTC TCACAAATAC CTCAGAGTCT 1080
 CATGTTTCAGC AGACAACACA ACTTCTACT TTAAATATTA GTATCTTTCA ACTCGAGTAA

A194 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 20 Signal sequence: none found
 Transmembrane domains: 24-40, 70-86, 95-111, 171-186, 253-269, 276-292, 314-330
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MGYQRQEPVI PPQVNKTFGF PGYLLSLVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIGVD 60
 PENVFIGRHF IIGLSTVTFT LPLSLYRNIA KLKGVSLIST GLTTLILGIV MARAISLGPH 120
 30 IPKTEDAWVF AKPNAIQAVG VMSFAFICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180
 ICIFATCGY LTFTGFTQGD LFENYCRNDD LVTFGRFCYG VTVILTYPME CFVTVREVIAN 240
 VFFGNNLSSV PHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCAATPLIF IIPSACYLKL 300
 SEEPRTSHDK IMSCVMLPIG AVVMVGFVFM AITNTQDCTH QGEMFYCFPD NFSLTNTSES 360
 HVQQTQLST LNISIFQLE

A195 DNA SEQUENCE:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 40 Nucleic Acid Accession #: N62096
 Coding sequence: 1-1389 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGACAGA GAGATTAGA TGACAGAGAA 60
 ACCCTTGTTT CTGAACATGA GTATAAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120
 GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT 180
 50 GGGTTTCCTT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTTACAGA CTTTTCCCTT 240
 GTTTTATTGA TAAAAGGAGG GGCCCTCTCT GGAACAGATA CCTACCAGTC TTTGGTCAAT 300
 AAAACTTTTC GCTTTCCAGG GTATCTGCTC CTCTCTGTTT TTCAGTTTGT GTATCCTTTT 360
 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAGT TTTTCAAAGA 420
 ATCCCAGGAG TTGATCCTGA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC 480
 ACAGTTACCT TTAATCTGCC TTTATCCTTG TACCGAAATA TAGCAAAGCT TGGAAAGGTC 540
 55 TCCCTCATCT CTACAGGTTT AACAACTCTG ATTCTTGGAA TTGTAATGGC AAGGGCAATT 600
 TCACTGGGTC CACACATACC AAAAACAGAA GACGCTTGGG TATTTGCAAA GCCCAATGCC 660
 ATTCAAGCGG TCGGGGTTAT GTCTTTTGCA TTTATTTGCC ACCATAACTC CTTCTTAGTT 720
 TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
 60 GTGATTTCTG TATTTATCTG TATATCTTTC GCTACATGTG GATACTTGAC ATTTACTGGC 840
 TTCACCCCAAG GGGACTTATT TGAATAATTAC TGCAGAAATG ATGACCTGGT AACATTGGA 900
 AGATTTTGTG ATGGTGTGAC TGTCATTTTG ACATACCCCTA TGGAAATGCTT TGTGACAAGA 960
 GAGGTAATAT CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTTCCT CATTGTTGTA 1020
 ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATTGATTG CCTCGGGATA 1080
 65 GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140
 TGTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200
 ATGCTTCCCA TTGGTGTCTG GGTGATGGTT TTTGGATTGC TCATGGCTAT TACAAATACT 1260
 CAAGACTCGA CCCATGGGCA GGAATGTTC TACTGCTTTC CTGACAATTT CTCTCTCACA 1320
 70 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380
 TTTCAATGA

A196 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 75 Signal sequence: none found
 Transmembrane domains: 37-53, 66-82, 109-125, 155-172, 180-196, 255-271, 338-354, 361-377, 399-415
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60

GFPLGILLLF WVSYVTFDFSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPF 120
 IAMISYNIIA GDTLISKVFR IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIKLGKV 180
 SLISTGLTTL ILGIVMARAI SLGPHIPKIE DAWVFAKPNIA IQAVGVMSFA FICHHNSFLV 240
 YSSLEETPVA KWSRLIHMSI VISVFICIFF ATCGYLTFTG FTQGDLEFENY CRNDLDTFTG 300
 RFCYGVTVIL TYPMECFVTR EVIANVFFGG NLSSVFHIVV TVMVITVATL VSLIDLCLGI 360
 VLELNGVLCA TPLIFIPSA CYLKLSEEPH THSKIMSCV MLPIGAVVMV FGFVMAINT 420
 QDCTHGQEMF YCFPDNFSLT NTSSEHVQQT TQLSTLNISI FQ

A197 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.31608
 Probeset Accession #: H18836
 Nucleic Acid Accession #: NM_017636
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGGAGGATG CCTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACACGCGATG ACACACCACG 60
 GAGAAGCCCA CCGATGCCTA CGGAGAGCTG GACTTCACGG GGGCCGGCCG CAAGCACAGC 120
 AATTTCCTCC GGCTCTCTGA CCGAACGGAT CCAGCTGCAG TTTATAGTCT GGTCAACAGC 180
 ACATGGGGCT TCCGTGCCCC GAACCTGGTG GTGTCACTGC TGGGGGGATC GGGGGGCCCC 240
 GTCTCCAGA CCTGGCTGCA GGACCTGCTG CGTCGTGGGC TGGTGCGGGC TGCCAGAGC 300
 ACAGGAGCCT GGATTGTAC CAGGAGCTG CACACGGGCA TCGGCGGCA TGTGGTGTG 360
 GCTGTACGGG ACCATCAGAT GGCCAGCACT GGGGGCACCA AGGTGGTGGC CATGGGTGTG 420
 GCCCCTGGG GTGTGGTCCG GAATAGAGAC ACCCTCATCA ACCCAAGGG CTCGTCCCT 480
 GCGAGGTACC GGTGCGCGG TGACCCGGAG GACGGGTCC AGTTTCCCTT GGACTACAAC 540
 TACTCGGCTT TCTTCTGGT GGACGACGGC ACACACGGCT GCCTGGGGGG CGAGAACCAG 600
 TTCCGCTTGC GCTTGGAGTC CTACATCTCA CAGCAGAAGA CGGGCGTGGG AGGGACTGGA 660
 ATTGATCATC CTGTCTGTCT CCTCTGATT GATGGTGTG AGAAGATGT GACGCGAATA 720
 GAGAAGCCCA CCGAGCTCA GCTCCCATGT CTCTCGTGG CTGGCTCAGG GGGAGCTGCG 780
 GACTGCCTGG CGGAGACCCT GGAAGACACT CTGGCCCCAG GGAGTGGGGG AGCCAGGCAA 840
 GGCGAAGCCC GAGATCGAAT CAGGCGTTTC TTTCCTCAAG GGGACCTTGA GGTCTCTCAG 900
 GCCCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCTCTA CAGTCTATTC TTCTGAGGAT 960
 GGGTCTGAGG AATTCGAGAC CATAGTTTTC AAGGCCCTTG TGAAGCCCTG TGGGAGCTCG 1020
 GAGGCTCAG CCTACTGGA TGAGCTGCGT TTGGCTGTGG CTGGAACCG CGTGGACATT 1080
 GCCCAGAGTG AACTCTTTTG GGGGACATC CAATGGCGGT CCTTCCATCT CGAAGCTTCC 1140
 CTCATGAGAG CCCTGCTGAA TGACCGGCTT GAGTTCTGTC GCTTGTCTAT TTCCACGGC 1200
 CTCAGCTGG GGCATCTCTT GACCCGATG CGCTGGGCC AACTCTACAG CGCGCGGCC 1260
 TCCAATCTGC TCATCGCAA CCTTTTGGAC CAGGCGTCCC ACACGCGAGG CACCAAGGCC 1320
 CCAGCCCTAA AAGGGGAGC TGCGGAGCTC CGGCCCTCG ACGTGGGGCA TGTGCTGAGG 1380
 ATGCTGTGG GGAAGATGTG CGCGCGAGG TACCCCTCCG GGGGCGCCTG GGACCTCAC 1440
 CCAGGCCAGG GCTTCGGGGA GAGCATGTAT CTGCTCTCG ACAAGGCCAC CTCGCCCTC 1500
 TCGCTGGATG CTGGCTCGG GCAGGCCCCC TGGAGCGACC TGCTTCTTTT GGCAGTGTG 1560
 CTGAACAGGG CACAGATGGC CATGTACTTC TGGGAGATGG GTTCCAATGC AGTTTCTCTA 1620
 GCTCTTGGGG CCTGTTTGTCT GCTCCGGGTG ATGGCACGCC TGGAGCCTGA CGCTGAGGAG 1680
 GCAGCACGGA GGAAGACCTT GCGTTCAAG TTTAGGGGA TGGCGTTGA CTTCTTTGGC 1740
 GAGTGTCTAT GCAGCAGTGA GGTGAGGGCT GCCCGCTCC TCCTCCGTCG CTGCCCGCTC 1800
 TGGGGGGATG CCACTTGCCT CCAGCTGGCC ATGCAAGCTG ACGCCCGTGC CTCTTTTGCC 1860
 CAGGATGGGG TACAGTCTCT GCTGACACAG AAGTGGTGGG GAGATATGGC CAGCACTACA 1920
 CCCATCTGGG CCTGTGTTCT GCGCTTCTTT TGCCCTCCAC TCATCTACAC CCGCTCATC 1980
 ACCTTCAGGA AATCAGAAGA GGAGCCACA CGGGAGGAGC TAGAGTTTGA CATGGATAGT 2040
 GTCATTAATG GGAAGGGGCC TGTGGGACG GCGGACCCAG CCGAGAAGAC GCCGCTGGG 2100
 GTCCCGCGCC AGTCGGGCGG TCCGGGTGTC TCGGGGGGCC GCTGCGGGGG GCGCCGGTGC 2160
 CTACGCGCTG GGTTCACCTT CTGGGGCGCG CCGGTGACCA TCTTCATGGG CAACGTGGTC 2220
 AGCTACCTGC TGTTCCTGCT GCTTTTCTCG CGGTGCTGC TCGTGGATT TCAGCCGGCG 2280
 CCGCCCGGCT CCTTGGAGCT GCTGCTCTAT TTCTGGGCTT TCACGCTGCT GTGCGAGGAA 2340
 CTGCGCCAGG CCGTGAAGCG AGGCGGGGCG AGCTCGCCA GCGGGGGCCC CGGGCTTGGC 2400
 CATGCTCTAC TGAGCCAGCG CCTGCGCTC TACCTCGCCG ACAGCTGGAA CCAGTGGCAG 2460
 CTAGTGGCTC TCACCTGCTT CCTCTGGGC GTGGGCTGCC GGCTGACCCC GGGTTTGTAC 2520
 CACCTGGGCC GCACCTGCTT CTGCTGACG TTCTATGGTT TCACGGTGGC GCTGCTTAC 2580
 ATCTTACAGG TCAACAACAG GCTGGGGCCC AAGATCGTCA TCGTGAGCAA GATGATGAAG 2640
 GACGTGTCTT TCTTCTCTT CTTCTCGGC GTGTGGCTGG TAGCCTATGG CGTGGCCAGC 2700
 GAGGGGCTCC TGAGGCCAGG GACACAGTAC TTCCCAAGTA TCCTGCGCCG CGTCTTCTAC 2760
 CGTCCCTACC TGCAGATCTT CCGGCAGATT CCCCAGGAG ACATGGACGT GGCCCTCATG 2820
 GAGCACAGCA ACTGCTCGTC GGAGCCCGGC TTCTGGGCAC ACCCTCTGGG GGCCAGGGC 2880
 GGCACCTGCG TCTCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCTCTGT CATCTTCTG 2940
 CTGCTGGCCA ACATCTGCT GGTCAACTTG CTCATTGCCA TGTTCAGTTA CACATTGGC 3000
 AAAGTACAGG GCAACAGCGA TCTCTACTGG AAGGCGCAGC GTTACCGCTT CATCCGGGAA 3060
 TTCCACTCTC GGGCCGCGCT GGGCCCGCCC TTTATCGTCA TCTCCACTT GCGCTCTCTG 3120
 CTAGGCAAT TGTGCAAGCG ACCCGGAGC CCCCAGCGCT CCTCCCGGCG CCGAGCAT 3180
 TTCCGGGTTT ACCTTTCTAA GGAAGCCGAG CGGAAGCTGC TAACGTGGGA ATCGGTGCAT 3240
 AAGGAGAACT TCTGCTGGC ACGGCTAGG GACAAGCGGG AGAGCGACTC CGAGCGTCTG 3300
 AAGCGCAAGT CCCAGAAGGT GACTTGGCA CTGAAACAGC TGGGACACAT CCGGAGTAC 3360
 GAACAGCGCC TGAAGTGTCT GGAGCGGAG GTCCAGCAGT GTAGCCCGCT CCTGGGGTGG 3420
 GTGGCCGAGG CCTTGGCCG CTCTGCCCTT CTGCCCCAG GTGGCGGCC ACCCCCTGAC 3480
 CTGCTGGGT CCAAGACTG A

A198 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.31608
 Probeset Accession #: H18836
 Protein Accession #: none found

Signal sequence: none found
 Transmembrane domains: 214-230, 537-556, 642-662, 730-752, 760-782, 815-837, 842-864, 877-899, 973-995
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MEDAFGAADV TVWSDAHTT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR 60
TWGFRAPNLV VSVLGGSGGP VLQTLWQDLL RRGLVRAAQS TGAWIVTGGL HTGIGRHVGV 120
AVRDHQMAST GGTKVVMGV APWGVVRNRD TLINPKGSFP ARYRWRGDPE DGVOFPLDYN 180
YSAFFLVDDG THGCLGGENR FRLRLSEYIS QQKTGVGGTG IDIPVLLLLI DGDEKMLTRI 240
ENATQAQLPC LLVAGSGGAA DCLAETLEDT LAPGSGGARQ GEARDRIIRF FPKGDLEVLQ 300
AQVERIMTRK ELLTVYSSD GSEEFETIVL KALVKACGSS EASAYLDEL R LAVANNRVDI 360
AQSELFRGDI QWRSFHLEAS LMDALLNDRP EFVRLISHG LSLGHFLTPM RLAQLYSAAP 420
15  SNSLIRNLD QASHSAGTKA PALKGGAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480
PGQGFESMY LLSDKATSP LSLDAGLGQAP WSDLLWALL LNRAQMAMYF WEMGSNAVSS 540
ALGACLLLRV MARLEPDABE AARRKDLAFK FEGMGVDLFG EYRSSEVRA ARLLLRRCPL 600
WGDATCLQLA MQADARAFFA QDGVQSLLTQ KWWGDMASTT PIWALVLAFF CPPLIYTRLI 660
20  TFRKSEBEPT REELEFDMDS VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGGRCCGRRC 720
LRRWFHFWGA PVTIFMGNVV SYLLFLLLF S RVLLVDFQPA PPGSLELLLY FWAFTLLCEE 780
LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840
HLGRTVLCID FMVFTVRLH IFTVNKQLGP KIVIVSKMMK DVFFFLFPLG VWLVAYGVAT 900
BGLLRPRDSD FPSILRRVFI RPYLQIFGQI PQEDMDVALM EHSNCSSEPG FWAHPGGAQA 960
25  GTCVSQYANW LVVLLLVIFL LVANILLVNL LIAMFSYTFG KVQGNSDLYW KAQRYRLIRE 1020
FHSRPAALAP FIVISHLRL LRQLCRRPRS PQSPSPALEH FRVYLSKEAE RKLLTWESVH 1080
KENFLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY BQRLKVLERE VQCSRVLGW 1140
VAEALSRSAL LPPGGPPPPD LPSKSD

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A199 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.40808
 Probeset Accession #: AA054237
 Nucleic Acid Accession #: AA054237
 Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCTTGGGG 60
CTGCTCGTCA CGGCATCTT CACCGACCAC TGGTACGAGA CCGACCCCGG GCGCCACAAG 120
40  GAGAGCTGCG AGCGCAGCCG CGCGGGCGCC GACCCCCCGG ACCAGAAGAA CCGCTGATG 180
CGCTGTCCGC ACCTGCGCGT CGCGGACTCG CCCCCTGTGG GCGCGCGGCT GCTCCCGGGC 240
GCGCCGGGGC GCGCGACCC CGAGTCTCGG CGCTCGCTCC TGGGGCTCGG CGGGCTGGAC 300
GCGAGTGGG GCGCGCCCT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
45  CTGGGCATCG ACCGGGACAT CGACACCCCT ATCCTGAAAG GTATTGCGCA GCGATGCACG 420
GCCATCAAGT ACCACTTTT TCAGCCCATC CGCTTCGGA ACATTCTTT TAATTAAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTTAA GAAGAATCAC TGCTGGCTTC 540
CTCGGCATGG CCGTAGCCGT CCTTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGACTCCTGT TCCTCATGAC AGGGATATTT 660
50  TGCAACATTT CCTCTGTGAC TTATGCGGCC AGTATCTCGT ATGATTTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCCTGCC TGCTGATGTG GAACATGGT ACAGCTGGTC CATCTTTTGC 780
GCTGTGTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT 840
ATTAGCCGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA

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A200 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.40808
 Probeset Accession #: AA054237
 Protein Accession #: none found
 Signal sequence: 1-18
 Transmembrane domains: 179-201, 209-231, 257-279
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DPPDQKNRLM 60
PLSHLPLRDS PPLGRRLLPG GPGRADPEW RSLGLGLGLD AECGRPLFAT YSGLWRKCYF 120
65  LGIDRDIDTL ILKGIAQRCT AIKYHFSQPI RLRNIPFNLT KTIQDEWHL LHLRRITAGF 180
LGMMAVAVLLC GCIVATVSFF WEESLTQHVA GLLFLMTGIF CTISLCTYAA SISYDLNRLP 240
70  KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

```

A201 DNA SEQUENCE

Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Nucleic Acid Accession #: NM_016570
 Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGAGGCGAC TGAATCGGAA AAAAAGTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTCCG 60
80  AAGGTTCTCT AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120

```

TTTACAACCTA TGGCTTTATT AACCATAAATG GAATTCCTCAG TATATCAAGA TACATGGATG 180
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240
 ACTGTTGCCA TGAAGTGTC AATATGTTGGA GCGGATGTAT TGGATTAGC AGAAACAATG 300
 GTTGCATCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACTT 420
 CAAGATGTGA TATTTAAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480
 GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCAATAAA 540
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCTCTG TGGTCATGCA 600
 CATTGGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTATAGAAAT AGATCATTTG 660
 TCTTTTGGAG AGCTTGTCTC AGCAATTATT AATCCTTTAG ATGGAATGTA AAAAAATGCT 720
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780
 TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAA 840
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTTCTCTT 900
 ATGGTGACAG TTACTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960
 ATGTTGGAG GAATCTTTTC AACCAACAGG ATGTTACATG GAATTGGAAA ATTTATAGTT 1020
 GAAATATTT GCTGCTCTT CAGACTTGGG TCCTATAAAC CTGTCAATTC TGTTCCTTTT 1080
 GAGGATGGCC ACACAGACAA CCATTACCT CTTTTAGAAA ATAATACACA TTGA

A202 Protein sequence:

Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Protein Accession #: NP_057654
 Signal sequence: none found
 Transmembrane domains: none found
 Cellular Localization: nuclear

1 11 21 31 41 51
 | | | | |
 MRRLNRKKT SLVKELDAFP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60
 KYEYEDKDF SSKLRINIDI TVAMKQYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120
 KEWQRMQLI QSRLQEEHSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVNK 180
 VAGNFHITVG KAIPHPRGHA HLAALVNHES YNFSHRIDHL SFGELVPAII NPLDGTETKIA 240
 IDHNQMFQYF ITVVPKTLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300
 MVTVTEHMP FWQFFVRLCG IVGGIFSTTG MLHGIGKPIV EIICCRFRLG SYKPVNSVPF 360
 EDGHTDNHLP LLENNTN

A203 DNA SEQUENCE

Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
 Unigene number: Hs.44926
 Probeset Accession #: S79876
 Nucleic Acid Accession #: NM_001935.1
 Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CGCGCGTCTC CGCGCCCGCG GTGACTTCTG CCTGCGCTCC TTCTCTGAAC GCTCACTTCC 60
 GAGGAGACGC CGACGATGAA GACACCGTGG AAGATTCTTC TGGGACTGCT GGGTGTCTGCT 120
 GCGCTTGTC CCAATCATCAC CGTGCCTGCTG GTTCTGCTGA ACAAGGCGAC AGATGATGCT 180
 ACAGCTGACA GTCGCAAAAC TTACACTCTA ACTGATTACT TAAAAAATAC TTATAGACTG 240
 AAGTTATACT CCTTAAGATG GATTTTCAGAT CATGAATATC TCTACAAACA AGAAAAATAAT 300
 ATCTTGGTAT TCAATGCTGA ATATGGAAAC AGCTCAGTTT TCTTGGAGAA CAGTACATTT 360
 GATGATTTTG GACATTCTAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTCTC 420
 TTAGAATACA ACTACGTGAA GCAATGGAGG CATTCTCTACA CAGCTTCATA TGACATTAT 480
 GATTAAATA AAAGGCAGCT GATTACAGAA GAGAGGATTC CAAACAACAC ACAGTGGGTC 540
 ACATGGTCAC CAGTGGGTCA TAAATTGGCA TATGTTTGGG ACAATGACAT TTATGTTAAA 600
 ATTGAAACCA ATTTACCAAG TTACAGAATC ACATGGACGG GGAAGAAGA TATAATATAT 660
 AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCTTCA GTGCCTACTC TGCTCTGTGG 720
 TGGTCTCCAA ACGGCACATT TTTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCCTT 780
 ATTGAAACT CCTTCTACTC TGATGAGTCA CTGCAGTACC CAAAGACTGT ACGGGTTCCA 840
 TATCCAAAGG CAGGAGCTGT GAATCCAAC GTAAAGTTCT TTGTGTGAAA TACAGACTCT 900
 CTCAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCCTGCTTC TATGTTGATA 960
 GGGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAAG AAAGAATTTC TTTGCAGTGG 1020
 CTCAGGAGGA TTCAGAACTA TTCGGTCATG GATATTTGTG ACTATGATGA ATCCAGTGGA 1080
 AGATGGAAGT GCTTAGTGCC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTGGA 1140
 AGATTAGGC CTTCAGAACC TCATTTTACC CTTGATGGTA ATAGCTTCTA CAAGATCATC 1200
 AGCAATGAAG AAGGTTACAG ACACATTTCG TATTTCCAAA TAGATAAAAA AGACTGCACA 1260
 TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAAG CTCTAACCAG TGATTATCTA 1320
 TACTACATTA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAATCCAA 1380
 CTTATTGACT ATACAAAAGT GACATGCCTC AGTTGTGAGC TGAATCCGGA AAGGTGTCAG 1440
 TACTATTCTG TGTCACTCAG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCCGGTCTC 1500
 GGTCTGCCCC TACTTACTCT ACACAGCAGC GTGAATGATA AAGGGCTGAG AGTCCTGGAA 1560
 GACATTCAG CTTTGGATAA AATGCTGCAG AATGTCCAGA TGCCCTCCAA AAACTGGGAC 1620
 TTCATTATT TGAAATGAAC AAAATTTTGG TATCAGATGA TCTTGCTTCC TCATTTTGAT 1680
 AAATCCAAGA AATATCTCTC ACTATTAGAT GTGTATGCAG GCCCATGTAG TCAAAAAGCA 1740
 GACACTGTCT TCAGATGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATTATAGTA 1800
 GCTAGCTTTG ATGGCAGAGG AAGTGGTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC 1860
 AGAAGACTGG GAACATTTGA AGTTGAAGAT CAAATGAAG CAGCCAGACA ATTTTCAAAA 1920
 ATGGGATTGG TGGACAACAA ACGAATTGCA ATTTGGGGCT GGTCAATAGG AGGGTACGTA 1980
 ACCTCAATTG TCCATGGGATC GGAAGTGGC GTGTTCAAGT GTGGAATAGC CGTGGCGCCT 2040

5
 10
 15
 20
 25
 30
 35

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GTATCCCGGT GGGAGTACTA TGACTCAGTG TACACAGAAC GTTACATGGG TCTCCCAACT 2100
CCAGAAGACA ACCTTGACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAAAAATTTT 2160
AAACAAGTTG AGTACCTCCT TATTCATGGA ACAGCAGATG ATAACGTTCA CTTTCAGCAG 2220
TCAGCTCAGA TCTCCAAAGC CCTGGTCGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT 2280
ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG 2340
AGCCACTTCA TAAAACAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCATTTA 2400
AAGCTTATTA AAATCATTTT TTGTTTTCAT TATCTCAAAA CTGCACTGTC AAGATGATGA 2460
TGATCTTTAA AATACACACT CAAATCAAGA AACTTAAGGT TACCTTTGTT CCCAAATTTT 2520
ATACCTATCA TCTTAAGTAG GGACTTCTGT CTTCACAACA GATTATTACC TTACAGAAGT 2580
TTGAATTATC CGGTCGGGTT TTATTGTTTA AAATCATTTT TGCATCAGCT GCTGAAACAA 2640
CAAAATAGGAA TTGTTTTTAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAATCTT 2700
TTTCTAACTG GACTGGTTCA AATGTTGTTT TCTTCTTTAA AGGGATGSCA AGATGTGGGC 2760
AGTGATGTCA CTAGGGCAGG GACAGGATAA GAGGGATTAG GGAGAGAAGA TAGCAGGGCA 2820
TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTGAG CTCCCTCGG 2880
AGAAGAGCTG TTCACACGA GACTGGCACA GTTTCTGAG AAAGACTATT CAAACAGTCT 2940
CAGGAAATCA AATATCGAAA GCACTGACTT CTAAGTAAAC CACAGCAGTT GAAAGACTCC 3000
AAAGAAATGT AAGGGAAACT GCCAGCAACG CAGCCCCCAG GTGCCAGTTA TGGCTATAGG 3060
TGCCTACAAA ACACAGCAAG GGTGATGGGA AAGCATTGTA AATGTGCTTT TAAAAAATAA 3120
TACTGATGTT CCTAGTGAAG GAGGCAGCTT GAAACTGAGA TGTGAACACA TCAGCTTGCC 3180
CTGTTAAAGG ATGAAAATAT TTGTATCACA AATCTTAACT TGAAGGAGTC CTTGCATCAA 3240
TTTTTCTTAT TTCAATTTCT TGAGTGCTCT AATTAAGAAGA ATATTTTAACT TTCCTTGGAC 3300
TCATTTTAAA AAATGGAACA TAAATACAA TGTATATGAT TATTATTTCC ATTCTACATA 3360
CTATGGAATT TCTCCCAGTC ATTTAATAAA TGTGCCCTCA TTTTTC
  
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A204 Protein sequence:

Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
 Unigene number: Hs.44926
 Probeset Accession #: S79876
 Protein Accession #: NP_001926.1
 Signal sequence: none found
 Transmembrane domains: 6-28
 DPPIV_N_term domain: 43-557
 Peptidase_S9 domain: 558-635
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 40 MKTPWKILG ILGAAALVTI ITVPVVLNKK GTDDATADSR KTYTLTDYK NTYRLKLYSL 60
 RWISDHELYL QKENNILVFN AEYGNSSVFL ENSTFDEFHG SINDYSISPD GQFILLEYN 120
 VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVTWSPV GHKLAYVWNN DIYVKIEPNL 180
 PSYRITWTGK EDIIYNGITD WYIEEVEVFA YSALWWSPNG TFLAYAQFND TEVPLIEYSF 240
 45 YSDESLQYPK TVRVYPKAG AVNPTVKFFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
 CDVTWATQER ISLQWLRRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGWVGRFRPS 360
 EPHFTLDGNS FYKIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYYISN 420
 EYKGMFGGRN LYKIGLIDYT KVTCLSCELN PERCQYYSVS FSKEAKYYQL RCSGPGPLPLY 480
 TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDIFIILN ETKFWYQMLL PPHFDKSKKY 540
 50 PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFDD RGSQYQGDKI MHAINRRLGT 600
 FEVEDQIEAA RQFSKMGFVD NKRIATWGS YGGYVISMVL GSGSGVFKCG IAVAPVSRWE 660
 YDVSVVTERY MGLPTPEDNL DHYRSTVMS RAENFKQVEY LLIHGTADDN VHFQQAQIS 720
 KALVDVGVDV QAMWYDDEDH GIASSTAHHQ IYTHMSHFIL QCFSLP

A205 DNA SEQUENCE

Gene name: predicted exon
 Unigene number: none found
 Probeset Accession #: none found
 Nucleic Acid Accession #: none found
 Coding sequence: 1-261 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 65 ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAATGACA ATGCCATCAG AGTTGACAAC 60
 AGAAGTGTGA TTAAAGTGCG TGCTAACCG TGTTCCTGCG ATGAGGCAGA AAGTGAATCC 120
 AGAAACCCCTC AGGAGCTCTG GATGGGCCTG CTCCTCTTGA TGGGGGTCCT AGAAGCATGT 180
 GTGGAATAGA GGCCTCTGTC AGTCTGGTCC CTGAGAGATG ACAAGGAGCA GAGCCCCCAC 240
 CAGCCACAC TGGATGCTCA A

A206 Protein sequence:

Gene name: predicted exon
 Unigene number: none found
 Probeset Accession #: none found
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 46-68
 Cellular Localization: not determined

1 11 21 31 41 51
 | | | | |
 MALAKVREPN ANDNAIRVDN RSVIKVRANQ CSLHAESES RNPQELWMGL LLLMGVLEAC 60
 VEMRPLSVWS LRDDKEQSPH QPTLDV

A207 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.222886
 Probeset Accession #: AI672225
 Nucleic Acid Accession #: none found
 Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTTGGAAGCA GTAAATGTTT AAAAACTGCT 60
CTCATACTTG CTGTATGTTG TGGATCAGCA AATATAGTCA GCCCTCTACT TGAGCAAAAT 120
ATTGATGTAT CTTCTCAAGA TCTGGACAGA CGGCCAGAGA GTATGCTGTT TCTAGTCATC 180
ATCATGTGGA CCAGTTTGTG GGAAGACAAT CTTCCATGG GCTGGGGGAA GCTAGAAGAT 240
TTTATGGCTA TTGAAGAAGA AATGAAGAAG CACGGAAGTA CTATGTGGG ATTCCAGAA 300
AACTGACTA ATGGTGGCCG TGCTGGCAAT GGTGATGATG GATTAATTCC TCCAAGGAAG 360
AGCAGAACAC CTGAAGGCCA GCAATTTCTT GACACTGAGA ATGAAGAGTA TCACAGGTTT 420
GTCAAAGATC AGATAGTTGT AGATATGCGG CGTATTCTCT GA

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A208 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.222886
 Probeset Accession #: AI672225
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 16-38
 Cellular Localization: not determined

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1      11      21      31      41      51
|      |      |      |      |      |
MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPLEQN IDVSSQDLDR RPESMLFLVI 60
IMWTSFVEDN LSMGWKLED FMAIEEMKK HGSTHVGFPF NLTNAGAAAGN GDDGLIPPRK 120
SRTPEQQPFP DTENEYHHRF VKDQIVVDMR RYF

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A209 DNA SEQUENCE

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
 Unigene number: Hs.23796
 Probeset Accession #: NM_014253
 Nucleic Acid Accession #: NM_014253
 Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

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 AAGCATCAGT AAGAAAGAAG GCGAAAAAGA GAAGTATAGC CTTTATGTCA GAAAAACATT 12480
 CTTTTTAGCT GCTTACTTTC TCATGAAAAG TAAAGATGTT TACAGTGTAT GCCAAGTTTT 12540
 CAGTTTCTGT ATAACAACAG GTAGAGGTTT TAATCATATT GAAAATTGTG TTATAATGGT 12600
 CTGAGCCATG TTGCTAGGAA ACAATAGGTT CCAATTTTGT ATTCCTGCTC TCCTGTGCTG 12660
 AAAAGTGACT GGATACTGTA CAGGTTTCATG TTCTCTGGCT GCAGTTAAAT GGTCTTTTGC 12720
 ATTTTGCTCT GGCTTTCAGG CCAGAAGCAT GCATTTTCTT ACAAGAGCAT CACAACAACA 12780
 TGCTGTAAAT ATTTAAAGTT AAACATTATG TGGTTGATATT TGAAAGAAAA GTACTTTGAA 12840
 TATTTTCATT TTAATAAATA AAATTGCCAA TGAAAAAATA

A210 Protein sequence:

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
 Unigene number: Hs.23796
 Probeset Accession #: NM_014253
 Protein Accession #: NP_055068
 Signal sequence: none found
 Transmembrane domains: 318-340
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MEQTDCKPYQ	PLPKVKHEMD	LAYTSSSDES	EDGRKPRQSY	NSRETLHEYN	QELRMNYSNQ	60
SKRKRKEVEKS	TQEMFECETS	HTLCSGYQTD	MHSVSRHGYQ	LEMGSVDVDE	TEGAASPDHA	120
LRMWIRGMKS	EHSCLSSRA	NSALSITDTD	HERKSDGENG	FKFSPVCCDM	EAQAGSTQDV	180
QSSPHNQFTF	RPLPPPPPPP	HACTCARKPP	PAADSLQRRS	MTRSQPSPA	APAPPTSTQD	240
SVHLHNSWVL	NSNIPLETRH	SLFKHSGSSS	AIFSAASQNY	PLTSNTVYSP	PPRPLPRSTF	300
SRPAFTFNKP	YRCNWKCTA	LSATAITVTL	ALLLAYVIAV	HLFGLTWQLQ	PVEGELYANG	360
VSKGNRGTES	MDTYSPIGG	KVSDKSEKKV	FQKGRAIDTG	EVDIGAQVMQ	TIPPGLFWRF	420
QTTIHHPIYL	KFNISLAKDS	LLGIYGRRNI	PPHTQDFDFV	KLMDGKQLVK	QDSKGSDDTQ	480
HSFRNLILTS	LQBTGPIEYM	DQGPWYLAFY	NDGKKMEQVF	VLTTAIEIMD	DCSTNCNGNG	540
ECISGHCHCF	PGLGPDCA	DSCPVLCCGN	GEYKKGHCVC	RHWKKGPECD	VPPEQCIDPT	600
CFGHGTCIMG	VCICVPGYKG	EICEEEDCLD	PMCSNHGICV	KGECHCSTGW	GGVNCETPLP	660
VCQEQCSGHG	TFLLDAGVCS	CDPKWTGSDC	STELCTMECG	SHGVCSRIGC	QCEEGWVGPT	720
CEERSCHSHC	TEHGQCKDGK	CECSPGWEGD	HCTIAHYLDA	VRDGCFLCF	GNRCCTLDQN	780
GWHCVQVGV	SGTGCNVVME	MLCGDNLND	GDGLTDCVDP	DCCQSQSNCYI	SPLCQGSPPD	840
LDLIQSQTL	FSQHTSRLFY	DRIKFLIGKD	STHVIPPEVS	FDSRRACVIR	QQVVAIDGTP	900
LVGNVVSFLH	HSYGFRTISR	QDGSFDLVAI	GGISVILIFD	RSPFLPEKRT	LWLPWNQFIV	960
VEKVTMRQVV	SDPPSCDISN	FISPNPIVLP	SPLTSFGGSC	PERGTIVPEL	QVVQEEIPI	1020
SSFVRLSYLS	SRTPGYKTL	RILLTHSTIP	VGMIKVHLTV	AVEGRLTQKW	FPAAILNVYT	1080
FAWNKTDIYG	QKVGWLAEL	VSVGYEYETC	PDFILWEQRT	VVLQGFEMDA	SNLGDWLSLNK	1140
HHILNQSGI	IHKNGENMNF	ISQQPPVIST	IMGNHGQRSV	ACTNCSNGPAH	NNKLFAPVAL	1200
ASGPDGSSVY	GDFNFVRIRF	PSGNSVSILE	LSTSPAHKYY	LAMPDVSSEL	YLSDTNTRKV	1260
YKLKSLVETK	DLSCNFEVVA	GTGDQCLPFD	QSHCGDGGRA	SEASLNSPRG	ITVDRHGFIY	1320
FVDGTMIRKI	DENAVITTVI	GSNGLTSTQP	LSCDSGMDIT	QVRLEWPTDL	AVNPMDSNLY	1380
VLDNNIVLQI	SENRRVRIIA	GRPIHCQVPG	IDHFLVSKVA	IHSTLESARA	ISVSHSGLLF	1440
IAETDERKVN	RIQQVTNNGE	IYI IAGAPTD	CDCKIDPNCD	CFSGDGGYAK	DARKMAPSSL	1500
AVSPDGTLYV	ADLGNVRIRI	ISRNQAHLND	MNIYEIASPA	DQELYQFTVN	GTHLHTLNLI	1560
TRYVYVNFY	NSBGDLGAIT	SSNGNSVHIR	RDAGGMPLWL	VVPGGQVYWL	TISSNGVLKR	1620
VSAQGYNPAL	MTYPGNTGLL	ATKSNENGWT	TVYEYDPEGH	LTNATFPTGE	VSSFHSDLEK	1680
LTKVELDTSN	RENVLMSTNL	TATSTIYILK	QENTQSTYRV	NPDSLSRVTF	ASGMEIGLSS	1740
EPHILAGAVN	PTLGKCNISL	PGEHNNALIE	WRQRKEQNGK	NVSAFERRLR	AHNRNLLSID	1800
FDHITRTGKI	YDHRKFTLR	ILYDQTCRPI	LWSPVSRVNE	VNITYSPSGL	VTFIQRTGWN	1860
EKMEYDQSGK	IISRTWADGK	IWSYTYLEKS	VMLLLHSQRR	YIFEYDQSDC	LLSVTMPSMV	1920
RHSLQTMLSV	GYRNIYTPP	DSSTSFIQDY	SRDGRLLQTL	HLGTGRRVLY	KYTKQARLSE	1980
VLXDTTQVTL	TYEESSGVIK	TIHLMHDGFI	CTIRYRQTGP	LIGRQIFRFS	EEGLVNARFD	2040
YSVNNFRVTS	MQAVINETPL	PIDLRYVDV	SGRTEQFGKF	SVINYDLNQV	ITTTVMKHTK	2100
IFSANGQVIE	VQYEILKAIA	YWMTIQYDNV	GRHGNMCIRV	GVDANITRYF	YEYDADGQLQ	2160
TVSVNDKTQW	RYSDYDNGDI	NLLSHGKSAR	LTPRLYDLRD	RITRLGELIQY	KMDEGDFLRQ	2220
RGNDIFEYNS	NGLLQKAYNK	ASGWTQVYYY	DGLGRRVASK	SSLGQHLQFF	VDATANPIRV	2280
THLYNHTSSE	ITSLYDYLQ	HLIAMELSSG	EEYVACDNT	GTPLAVFSSR	GQVIKEILYT	2340
PYGDYIHDY	PDFQVIIGFH	GGLYDFLTKL	VHLQQRDYDV	VAGRWTAYH	HIWKQLNLLP	2400
KPFNLVSFEN	NYPVGKIQDV	AKYTTDIRSW	LELFGFQLHN	VLPGFPPKPEL	ENLELTYELL	2460
RLQTKTQEW	PGKITLGIQC	ELQQLRNFI	SLDQLPMTPR	YNDGRCLGEG	KQPRFAAVPS	2520
VFGKGIKFAI	KDGIVTADII	GVANEDSRRL	AAILNNAHYL	ENLHFTIEGR	DTHYFIKLSG	2580
LEEDLVLLIG	TGRRIRILENG	VNVTVSQMIS	LLNGRTRRFA	DIQLQHGALE	FNIRYGTIVE	2640
EEKNHVLEIA	RQRAVAQAWT	KEQRRLQEGE	EGIRAWTEGE	KQQLLSTGRV	QGYDGYFVLS	2700
VEQYLELSDS	ANNHIFMRQS	EIGRR				

A211 DNA SEQUENCE:

Gene name: Solute carrier family 26, member 4
 Unigene number: Hs.159275
 Probeset Accession #: AF030880
 Nucleic Acid Accession #: NM_000441
 Coding sequence: 225-2567 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
CTCAGCCTTC	CCGGTTCGGG	AAAGGGAAG	AATGCAGGAG	GGGTAGGATT	TCTTCTCTGA	60
TAGGATCCGT	TGGGAAAGAC	CGCAGCCTGT	GTGTGTCTTT	CCCTTCGACC	AAGGTGTCTG	120
TTGCTCCGTA	ATAAAACGT	CCCACTGCCT	TCTGAGAGCG	CTATAAAGGC	AGCGGAAGGG	180
TAGTCCGCGG	GGCATTCGGG	GCGGGGCGCG	AGCAGAGACA	GGTCATGGCA	GCGCCAGGCG	240
GCAGGTCCGA	GCCGCGCGAG	CTCCCCGAGT	ACAGCTGCAG	CTACATGGTG	TCGCGGCCCG	300
TCTACAGCGA	GCTCGCTTTC	CAGCAACAGC	ACGAGCGGCG	CCTGCAGGAG	CGCAAGACGC	360

5 TGCGGGAGAG CCTGGCCAAG TGCTGCAGTT GTTCAAGAAA GAGAGCCTTT GGTGTGCTAA 420
 AGACTCTTGT GCCCATCTTG GAGTGGCTCC CCAAATACCG AGTCAAGGAA TGGCTGCTTA 480
 GTGACGTCAT TTCGGGAGTT AGTACTGGGC TAGTGGCCAC GCTGCAAGGG ATGGCATATG 540
 CCCTACTAGC TGCAGTTCCT GTCGGATATG GTCTCTACTC TGCTTTTTTC CCTATCCTGA 600
 CATACTTTAT CTTTGGAAACA TCAAGACATA TCTCAGTTGG ACCTTTTCCA GTGGTGAGTT 660
 TAATGGTGGG ATCTGTTGTT CTGAGCATGG CCCCOCGACGA ACACTTTCTC GTATCCAGCA 720
 GCAATGGAAC TGTATTAAT ACTACTATGA TAGACACTGC AGCTAGAGAT ACAGCTAGAG 780
 TCCTGATTGC CAGTGCCCTG ACTCTGCTGG TTGGAATTAT ACAGTTGATA TTTGGTGGCT 840
 10 TGCAGATTGG ATTCATAGTG AGGTACTTGG CAGATCCTTT GGTGGTGGC TTCACAACAG 900
 CTGCTGCCTT CCAAGTGGTG GTCTCACAGC TAAAGATTGT CCTCAATGTT TCAACCAAAA 960
 ACTACAATGG AGTTCTCTCT ATTATCTATA CGCTGGTTGA GATTTTCAA AATATTGGTG 1020
 ATACCAATCT TGCTGATTTC ACTGCTGGAT TGCTCACCAT TGTCGTCTGT ATGGCAGTTA 1080
 AGGAATTAAA TGATCGGTTT AGACACAAAA TCCCAGTCCC TATTCCTATA GAAGTAATTG 1140
 15 TGACGATAAT TGCTACTGCC ATTTCTATATG GAGCCAACTT GGAAAAAAT TACATGCTG 1200
 GCATTGTTAA ATCCATCCCA AGGGGGTTTT TGCTTCTGA ACTTCCACT GTGAGCTTGT 1260
 TCTCGGAGAT GCTGGCTGCA TCAATTTTCCA TCGCTGTGGT GGCTTATGCT ATTGCAGTGT 1320
 CAGTAGGAAA AGTATATGCC ACCAAGTATG ATTACACCAT CGATGGGAAC CAGGAATTCA 1380
 TTGCCTTTGG GATCAGCAAC ATCTTCTCAG GATTCTTCTC TGTGTTTGTG GCCACCACTG 1440
 20 CTCTTTCCTG CACGGCCGTC CAGGAGAGCA CTGGAGGAAA GACACAGGTT GCTGGCATCA 1500
 TCTCTGCTGC GATTGTGATG ATCGCCATTC TTGCGCTGGG GAAGCTTCTG GAACCTTGC 1560
 AGAAGTCGGT CTTCGCAGCT GTTGTAATTG CCAACCTGAA AGGGATGTTT ATGCAGCTGT 1620
 GTGACATTCC TCGTCTGTGG AGACAGAATA AGATTGATGC TGTATCTGG GTGTTTACGT 1680
 GTATAGTGTC CATCATTCG GGGCTGGATC TCGGTTTACT AGCTGGCCTT ATATTGGAC 1740
 25 TGTGACTGT GGTCTGAGA GTTCAGTTTC CTCTTGGAA TGGCCTTGA AGCATCCCTA 1800
 GCACAGATAT CTACAAAAGT ACCAAGAATT ACAAAAACAT TGAAGAACCT CAAGGAGTGA 1860
 AGATTCTTAG ATTTCCAGT CCTATTTCT ATGGCAATGT CGATGGTTT AAAAAATGTA 1920
 TCAAGTCCAC AGTTGGATTG GATGCCATTA GAGTATATAA TAAGAGGCTG AAAGCGCTGA 1980
 GGAAAAATCA GAACTAATA AAAAGTGGAC AATTAAGAGC AACAAGAAT GGCATCATAA 2040
 30 GTGATGCTGT TCAACAAAT AATGCTTTTG AGCCTGATGA GGATATTGAA GATCTGGAGG 2100
 AACTTGATAT CCCAACCAAG GAAATAGAGA TTCAAGTGA TTGGAACCTC GAGCTTCCAG 2160
 TCAAGTGAA CGTTCCTCAA GTGCCAATCC ATAGCCTTGT GCTTGACTGT GGAGCTATAT 2220
 CTTTCTCGGA CGTGTGGA GTGAGATCAC TGCGGTGAT TGTCAAAGAA TTCCAAGAA 2280
 TTGATGTGAA TGTGATTTT GCATCACTTC AAGATTATGT GATAGAAAAG CTGAGCAAT 2340
 35 GCGGGTTCTT TGACGACAAC ATTAGAAAGG ACACATCTT TTTGACGGTC CATGATGCTA 2400
 TACTCTATCT ACAGAACCAA GTGAAATCTC AAGAGGGTCA AGGTTCCATT TTAGAAACGA 2460
 TCACTCTCAT TCAGGATTGT AAAGATACCC TTGAATTAAT AGAAACAGAG CTGACGGAAG 2520
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 55 TGACCACTTA AAAAAAATC TAAAAATTGA ACTACCTATA GTAGTCTGTG TTTAAAGTGA 3600
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 60 GTTATACCCA GGTCCCAAT TGAGAAATGTC TTGCTTGATT GAAAACGACA TCATCCCTTG 3900
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 TCCTGCAGTC ACCCTGCTT AAAGATAGAA TGGCTTCTCT GTTTTCTTC TGAATACAA 4020
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 65 TCACAGCACT ACTGCTTAT ATTGACACA AATCATCTCG CTAAAGAGTG AATGTAGGCC 4200
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 GGAGGCTAAG GCAGGAGAAT GGCCTGAACC CGGGAGGCGG AGCTTGAGT GAGCCGAGGT 4440
 70 CGTGCCACTG CACTCCAGCC TGGGCGACAG AGCAAGACTC CGTCTCAAAA AAAAAAATAA 4500
 AAAAAAATAA AGAGTGAATG TAATAGTCTT GCAGAAAATG AATGAATACC TTTGTTCAAT 4560
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 75 GAAAAATTTCA CTTGAAATTA AAGCTGCCTT TTGTTATATT TTTAACCTAT AGGATAAGAT 4800
 TCCAGTATTG TATATGAGTT TTAACAAAT AAAAAATCAA ATCATGTACA TTTGAAAAAT 4860
 TTTGCACACA TTTAAAAATA AATGTAAAGT TGTCTTTTAA ACTACTCGGA TGTGTCCTTT 4920
 CTGAACAAA

A212 Protein sequence:

Gene name: Solute carrier family 26, member 4
 Unigene number: Hs.159275
 Probeset Accession #: AF030880
 Protein Accession #: O43511
 Signal sequence: none found

Transmembrane domains: 81-103, 109-131, 136-158, 185-207, 221-243, 245-267, 270-291, 295-317,
347-369, 386-408, 420-442, 448-470, 486-508
Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MAAPGGRSEP PQLPEYSCSY MVSRPVYSEL AFQQQHERRL QERKTLRESL AKCCSCSRKR 60
AFGLVLTLPV ILEWLPKYRV KEWLLSDVIS GVSTGLVATL QGMAYALLAA VPVGYYGLYSA 120
FFPILTYFIF GTSRHSISVGP FPVVSMLVGS VVLSMAPDEH FLVSSSNGTV LNTTMDTAA 180
RDTARVLIAS ALTLVLGIQ LIFGGLQIGF IVRYLADPLV GGFTTAAAFQ VLVSQKIVL 240
NVSTKNYNGV LSIITYLVEI FQNIGDTNLA DFTAGLLTIV VCMAYKELND RFRHKIPVPI 300
PIEVIVTIIA TAISYGANLE KNYNAGIVKS IPRGFLPPEL PPVSLFSEML AASFIAVVA 360
YAIASVGVKV YATKYDYTID GNQEFIAFGI SNIFSGFFSC FVATTALSRT AVQESTGGKT 420
QVAGIISAAI VMIAIALGK LLEPLQKSVL AAVVIANLKG MFMQLCDIPR LWRQNKIDAV 480
IWVFTCIVSI ILGLDLGLLA GLIFGLLTIV LRVQFPWSNG LGSIPSTDYI KSTKNYKNIE 540
EPQGVKILRF SPSIFPYGNDV GFKKCIKSTV GFDAIRVYNK RLKALRKIQK LIKSGQLRAT 600
KNGIISDAVS TNNAFEPDED IEDLEELDIP TKEIEIQVDW NSELPVKVNK PKVPIHSLVL 660
DCGAISFLDV VGVRSRLRVIV KEFQRIDNVN YFASLQDYVI EKLEQCGFFD DNIRKDTFFL 720
TVHDAIYLQ NVQKSQEGQG SILETITLIQ DCKDTLELIE TELTEELDVL QDEAMRTLAS 780
QDEAMRTLAS

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25

A213 DNA SEQUENCE:

Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]
Unigene number: Hs.98280
Probeset Accession #: AA418000
Nucleic Acid Accession #: NM_021614
Coding sequence: 458-2197 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
CGGCGGCAGC AGCCCATGCC TCCGGTGCAA CAGCTGCGCC TCCTCCGGTG CCCCAGCGGC 60
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GACCCCGCACC TCCTCGCCGC TGTCGGGCTC GTCTGCTGCT TGCTGCTGCT GCTCGTCGCG 180
CCGGGGGAGC CAGCTCAATG TGAGCGAGCT GACGCCGTCC AGCCATGCCA GTGCGCTCCG 240
CGAGCAGTAC GCGCAGCAGT CCGCGCAGCA GTCGGCGTCC GCCTCCAGT ACCACCACTG 300
CCACAGCCTC CAGCCCGCCG CCAGCCCCAC GGGCAGCCTC GGCAGTCTGG GCTCCGCGCC 360
CCCGCTCTCG CACCACCACC ACCACCCGCA CCGGGCGCAC CACCAGCACC ACCAGCCCCA 420
GGCGCGCCCG GAGAGCAACC CCTTCAACCGA AATAGCCATG AGCAGCTGCA GGTACAACCG 480
GGCGCTCATG CGGCCGCTCA GCAACTTGAG CGCGTCCC GCAGAACCTCC ACGAGATGGA 540
CTCAGAGCGC CAGCCCTGCT AGCCCCCGCG GTCTGTGCGG GAGAGTGGCG GCGCGTCTCT 600
CCCGTCTGCA GAGCTGCGCG CCGCGCGCGC TGTTCGTGTC TCAGCCCCCG AGATCGTGGT 660
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CATGACTTAT GAGCGTATTT TCTTCATCTG CTTGGAATA CTGGTGTGTG CTATTCATCC 1140
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GATTGCCAGA GTCATGCTTT TACATAGCAA ACTTTTCACT GATGCCCTCT CTAGAAGCAT 1320
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AAGAAAACAT CAACGAAAAT TCCTGCAAGC TATTCATCAA TTAAGAAGTG TAAAAATGGA 1860
GCAGAGGAAA CTGAATGACC AAGCAACAC TTTGGTGGAC TTGGCAAGA CCCAGAACAT 1920
CATGTATGAT ATGATTTCTG ACTTAAACGA AAGGAGTGAA GACTTCGAGA AGAGGATGTT 1980
TACCTTGAA ACAAACCTAG AGACTTTGAT TGGTAGCATC CACGCCCTCC CTGGGCTCAT 2040
AAGCGAGAC ACTAGGCGAG AGCAGAGAGA TTTCAATTGAG GCTCAGATGG AGAGCTACGA 2100
CAAGCACGTC ATTTACAATG CTGAGCGGTC CCGGTCTCTG TCCAGGAGGC GCGGCTCTCT 2160
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CTAATCAGCG TTATCCGGGT TCTGATGTCA GAATCCTGGG AACCTGAACA CTAAGTTTTA 2340
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AACTTTACTA CTACATTATA TGATATATAA TAAAAAAGT TAATTTCCGA

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80

A214 Protein sequence:

Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]
Unigene number: Hs.98280
Probeset Accession #: AA418000
Protein Accession #: NP_067627
Signal sequence: none found
Transmembrane domains: 135-157, 168-190, 208-230, 254-276, 306-328, 342-364, 373-394

Calmodulin binding domain: 412-488
Cellular Localization: plasma membrane

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5      1      11      21      31      41      51
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      S S A P E I V V S K P E H N N S N N L A L Y G T G G G G S T G G G G G G G S G H G S S S G T K S S K K N Q N I G Y K 120
      L G H R R A L F E K R K R L S D Y A L I F G M F G I V V M V I E T E L S W G A Y D K A S L Y S L A L K C L I S L S T I I 180
      L L G L I I V Y H A R E I Q L F M V D N G A D D W R I A M T Y E R I F F I C L E I L V C A I H P I P G N Y T F T W T A R 240
      L A F S Y A P S T T A D V D I I L S I P M F L R L Y L I A R V M L L H S K L F T D A S S R S I G A L N K I N F N T R F 300
      V M K T L M T I C P G T V L L V F S I S L W I I A A W T V R A C E R Y H D Q Q D V T S N F L G A M W L I S I T F L S I G 360
      Y G D M V P N T Y C G K G V C L L T G I M G A G C T A L V V A V V A R K L E L T K A E K H V H N F M M D T Q L T K R V K 420
      N A A A N V L R E T W L I Y K N T K L V K K I D H A K V R K H Q R K F L Q A I H Q L R S V K M E Q R K L N D Q A N T L V 480
      D L A K T Q N I M Y D M I S D L N E R S E D F E K R I V T L E T K L E T L I G S I H A L P G L I S Q T I R Q Q Q R D F I 540
      E A Q M E S Y D K H V T Y N A E R S R S S S R R R R S S T A P T S S E S S

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A215 DNA SEQUENCE:

Gene name: CGI-86 protein
Unigene number: Hs.109201
Probeset Accession #: AW161450
Nucleic Acid Accession #: NM_016029
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

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25      1      11      21      31      41      51
      |      |      |      |      |      |
      C T G C G A T C C C G C A G G G C A G C G A C G C G A C T T G G T G C G G G C C G T C T T C T T C C C C C G A G C T 60
      G G G C G T G C G C G G C C G C A A T G A A C T G G G A G C T G C T G C T G T G G C T G C T G C G T G C T G T G C C G C G C 120
      T G C T C C T G C T C T T G G T G C A G C T G C T G C G C T T C C T G A G G G C T G A C G G C G A C C T G A C G C T A C 180
      T A T G G G C C G A G T G G C A G G G A C G A C G C C C A G A A T G G G A G C T G A C T G A T A T G T G G T G T G G G 240
      T G A C T G G A G C C T C G A G T G G A A T T G G T G A G G A G C T G G C T T A C C A G T T G T C T A A A C T A G G A G 300
      T T T C T C T T G T G C T G T C A G C C A G A A G A G T G C A T G A G C T G G A A A G G G T G A A A A G A A G A T G C C 360
      T A G A A A T G G C A A T T T A A A A G A A A A G A T A T A C T T G T T T T G C C C C T T G A C C T G A C C G A C A C 420
      C T G G T T C C C A T G A A G C G G C T A C C A A A G C T G T T C T C C A G G A G T T G G T A G A A T C G A C A T T C 480
      T G G T A C A C A A T G G T G G A A T G T C C A G C G T T C T C T G T G C A T G G A T A C C A G C T T G G A T G T C T 540
      A C A G A A A G C T A A T A G A G C T T A A C T A C T T A G G G A C G G T G T C C T T G A C A A A A T G T G T T C T G C 600
      C T C A C A T G A T C G A G A G A A A G C A A G A A A G A T T G T T A C T G T G A A T A G A T C C T G G G T A T C A 660
      T A T C T G T A C C T C T T T C C A T T G G A T A C T G T C T A G C A A G C A T G C T C T C C G G G T T T T T T A 720
      A T G G C C T T C G A A C A G A A C T T G C C A C A T A C C A G G T A T A A T A G T T T C T A A C A T T T G C C C A G 780
      G A C C T G T G C A A T C A A A T A T T G T G A G A A T T C C T A G C T G G A G A A G T C A C A A G A C T A T A G 840
      G C A A T A A T G G A G A C C A G T C C C A C A A G A T G A C A A G T C G T T G T G C G G C T G A T G T T A A 900
      T C A G C A T G G C C A A T G A T T T G A A G A A G T T T G G A T C T C A G A C A A C C T T T C T G T T A G T A A 960
      C A T A T T T G T G C A A T A C A T C C A A C C T G G G C C T G G T G G A T A A C C A C A A G A T G G G G A A G A 1020
      A A A G G A T T G A G A A C T T A A G A G T G G T G T G G A T G C A G A C T C T T C T T A T T T T A A A A T C T T T A 1080
      A G A C A A A C A T G A C T G A A A A G A G C A C C T G T A C T T T C A A G C C A C T G G A G G A G A A A T G G A 1140
      A A A C A T G A A A A C A G C A A T C T T C T A T G C T T C T G A A T A A T C A A G A C A A T A T T G T G A T T T T 1200
      A C T T T T T A A T A G A T A T G A C T T T G C T T C C A A C A T G G A A T G A A A T A A A A A A T A A T A A T A A A 1260
      A G A T T G C C A T G A A T C T T G C A A A

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A216 Protein sequence:

Gene name: CGI-86 protein
Unigene number: Hs.109201
Probeset Accession #: AW161450
Protein Accession #: NP_057113
Signal sequence: 1-26
Transmembrane domains: 183-206, 221-243
Cellular Localization: plasma membrane

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65      1      11      21      31      41      51
      |      |      |      |      |      |
      M N W E L L L W L L V L C A L L L L L V Q L L R F L R A D G D L T L L W A E W Q G R R P E W E L T D M V V W V T G A S S 60
      G I G E E L A Y Q L S K L G V S L V L S A R R V H E L E R V K R R C L E N G N L K E K D I L V L P L D L T D T G S H E A 120
      A T K A V L Q E F G R I D I L V N N G G M S Q R S L C M D T S L D V Y R K L I E L N Y L G T V S L T K C V L P H M I E R 180
      K Q G K I V T V N S I L G I I S V P L S I G Y C A S K H A L R G F F N G L R T E L A T Y P G I I V S N I C P G P V Q S N 240
      I V E N S L A G E V T K T I G N N G D Q S H K M T T S R C V R L M L I S M A N D L K E V W I S E Q P F L L V T Y L W Q Y 300
      M P T W A W W I T N K M G K K R I E N F K S G V D A D S S Y F K I F K T K H D

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A217 DNA SEQUENCE:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
Unigene number: Hs.27373
Probeset Accession #: F13036
Nucleic Acid Accession #: AC012478
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

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80      1      11      21      31      41      51
      |      |      |      |      |      |
      A T G C G C G C G C T G C C G C T G C C G C C C G C T C T G C C G C T G C T G C T G C T G C T C C T G G C C 60
      G C T C C C G C G C C C C G C G C C A G C A G A C C G A G T C C G T C T C C G C G C C G T G G C C G A A C C C G A G 120
      C G C G A G T C G C G G C C A C C G C C C G G C C C C G G A A C A C C A C C G G T T T G G G T C T G G G 180
      G C G G C G G G C G C A G C G G C A G C T C C A G C T C C A A C A G C A G T G C G A C G C G C T T G G T A C C C G C 240

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ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAAGGCAG CCGTGATCGT GGC GTTCGCC 300
 TTATACACCC TCCTCATCGC CTGCGTCTG CTGCGCGTCT TCAGGTCGGG AAAGAGGTTA 360
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGCGCCA 420
 CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
 TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCTT 540
 GTGCCCCAC CCTTCATCCT CGACATGAC CTTCACGCAA GATGCAGTGG AAGGCCTGAT 600
 GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCTGGT GGCATCCTGT GGAAAGTTGG 660
 TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGCCT CGGAGGTGTT 720
 GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTC AGGCATCTGC 780
 TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCACCACAA TGGAGTTGCT TCTGCCACCC 840
 TTTGGGCATC CCTTTAAAGT GCGCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG 900
 CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGCTCCATCT 960
 GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
 CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAAACCATG 1080
 AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCGGCGCAGC GGGGCACCTT TGTGAAGAC 1140
 AGAGCAGTGA CTAAGGTTCT CCAGGGTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
 GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
 ACCATCCTG TCAGGTTGGC TCGTTCAGAT GCCCGGGAGC AAGCCAGCCT GACGGGGAGG 1320
 AGGGTGTTC GCGCTCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380
 TGCTTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTCTACAAA 1440
 ATCTGTCTCC CCGTCTGTGC CGTGGAAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
 GTCCTTGCCT CATTTGAGCA GAGCCACAAA AAGGCAGCTG CTGCCACCGG GGAGCCTGTC 1560
 AAACGAGGCG CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
 GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCAGTGA GGATGTCATC 1680
 CACCCCTGGG GAGACTTGGG TGGGGTGGCA AATTTCTATT TGGAGGAAGA GGGTTTCCAG 1740
 GATGGCAGAT GCCAGAGATG GGTCTGTATG TCTGAGGAAG GGCACCTAG TTTGACAGGA 1800
 TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCTCT 1860
 TCCCCCGAC AGCCCCGTGT TCTGTCCAGG CCCTGA

A218 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
 Unigene number: Hs.27373
 Probeset Accession #: F13036
 Protein Accession #: FGENESH predicted
 Signal sequence: 1-27
 Transmembrane domains: 94-115, 448-469
 Cellular Localization: not determined

1 11 21 31 41 51
 MRVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG 60
 AAGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FTTLLIACLL LRVFRSGKRL 120
 KKTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGCTLLTVP 180
 VPPFILDID LPARCSGRPD GGIRPGKTCF PAWHPVESW SAATWGVKDW TWKPSCVGGV 240
 ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPP FGHPFKVPPT STPHGFRQLQ 300
 LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAAESDLFN PWWHFSATGS PIKTLTYQTM 360
 STLGLDVFEG AGQRTFCEG RAVTKVLQGS SFSQRLRWKP ALESGFPFHL RLLRECPPLS 420
 THPVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
 ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHAHGEVP KRGPSSQLTR HTCPCGWGITH 540
 ANLQITPDTP QGEGPREVDV HPGGDLGVA NFYLEEGFQ DGRQCQKMLM SEEGPPSLTG 600
 CERLTGSHHF SSHSKSWSFL SPRQPLFLSR P

A219 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAAGAGAGTGGG 60
 GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATGT 120
 CAGCAAAAGT ACACACACCT GGTTCGAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
 TCCATATTGA GCTATTACAC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGRAG CCAAGAACTG GGCTCCAGGT 300
 GAACCCAACA ATAGGCAAAA AGATGAGGAC TGCCTGGAGA TCTACATCAA GAGAGAAAAA 360
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
 GCTGCCTGTA CCAATACATC CTGCACTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAACCTGT 540
 ACAGCCCTGG AATCCCTCTG GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAACTTC 600
 AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 ACCATGCAGT GTATGTCTTC TGGAGAATGG AGTGTCTCTA TTCCAGCCTG CAATGTGGTT 720
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTGGA 780
 AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTTGA ACTAATGGGA 840
 GCGCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
 GCTGTGACAT GCAGGGCCGT CGGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
 CCTGTGGGAG AGTTACCTTC CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
 TTGCAGGGAC CAGCCAGGTG TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAAATCCCA 1080
 GTTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
 CTTCTAGTGT CTTCTGGCAG TTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200
 GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260

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GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
GTGAGGTGTG CTCAATTCCTT TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCCTTCAGC 1380
TGTGAGGAGG GATT'TGAATT ATATGGATCA ACTCAACTTG AGTGCACATC TCAGGGACAA 1440
TGGACAGAAG AGGTTCTCTTC CTGCCAAGTG GTAAAAATGT CAAGCCTGGC AGTTCGGGA 1500
AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCCTGT 1560
CCTGAAGGAT GGCAGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
CTTTCTGCTG CTGGACTCTC CCTCCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740
TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

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A220 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Protein Accession #: NP_000441
 Signal sequence: 1-22
 Transmembrane domains: 555-573
 C-lectin domain: 23-139
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRTHLVAI QNKEEIEYLN 60
 SILSYSPSY WIGIRKNNV WVWVGTKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120
 DVMGNWDERC SKKKLALCYT AACTNTSCSG HGECEVETINN YTKCDPGRS GLKCEQIVNC 180
 TALESPHEGS LVCSHPILGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
 ECDAVTNPAN GFVECFQNPFG SFPWNTTCTF DCEEGFELMG AQLSQCTSSG NWDNEKPTCK 300
 AVTCRAVRQP QNGSVRCSSH PAGEFTFKSS CNFTCEGFM LQGPQVVECT TQGQWTQQIP 360
 VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCQFTGEWDN 420
 EKPTCEAVRC DAVHQPPKGL VRCASPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
 WTEEVPSQCV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
 SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLWLRLK CLRKAKKFVP ASSCQSLESD 600
 GSQKPSYIL

Taxol ProstateA221 DNA SEQUENCE

Gene name: ESTs; Liprin A2
 Unigene number: Hs.306480
 Probeset Accession #: N51002
 Nucleic Acid Accession #: N51002
 Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ATGATGTGTG AAGTGATGCC CACGATTAAT GAGGACACCC CAATGAGCCA AAGGGGGTCC 60
 CAAAGCAGTG GCTCGGACTC AGACTCCCAT TTTGAGCAGC TGATGGTGAA TATGCTAGAT 120
 GAAAGGGATC GTCTTCTAGA CACCCTTCGG GAGACCCAGG AAAGCCTCTC ACTTGCCAG 180
 CAAAGACTTC AGGATGTCAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTGAGCC 240
 CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GGCTGATCCA 300
 CCGGAATTGT CTGCACTGAC AAAAGAATTA AATGCCCTGCA GGGAAACAAC TCTAGAAAAG 360
 GAAGAAAGAA TCCTCTGAAT TAAAGCTGAA AGAAACAACA CAAGACTATT ACTGGAGCAT 420
 TTGGAGTGCC TTGTGTCCAG ACATGAAAGA TCACTAAGAA TGACGGTGGT AAAACGGCAA 480
 GCCCAGTCTC CCTCAGGAGT ATCCAGTGAA GTTGAAGTTC TCAAGGCACT GAAATCTTTG 540
 TTTGAGCACC ACAAGGCCTT GGATGAAAAG GTAAGGGAGC GACTGAGGGT TTCTTTAGAA 600
 AGAGTCTCTG CACTGGAAGA AGAACTAGCT GCTGCTAATC AGGAGATTGT TGCCTTCCGT 660
 GAACAAAATG TTCATATACA AAGAAAAATG GCATCAAGCG AGGGATCCAC AGAGTCAGAA 720
 CATCTTGAAG GGATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTTGTG CAATGGTTCT 780
 ATAGACTCAA CCGATGAAAC TAGTCAAATA GTTGAACCTAC AAGAATTGCT TGAAAAGCAA 840
 AACTATGAAA TGGCCCAGAT GAAAGAACGT TTAGCAGCCC TTTCTTCCCG AGTGGGAGAG 900
 GTGGAACAGG AAGCAGAGAC AGCAAGAAAG GATCTCATTA AAACAGAAGA AATGAACACC 960
 AAGTATCAAA GGGACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAGAATT 1020
 ACAACCTTG AAAAGCGTTA CCTCAGTGCT CAGAGAGAAT CTACCTCCAT ACATGACATG 1080
 AATGATAAAC TAGAAAATGA GTTAGCAAAT AAAGAAGCTA TCCTACGGCA GATGGAAGAG 1140
 AAAAACAGAC AGTTACAAGA ACGTCTTGAG CTAGCTGAAC AAAAGTTGCA GCAGACCATG 1200
 AGAAAGGCTG AAACCTTGCC TGAAGTAGAG GCTGAAGTGG CTCAGAAAT TGCAGCCCTA 1260
 ACCAAGGCTG AAGAGAGACA TGGAAATATT GAAGAACGTA TGAGACATTT AGAGGGTCAA 1320
 CTTGAAGAGA AGAATCAAGA ACTTCAAAGA GCTAGGCAAA GAGAGAAAAA GAATGAGGAG 1380
 CATAACAAGA GATTATCGGA TACGGTTGAT AGACTTCTGA CTGAATCCAA TGAACGCCTA 1440
 CACTACACT TAAGGAAAG AATGGCTGCT CTAGAAGAAA AGAATGTTTT AATTCAAGAA 1500
 TCAGAAACTT TCAGAAAGAA TCTTGAAGAA TCTTTACATG ATAAGGAAAG ATTAGCAGAA 1560
 GAAATTGAAA AGCTGAGATC TGAACCTGAC CAATTGAAA TGAGAACTGG CTCTTTAATT 1620
 GAACCCACAA TACCAAGAAC TCATCTAGAC ACCTCAGCTG AGTTGCGGTA CTGAGTGGGA 1680
 TCCCTAGTGT ACAGCCAGTC TGATTACAGA ACAACTAAAG TAATAAGAAG ACCAAGGAGA 1740
 GGCCGCATGG GTGTGCCAAG AGATGAGCCA AAGGTGAAAT CTCTTGGGGA TCACGAGTGG 1800
 AATAGAACTC AACAGATTGG AGTACTAAGC AGCCACCCTT TTGAAAGTGA CACTGAAATG 1860
 TCTGATATTG ATGATGATGA CAGAGAAACA ATTTTATGCT CAATGGATCT TCTCTCTCCA 1920
 AGTGGTCATT CCGATGCCCA GACGCTAGCC ATGATGCTTC AGGAACAATT GGATGCCATC 1980
 AACAAAGAAA TCAGGCTAAT TCAGGAAGAA AAAGAATCTA CAGAGTTGCG TGCTGAAGAA 2040
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5 GGTACCTCCA TTA CTGCTC TGTTACAGCT TCATCGCTGG CCAGTTCATC TCCCCCAGT 2160
 GGACACTCAA CTCCAAAGCT CACCCTCGA AGCCCTGCCA GGGAAATGGA TCGGATGGGA 2220
 GTCATGACAC TGCCTAGTGA TCTGAGGAAA CATCGGAGAA AGATTGCAGT TGTGGAAGAA 2280
 GATGGTTCGAG AGGACAAAGC AACAATTAAA TGTGAACTT CTCTCTCTCC TACCCTTAGA 2340
 GCCCTCAGAA TGACTCACAC TCTCCCTTCT TCCTACCACA ATGATGCTCG AAGTAGTTTA 2400
 TCTGTCTCTC TTGAGCCAGA AAGCCTCGGG CTGTGTAGTG CCAACAGCAG CCAAGACTCT 2460
 CTTCAAAAAG CCCCCAAGAA GAAAGGAATC AAGTCTTCAA TAGGACGTTT GTTTGGTAAA 2520
 AAAGAAAAAG CTCGACTTGG GCAGCTCCGA GGCTTTATGG AGACTGAAGC TGCAGCTCAG 2580
 10 GAGTCCCTGG GGTTAGGCAA ACTCGGAAC CAAGCTGAGA AGGATCGAAG ACTAAAGAAA 2640
 AAGCATGAAC TTCTTGAAGA AGCTCGGAGA AAGGGATTAC CTTTGGCCCA GTGGGATGGG 2700
 CCAACTGTGG TCGCATGGCT AGAGCTTTGG TTGGGAATGC CTGCGTGGTA CGTGGCAGCC 2760
 TGCCGAGCCA ACGTGAAGAG TGGTGCCATC ATGTCTGCTT TATCTGACAC TGAGATCCAG 2820
 AGAGAAATTG GAATCAGCAA TCCACTGCAT CGCTTAAAC TTGATTAGC AATCCAGGAG 2880
 15 ATGTTTCCCT TAACAAGTCC TTCAGTCTCT CCAACATCTC GAATCTCTT AGGCAACGTT 2940
 TGGGTGACTC ATGAAGAAAT GGAATATCTT GCAGCTCCAG CAAAAACGAA AGAATCTGAG 3000
 GAAGGAAGCT GGGCCAGTGT TCCGGTTTTT CTACAGACCC TGGCTTATGG AGATATGAAT 3060
 CATGAGTGGG TTGGAATGA ATGGCTTCCC AGCTTGGGGT TACCTCAGTA CAGAAGTTAC 3120
 TTTATGGAAT GCTTGGTAGA TGCAAGAATG TTAGATCACC TAACAAAAA AGATCTCCGT 3180
 20 GTCCATTTAA AAATGGTGGG TAGTTTCCAT CGAACCAAGT TACAATATGG AATTATGTGC 3240
 TTAAGAGAGT TGAATTTATG CAGAAAAGAA CTAGAAAGAA GACGGGAAGC AAGCCAACAT 3300
 GAAATAAAG ACGTGTGGT GTGGAGCAAT GACCGAATTA TTGCTGGAT ACAAGCAAT 3360
 GGAATTCGAG AATATGCAAA TAATATACTT GAGAGCGGTG TGCATGGCTC ACTTATAGCC 3420
 CTGGATGAAA ACTTTGACTA CAGCAGCTTA ACTTTATTAT TACAGATTCC AACACAGAAC 3480
 25 ACCCAGGCAA GGCAGATTCT TGAAAGAGAA TACAATAACC TCTTGGCCCT GGGAACTGAA 3540
 AGCGCACTGG ATGAAAGTGA TGACAAGAAC TTCAGACGTG GATCAACCTG GAGAAGGCAG 3600
 TTTCTCTCTC GTGAAGTACA TGAATCAGC ATGATGCTCG GGTCTCAGA AACATTACCA 3660
 GCTGGATTGA GGTAAACAC AACCTCTGGG CAATCAAGAA AAATGACAAC AGATGTTGCT 3720
 TCATCAAGAC TGCAGAGGTT AGACAACCTC ACTGTTTCGCA CATACTCATG TCTCGAGTAA 3780
 30 GCGGCCGCTT TAA

A222 Protein sequence:

Gene name: ESTs; Liprin A2
 Unigene number: Hs.306480
 35 Probeset Accession #: N51002
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: none found
 40 AAA domain: 286-539
 SAM domains: 895-964, 1017-1084, 1105-1177
 Cellular Localization: not determined

1 11 21 31 41 51
 45 MMCEVMPTIN EDTPMSQRGS QSSGSDSDSH FEQLMVNMLD ERDRLDLTLR ETQESLSLAQ 60
 QRLQDVIYDR DSLQRQLNSA LPQDIESLTG GLAGSKGADP PEFAALTKEL NACREQLLEK 120
 EEBISELKAE RNNTRLLEH LECLVSRHER SLRMTVVKRQ AQSPSGVSSE VEVLKALKSL 180
 FEHHKALDEK VRERLRVSLR RVSALEEEEL AANQEIVALLR EQNVHIQRKM ASSEGSTESE 240
 50 HLEGMEPQOK VHEKRLNSGS IDSTDETSQI VELQELLEKQ NYEMAQMKER LAALSSRVGE 300
 VEQEAETARK DLIKTEEMNT KYQRDIREAM AQKEDMEERI TTLEKRYLSA QRESTSIHDM 360
 NDKLENELAN KEAILRQMEE KNRQLQERLE LAEQKLQQT M RKAETLPEVE AELAQRIAL 420
 TKABERHGN EERMRLHEGQ LEEKNQELQR ARQREKMNEE HNKRLSDTVD RLLTESNERL 480
 QLHLKERRMA LEEKNVLIQE SETFRKNLEE SLHDKERLAE EIEKLRLSEL QLMKRTGSLI 540
 55 EPTTPRTHLD TSABLRYSVG SLVDSQSDYR TTKVIRRRPR GRMGVRRDEP KVKSLGDHEW 600
 NRTQIGVLS SHPFESDTEM SDIDDDRET IFSSMDLLSP SGHSDAQTLA MMLQEQLDAI 660
 NKEIRLIQEE KESTELRAEE IENRVASVSL EGLNLARVHP GTSITASVTA SSLASSPPPS 720
 GHSTPKLTPR SPAREMDRMG VMTLPDLRK HRRKIIVVEE DGREDKATIK CETSPPTPR 780
 60 ALRMTHTLPS SYHNDARSSL SVSLEPESLG LGSANSSQDS LHKAPKKKGI KSSIGRLFGK 840
 KEKARLQQLR GFMEATEAAQ ESLGLGKLTG QAEKDRRLKK KHELLEEARR KGLPFAQWDG 900
 PTVVWALELW LGMPAWYVAA CRANVKSAGI MSALSDTEIQ REIGISNPLH RLKRLRAIQE 960
 MVLSTSPSP PTSTRTPSGNV WVTHEEMENL AAPAKTKESE EGSWAQCPVF LQTLAYGDMN 1020
 HEWIGNEWLP SLGLPQYRSY FMECLVDARM LDHLTKKDLR VHLKMDVSFH RTSLOQYIMC 1080
 65 LKRLNYDRKE LERRREASQH EIKDVLVWSN DRIIRWIQAI GLREYANNIL ESGVHGLIA 1140
 LDENFDYSSL TLLQIPTQN TQARQILERE YNNLLALGTE RRLDESDDKN FRRGSTWRRQ 1200
 FPPREVHGIS MMPGSSETLP AGFRLTTTSG QSRKMTTDVA SSRLQRLDNS TVRTYSCLE

A223 DNA SEQUENCE

Gene name: CDA14
 70 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Nucleic Acid Accession #: NM_016570
 Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 ATGAGGCGAC TGAATCGGAA AAAAACTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTCCG 60
 AAGGTTCTCT AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
 80 TTTACAACATA TGGCTTTTAT AACCATAATG GAATTCCTAG TATATCAAGA TACATGGATG 180
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAT TAAGAATTAA TATAGATATT 240
 ACTGTTGCCA TGAAGTGTCA ATATGTTGGA GCGGATGTAT TGGATTTAGC AGAAACAATG 300
 GTTGATCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACTT 420
 CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480

5 GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCAATAAA 540
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600
 CATTITGGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTCATAGAAT AGATCATTTG 660
 TCTTTTGGAG AGCTTGTTC AGCAATTATT AATCCTTTAG ATGGAACCTGA AAAAATGTCT 720
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAAACAAA ACTACATACA 780
 TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAC 840
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTTCTCTT 900
 ATGGTGACAG TTACTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960
 10 ATTGTGGAG GAATCTTTT AACAACAGGC ATGTTACATG GAATTGGAAA ATTTATAGTT 1020
 GAAATAATT GCTGTCGTTT CAGACTTGA TCCTATAAAC CTGTCAATTC TGTTCCTTT 1080
 GAGGATGGCC ACACAGACAA CCACTTACCT CTTTATAGAAA ATAATACACA TGA

A224 Protein sequence:

15 Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Protein Accession #: NP_057654
 20 Signal sequence: none found
 Transmembrane domains: none found
 Cellular Localization: nuclear

25 1 11 21 31 41 51
 | | | | | |
 MRRLNRKKTL SLVKELDAFP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60
 KVEYEVDKDF SSKLRINIDI TVAMKQYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120
 KEWQRLQLI QSRLOEBSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVVK 180
 30 VAGNPHITVG KAIPHRGHA HLAALVNHEB YNFSHRIDHL SFGEIVPAII NPLDGTEDIA 240
 IDHNQMFQYF ITVVPFKLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300
 MVTVTEEHMP FWQFFVRLCG IVGGIFSTTG MLHGIGKFIV EIICCRFRLG SYKPVNSVPF 360
 EDGHTDNHLP LLENNTNTH

Uterine

A225 DNA SEQUENCE:

35 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 40 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 | | | | | |
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
 CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGCTCAGAG TTTCTTCCAA CCTTGCCATT 120
 GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
 ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
 50 ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGCCC 300
 CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
 GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
 TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
 55 CAGTCAGAGC TATAAGAGAT GATAGAAAA AGCCTTCACT TCAAAGAGT CAAATTCAT 600
 GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAA 660
 TTACTATTTA GTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTAA 720
 TCTGAAAAA AAAAAA AAAAAA

A226 Protein sequence:

60 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 65 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

70 1 11 21 31 41 51
 | | | | | |
 MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLRSGWGD DITWVQTYEE GLFYAQSKSK 60
 PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM 120
 75 FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

A227 DNA SEQUENCE

80 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Probeset Accession #: AA460530
 Nucleic Acid Accession #: NM_003667
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GTGGCGGCAA	CCGGCACCTC	AGTCCCCGCC	GCGCTTCTCC	TCGCGGCCCA	CGCCGTGGGG	60
5	TCAGGAACGC	GGCGTCTGGC	GCTGCAGACG	CCCCGTGAGT	TGCAGAAGCC	CACGGAGCGG	120
	CGCCCGGCGC	GCCACGGGCC	GTAGCAGTCC	GGTGTCTGTC	TCCGCCCGCG	TCCGGCTCGT	180
	GGCCCCCTAC	TTCCGGGCACC	ATGGACACCT	CCCCGCTCGG	TGTGCTCCTG	TCCTTGCTCG	240
	TGCTGTCTGA	GCTGGCGACC	GGGGGACAGT	CTCCGAGTCC	TGGTGTGTGT	CTGAGGGGCT	300
	GCCCCACACA	CTGTCAATTGC	GAGCCCGACG	GCAGGATGTT	GCTCAGGGTG	GACTGCTCCG	360
10	ACCTGGGGCT	CTCGGAGCTG	CCTTCCAACC	TCAGGCTCTT	CACCTCCTAC	CTAGACCTCA	420
	GTATGAACAA	CATCAGTCAG	CTGCTCCCCG	ATCCCTTGCC	CAGTCTCCCG	TTCTTGGAGG	480
	AGTTACGCTC	TGCGGGAAAC	GCTCTGACAT	ACATTCCTCA	GGGAGCATTC	ACTGGCCTTT	540
	ACAGTCTTAA	AGTTCTTTATG	CTGCAGAATA	ATCAGCTAAG	ACACGTACCC	ACAGAAGCTC	600
	TGCAGAAATT	GCGAAGCCTT	CAATCCCTGC	GTCTGGATGC	TAACCAATC	AGCTATGTGC	660
15	CCCCAAGCTG	TTTCAGTGGC	CTGCATTCCC	TGAGGCACCT	GTGGCTGGAT	GACAATGCGT	720
	TAACAGAAAT	CCCCGTCCAG	GCTTTTAGAA	GTTTATCGGC	ATTGCAAGCC	ATGACCTTGG	780
	CCCTGAACAA	AATACACCAC	ATACCAGACT	ATGCCTTTGG	AAACCTCTCC	AGCTTGGTAG	840
	TTCTACATCT	CCATAACAA	AGAATCCACT	CCCTGGGAAA	GAAATGCTTT	GATGGGCTCC	900
	ACAGCCTAGA	GACTTTAGAT	TTAAATTACA	ATAACCTTGA	TGAATTCCTC	ACTGCAATTA	960
20	GGACACTCTC	CAACCTTAAA	GAACCTAGGAT	TTCATAGCAA	CAATATCAGG	TCGATACCTG	1020
	AGAAAGCATT	TGTAGGCAAC	CCTTCTCTTA	TTACAATACA	TTTCTATGAC	AATCCCATTCC	1080
	AATTTGTTGG	GAGATCTGCT	TTTCAACATT	TACCTGAACT	AAGAACACTG	ACTCTGAATG	1140
	GTGCCTCACA	AATAACTGAA	TTTCTGTGAT	TAACCTGGAAC	TGCAAACTCG	GAGAGTCTGA	1200
	CTTTAACTGG	AGCAGAGATC	TCATCTCTTC	CTCAACCGCT	CTGCAATCAG	TTACCTAATC	1260
25	TCCAAGTGCT	AGATCTGTCT	TACAACCTAT	TAGAAGATT	ACCCAGTTT	TCAGTCTGCC	1320
	AAAAGCTTCA	GAAATTTGAC	CTAAGACATA	ATGAAATCTA	CGAAATTTAA	GTTGACACTT	1380
	TCCAGCAGTT	GCTTAGCCTC	CGATCGCTGA	ATTTGGCTTG	GAACAAAATT	GCTATTATTC	1440
	ACCCCAATGC	ATTTTCCACT	TTGCCATCCC	TAATAAAGCT	GGACCTATCG	TCCAACCTCC	1500
	TGTCGTCTTT	TCCTATAACT	GGGTACATG	GTTTAACTCA	CTTAAATTA	ACAGGAAATC	1560
	ATGCCTTACA	GAGCTTGATA	TCATCTGAAA	ACTTCCGAGA	ACTCAAGGTT	ATAGAAATGC	1620
30	CTTATGCTTA	CCAGTGCTGT	GCATTTGGAG	TGTGTGAGAA	TGCCTATAAG	ATTTCTAATC	1680
	AATGGAATAA	AGGTGACAAC	AGCAGTATGG	ACGACCTTCA	TAAGAAAGAT	GCTGGAATGT	1740
	TTCAGGCTCA	AGATGAACGT	GACCTTGAAG	ATTTCTGTCT	TGACTTTGAG	GAAGACCTGA	1800
	AAGCCCTTCA	TTCAGTGCAG	TGTTACCTT	CCCCAGGCC	CTTCAAAACC	TGTGAACACC	1860
35	TGCTTGATGG	CTGGCTGATC	AGAATTGGAG	TGTGGACCAT	AGCAGTTCTG	GCACCTACTT	1920
	GTAATGCTTT	GGTGACTTCA	ACAGTTTTC	GATCCCTCT	GTACATTTC	CCCATTAAC	1980
	TGTTAATTGG	GGTCATCGCA	GCAGTGAACA	TGCTCACGGG	AGTCTCCAGT	GCCGTGCTGG	2040
	CTGGTGTGGA	TGCGTTCACT	TTTGGCAGCT	TTGCACGACA	TGGTGCCTGG	TGGGAGAAATG	2100
	GGGTGTTGGT	CCATGTCATT	GGTTTTTGT	CCATTTTTC	TTTCAAGTCA	TCTGTTTTCC	2160
40	TGCTTACTCT	GGCAGCCCTG	GAGCGTGGGT	TCCTGTGAA	ATATTCTGCA	AAATTGAAA	2220
	CGAAAGCTCC	ATTTCTAGC	CTGAAAGTAA	TCATTTTGCT	CTGTGCCCTG	CTGGCCTTGA	2280
	CCATGGCCGC	AGTTCCCTCG	CTGGGTGGCA	GCAAGTATGG	CGCCTCCCT	CTCTGCCTGC	2340
	CTTTGCCTTT	TGGGGAGCCC	AGCACCATGG	GCTACATGGT	CGCTCTCATC	TTGCTCAATT	2400
	CCCTTTGCTT	CCTCATGATG	ACCATTGCTT	ACACCAAGCT	CTACTGCAAT	TTGGACAAGG	2460
45	GAGACCTGGA	GAATATTGTT	GACTGCTCTA	TGGTAAACA	CATTGCCCTG	TTGCTCTTCA	2520
	CAACTGCAAT	CCTAAACTGC	CCTGTGGCTT	TCTTGCTCTT	CTCCTCTTTA	ATAAACCTTA	2580
	CATTTATCAG	TCTGAAGTA	ATTAAGTTTA	TCCTTCTGGT	GGTAGTCCCA	CTTCTGTCAT	2640
	TGCTCAATCC	CCTTCTCTAC	ATCTTGTTC	ATCCTCACTT	TAAGGAGGAT	CTGGTGAGCC	2700
	TGAGAAAGCA	AACCTACGTG	TGGACAAGAT	CAAAACACCC	AAGCTTGATG	TCAATTAAC	2760
50	CTGATGATGT	CGAAAAACAG	TCCTGTGACT	CAACTCAAGC	CTTGGTAAAC	TTTACCAGCT	2820
	CCAGCATCAC	TTATGACCTG	CCTCCAGTT	CCGTGCCATC	ACCAGCTTAT	CCAGTGACTG	2880
	AGAGCTGCCA	TCCTTCTCT	GTGGCATTTG	TCCCATGTCT	CTAATTAATA	TGTGAAGGAA	2940
	AATGTTTTCA	AAGGTTGAGA	ACCTGAAAAT	GTGAGATTGA	GTATATCAGA	GCAGTAATTA	3000
	ATAAGAAAG	CTGAGGTGAA	ACTCGGTTTA	AA			

A228 Protein sequence

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Protein Accession #: NP_003658.1
 Signal sequence: 1-22
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
65	MDTSRLGVLL	SLPVLQLLAT	GGSSPRSGVL	LRGCPHCHC	EPDGRMLLRV	DCSDLGLSEL	60
	PSNLSVFTSY	LDLSMNNISQ	LLPNPLPSLR	FLEELRLAGN	ALTYIPKGF	TGLYSKVLML	120
	LQNNQLRHVP	TEALQNLRLS	QSLRLDANHI	SYVPPSCFSG	LHSLRLHLWD	DNALTEIPVQ	180
70	AFRLSLALQA	MTLALNKIHH	IPDYAFGNLS	SLVVLHLHNN	RIHSLGKKCF	DGLHSLETLD	240
	LNYNLDEFP	TAIRTLNLK	ELGFHSNNIR	SIPEKAFVGN	PSLTIHFYD	NPIQFVGRSA	300
	FQHLPELRTL	TLNGASQITE	FPDLTGATNL	ESLTLTGAQI	SSLPQTVCNQ	LPNLQVLDLS	360
	YNLLEDLPF	SVQKLQKID	LRHNEIYEIK	VDTFQQLSL	RLNLAWNKI	AIHPNAFST	420
	LPSLIKLDDL	SNLLSSFPIT	GLHGLTHLKL	TGNHALQSLI	SSNFPELVK	IEMFYAQCC	480
75	AFGVCENAYK	ISNQWNKGDN	SSMDDLHKKD	AGMFOAQDER	DLEDFLDPE	EDLKALHSVQ	540
	CSPSPGPFKP	CEHLLDGWLI	RIGVWTIAVL	ALTCNALVTS	TVFRSPLYIS	PIKLLIGVIA	600
	AVNMLTGVS	AVLAGVDAFT	PGSFARHGAW	WENGVGCHVI	GFLSIFASES	SVFLTLAAL	660
	ERGSVKYSA	KFETKAPFSS	LKVILLCAL	LALTMVAVPL	LGGSKYGASP	LCLPLPFGE	720
	STMGYMLALI	LLNSLCFEMM	TIATYTKLYCN	LDKGDLENIW	DCSMVKHIAL	LLFTNCILNC	780
80	PVAFLSFSSL	LNLFISPEV	IKFILLVVP	LPACLNPLY	ILFNPFPKED	LVSLRKQTYV	840
	WTRSKHPSLM	SINSDDVEKQ	SCDSTQALVT	FTSSSITYDL	PPSSVPSPAY	PVTESCHLSS	900
	VAFVPC						

Table 75: See Table 1

Table 76A depicts Seq ID No; UnigenelD; UnigeneTitle; PKey; Predicted Cellular Localization; and Exemplar Accession for each of the sequences in Table 78. The information in

Table 76A is linked by SeqID No to Table 78.

Seq ID No:	Sequence ID No for sequences in table				
Pkey:	Unique Eos probeset identifier number				
ExAccn:	Exemplar Accession number, Genbank accession number				
UnigenelD:	Unigene number				
Unigene Title:	Unigene gene title				
Pred Subcell Loc:	Predicted sub-cellular localization				
Seq ID No	Pkey	ExAccn	UnigenelD	Unigene Title	Pred Subcell Loc
Seq ID 1 & 2	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	plasma membrane
Seq ID 3 & 4	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	plasma membrane
Seq ID 5 & 6	429423	AI016712	Hs.287797	integrin, beta 1 (fibronectin receptor,	plasma membrane
Seq ID 7 & 8	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	secreted
Seq ID 9 & 10	419172	AW338625	Hs.22120	ESTs; similar to TRANSMEMBRANE 4 SUPERF	plasma membrane
Seq ID 11 & 12	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 13 & 14	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 15 & 16	407836	T79340	Hs.200272	B-cell CLL/lymphoma 6, member B, zinc fi	intracell
Seq ID 17 & 18	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	secreted
Seq ID 19 & 20	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	plasma membrane
Seq ID 21 & 22	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	secreted
Seq ID 23 & 24	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	secreted
Seq ID 25 & 26	429276	AF056085	Hs.198612	G protein-coupled receptor 51	plasma membrane
Seq ID 27 & 28	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecuol	plasma membrane
Seq ID 29 & 30	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	secreted
Seq ID 31 & 32	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	intracell
Seq ID 33 & 34	418506	AA084248	Hs.85339	G protein-coupled receptor 39	plasma membrane
Seq ID 35 & 36	423961	D13666	Hs.136348	periostin (OSF-2os)	secreted
Seq ID 37 & 38	414812	X72755	Hs.77367	monokine induced by gamma interferon	secreted
Seq ID 39 & 40	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 41 & 42	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 43 & 44	424399	AI905687	AI905687:IL-BT095-190199-019 BT095 Homo	secreted	secreted
Seq ID 45 & 46	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	secreted
Seq ID 47 & 48	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	secreted
Seq ID 49 & 50	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	secreted
Seq ID 51 & 52	439569	AW602166	Hs.222399	CEGP1 protein	secreted
Seq ID 53 & 54	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 55 & 56	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	plasma membrane
Seq ID 57 & 58	411789	AF245505	Hs.72157	Adlcan	secreted
Seq ID 59 & 60	428698	AA852773	Hs.334838	KIAA1866 protein	plasma membrane
Seq ID 61 & 62	450098	W27249	Hs.8109	hypothetical protein FLJ21080	intracell
Seq ID 63 & 64	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	secreted
Seq ID 65 & 66	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	plasma membrane
Seq ID 67 & 68	415539	AI733881	Hs.72472	BMP-R1B	plasma membrane
Seq ID 69 & 70	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 71 & 72	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 73 & 74	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	plasma membrane
Seq ID 75 & 76	442082	R41823	Hs.7413	ESTs	plasma membrane
Seq ID 77 & 78	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	plasma membrane
Seq ID 79 & 80	451398	AI793124	Hs.144479	ESTs	intracell
Seq ID 81 & 82	429220	AW207206		ESTs	plasma membrane
Seq ID 83 & 84	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	plasma membrane
Seq ID 85 & 86	423242	AL039402	Hs.125783	DEME-6 protein	plasma membrane
Seq ID 87 & 88	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 89 & 90	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 91 & 92	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 93 & 94	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 95 & 96	325372			Phase 2 & 3 Exons	cytoplasmic
Seq ID 97 & 98	450375	AA009647		a disintegrin and metalloproteinase doma	plasma membrane
Seq ID 99 & 100	426215	AW963419	Hs.155223	stanniocalcin 2	secreted
Seq ID 101 & 102	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	secreted
Seq ID 103 & 104	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 105 & 106	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 107 & 108	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	plasma membrane
Seq ID 109 & 110	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	secreted
Seq ID 111 & 112	446163	AA026880	Hs.25252	prolactin receptor	plasma membrane
Seq ID 113 & 114	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	plasma membrane
Seq ID 115 & 116	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-li	intracell
Seq ID 117 & 118	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	plasma membrane
Seq ID 119 & 120	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 121 & 122	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 123 & 124	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 125 & 126	115522	BE614387	Hs.333893	c-Myc target JPO1	intracell
Seq ID 127 & 128	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	plasma membrane
Seq ID 129 & 130	446051	BE048061	Hs.37054	ephrin-A3	plasma membrane
Seq ID 131 & 132	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	secreted
Seq ID 133 & 134	410418	D31382	Hs.63325	transmembrane protease, serine 4	plasma membrane
Seq ID 135 & 136	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	plasma membrane
Seq ID 137 & 138	422260	AA315993	Hs.105484	regenerating gene type IV	secreted

5	Seq ID 139 & 140	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 141 & 142	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 143 & 144	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 145 & 146	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 147 & 148	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 149 & 150	104888	AW939591	Hs.5940	mucin 13, epithelial transmembrane	plasma membrane
	Seq ID 151 & 152	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ1245 fis, clone C	plasma membrane
	Seq ID 153 & 154	422330	D30783	Hs.115263	epiregulin	plasma membrane
10	Seq ID 155 & 156	452461	N78223	Hs.108106	transcription factor	intracell
	Seq ID 157 & 158	413324	V00571	Hs.75294	corticotropin releasing hormone	secreted
	Seq ID 159 & 160	412420	AL035668	Hs.73853	bone morphogenetic protein 2	secreted
	Seq ID 161 & 162	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	secreted
	Seq ID 163 & 164	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	secreted
15	Seq ID 165	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (intracell
	Seq ID 166 & 167	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (intracell
	Seq ID 168 & 169	432829	W60377	Hs.57772	ESTs	intracell
	Seq ID 170 & 171	425721	AC002115	Hs.159309	uropalakin 1A	plasma membrane
	Seq ID 172 & 173	420370	Y13645	Hs.97234	uropalakin 2	plasma membrane
20	Seq ID 174 & 175	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	plasma membrane
	Seq ID 176 & 177	402075			ENSP00000251056*:Plasma membrane calcium	secreted
	Seq ID 178 & 179	421110	AJ250717	Hs.1355	cathepsin E	secreted
	Seq ID 180 & 181	451668	Z43948	Hs.326444	cartilage acidic protein 1	plasma membrane
	Seq ID 182 & 183	451668	Z43948	Hs.326444	cartilage acidic protein 1	secreted
25	Seq ID 184 & 185	451668	Z43948	Hs.326444	cartilage acidic protein 1	intracell
	Seq ID 186 & 187	408243	Y00787	Hs.624	interleukin 8	secreted
	Seq ID 188 & 189	422282	AF019225	Hs.114309	apolipoprotein L	secreted
	Seq ID 190 & 191	425852	AK001504	Hs.159551	death receptor 6, TNF superfamily member	plasma membrane
	Seq ID 192 & 193	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	plasma membrane
30	Seq ID 194 & 195	404875			NM_022819*:Homo sapiens phospholipase A2	intracell
	Seq ID 196 & 197	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	plasma membrane
	Seq ID 198 & 199	404977			Insulin-like growth factor 2 (somatomedi	secreted
	Seq ID 200 & 201	420876	AA918425	Hs.177744	ESTs	plasma membrane
	Seq ID 202 & 203	427747	AW411425	Hs.180655	serine/threonine kinase 12	intracell
35	Seq ID 204 & 205	420281	AI623693	Hs.323494	Predicted cation efflux pump	plasma membrane
	Seq ID 206 & 207	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	intracell
	Seq ID 208	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 209 & 210	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 211 & 212	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
40	Seq ID 213 & 214	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 215 & 216	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 217 & 218	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 219 & 220	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0	intracell
	Seq ID 221 & 222	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0	intracell
45	Seq ID 223 & 224	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 225 & 226	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 227 & 228	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 229 & 230	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	secreted
50	Seq ID 231 & 232	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	secreted
	Seq ID 233 & 234	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	secreted
	Seq ID 235 & 236	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 237 & 238	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 239 & 240	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 241 & 242	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	intracell
55	Seq ID 243 & 244	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	secreted
	Seq ID 245 & 246	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	plasma membrane
	Seq ID 247 & 248	430890	X54232	Hs.2699	glypican 1	plasma membrane
	Seq ID 249 & 250	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	plasma membrane
	Seq ID 251	429466	M85835	Hs.12827	ESTs	
60	Seq ID 252	429466	M85835	Hs.12827	ESTs	
	Seq ID 253 & 254	419721	NM_001650	Hs.288650	aquaporin 4	plasma membrane
	Seq ID 255 & 256	407034	U84540		gb:Human dystrobrein isoform DTN-3 (DTN	secreted
	Seq ID 257 & 258	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	plasma membrane
	Seq ID 259 & 260	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	secreted & plasma membrane
65	Seq ID 261 & 262	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	secreted
	Seq ID 263 & 264	419704	AA429104	Hs.45057	ESTs	intracell
	Seq ID 265 & 266	444471	AB020684	Hs.11217	KIAA0877 protein	plasma membrane
	Seq ID 267 & 268	409395	U46745	Hs.336678	dystrobrein, alpha	secreted
	Seq ID 269 & 270	413053	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	secreted
70	Seq ID 271 & 272	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	plasma membrane
	Seq ID 273	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 274	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 275 & 276	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	plasma membrane
	Seq ID 277 & 278	424998	U58515	Hs.154138	chitinase 3-like 2	secreted
75	Seq ID 279 & 280	412709	AL022327	Hs.74518	KIAA0027 protein	plasma membrane
	Seq ID 281 & 282	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	plasma membrane
	Seq ID 283 & 284	404049			NM_018937*:Homo sapiens protocadherin be	plasma membrane
	Seq ID 285 & 286	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	plasma membrane
	Seq ID 287 & 288	404029			NM_018936*:Homo sapiens protocadherin be	plasma membrane
80	Seq ID 289 & 290	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	intracell
	Seq ID 291 & 292	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 293 & 294	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 295 & 296	436895	AF037335	Hs.5338	carbonic anhydrase XII	plasma membrane
	Seq ID 297 & 298	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospho	plasma membrane

5	Seq ID 299 & 300	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	plasma membrane
	Seq ID 301 & 302	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	plasma membrane
	Seq ID 303 & 304	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	plasma membrane
	Seq ID 305 & 306	410407	X66839	Hs.63287	carbonic anhydrase IX	plasma membrane
	Seq ID 307 & 308	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	plasma membrane
	Seq ID 309 & 310	420737	L08096	Hs.99899	CD70 ; tumor necrosis factor (ligand) s	plasma membrane
	Seq ID 311 & 312	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	plasma membrane
10	Seq ID 313 & 314	412719	AW016610	Hs.816	ESTs	intracell
	Seq ID 315 & 316	417034	NM_006183	Hs.80962	neurotensin	secreted
	Seq ID 317 & 318	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	plasma membrane
	Seq ID 319 & 320	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	secreted
	Seq ID 321 & 322	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	plasma membrane
	Seq ID 323 & 324	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	secreted
15	Seq ID 325 & 326	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 327 & 328	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 329 & 330	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	secreted
	Seq ID 331 & 332	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	plasma membrane
	Seq ID 333 & 334	431846	BE019924	Hs.271580	uroplakin 1B	plasma membrane
20	Seq ID 335 & 336	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	secreted
	Seq ID 337 & 338	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane
	Seq ID 339 & 340	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	plasma membrane
	Seq ID 341 & 342	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	plasma membrane
	Seq ID 343 & 344	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	plasma membrane
25	Seq ID 345 & 346	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	secreted
	Seq ID 347 & 348	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	plasma membrane
	Seq ID 349 & 350	417542	J04129	Hs.82269	progestagen-associated endometrial prote	secreted
	Seq ID 351 & 352	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	plasma membrane
	Seq ID 353 & 354	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
30	Seq ID 355 & 356	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 357 & 358	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	secreted
	Seq ID 359 & 360	418462	BE001596	Hs.85266	integrin, beta 4	plasma membrane
	Seq ID 361 & 362	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	secreted
	Seq ID 363 & 364	439606	W79123	Hs.58561	G protein-coupled receptor 87	plasma membrane
35	Seq ID 365 & 366	404877			NM_005365:Homo sapiens melanoma antigen,	intracell
	Seq ID 367 & 368	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	plasma membrane
	Seq ID 369 & 370	109424	NM_005329	Hs.85962	hyaluronan synthase 3	plasma membrane
	Seq ID 371 & 372	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 373 & 374	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
40	Seq ID 375 & 376	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 377 & 378	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 379 & 380	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 381 & 382	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 383 & 384	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	plasma membrane
45	Seq ID 385 & 386	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 387 & 388	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 389 & 390	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	secreted
	Seq ID 391 & 392	332180	AF134160	Hs.7327	claudin 1	plasma membrane
50	Seq ID 393 & 394	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 395 & 396	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 397 & 398	439223	AW238299	Hs.250618	UL16 binding protein 2	plasma membrane
	Seq ID 399 & 400	409757	NM_001898	Hs.123114	cystatin SN	secreted
	Seq ID 401 & 402	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 403 & 404	428969	AF120274	Hs.194689	artemin	secreted
55	Seq ID 405 & 406	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 407 & 408	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 409 & 410	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 411 & 412	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 413 & 414	414774	X02419	Hs.77274	plasminogen activator, urokinase	secreted
60	Seq ID 415 & 416	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 417 & 418	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 419 & 420	428486	AW583497	Hs.184604	pancreatic polypeptide	secreted
	Seq ID 421 & 422	457489	AI693815	Hs.127179	cryptic gene	secreted
	Seq ID 423 & 424	432874	W94322	Hs.279651	melanoma inhibitory activity	secreted
65	Seq ID 425 & 426	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 427 & 428	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 429 & 430	404682			C9001188*:gi12738842[ref]NP_073725.1] p	secreted
	Seq ID 431 & 432	429547	AW009166	Hs.99376	ESTs	secreted
70	Seq ID 433 & 434	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter)	plasma membrane
	Seq ID 435 & 436	407242	M18728		gb:Human nonspecific crossreacting antig	plasma membrane
	Seq ID 437 & 438	407242	M18728		gb:Human nonspecific crossreacting antig	plasma membrane
	Seq ID 439 & 440	407242	M18728		gb:Human nonspecific crossreacting antig	plasma membrane
	Seq ID 441 & 442	432596	AJ224741	Hs.278461	matrilin 3	secreted
	Seq ID 443 & 444	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	plasma membrane
75	Seq ID 445 & 446	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	intracell
	Seq ID 447 & 448	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	secreted
	Seq ID 449 & 450	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 451 & 452	448030	N30714	Hs.325360	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 453 & 454	422109	S73265	Hs.1473	gastrin-releasing peptide	secreted
80	Seq ID 455 & 456	419235	AW470411	Hs.288433	neurotrophin	plasma membrane
	Seq ID 457 & 458	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	plasma membrane
	Seq ID 459 & 460	427333	AF067797	Hs.176658	aquaporin 8	plasma membrane
	Seq ID 461 & 462	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	secreted
	Seq ID 463 & 464	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	secreted

5	Seq ID 465 & 466	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	secreted
	Seq ID 467 & 468	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	secreted
	Seq ID 469 & 470	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10???	plasma membrane
	Seq ID 471 & 472	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10???	plasma membrane
	Seq ID 473 & 474	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	secreted
10	Seq ID 475 & 476	429010	Y18198	Hs.194725	one cut domain, family member 2	intracell
	Seq ID 477 & 478	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	secreted
	Seq ID 479 & 480	448243	AW369771	Hs.52620	integrin, beta 8	plasma membrane
	Seq ID 481 & 482	426427	M86699	Hs.169840	TTK protein kinase	intracell
	Seq ID 483 & 484	428187	AI687303	Hs.285529	G protein-coupled receptor 49	plasma membrane
15	Seq ID 485 & 486	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 487 & 488	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 489 & 490	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 491 & 492	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 493 & 494	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	secreted
20	Seq ID 495 & 496	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	plasma membrane
	Seq ID 497 & 498	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum corn	secreted
	Seq ID 499 & 500	406400			kallikrein 8 (neurosin/ovasin) (KLK8)	secreted
	Seq ID 501 & 502	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	secreted
	Seq ID 503 & 504	420440	NM_002407	Hs.97644	mammaglobin 2	secreted
25	Seq ID 505 & 506	428450	NM_014791	Hs.184339	KIAA0175 gene product	intracell
	Seq ID 507 & 508	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	secreted
	Seq ID 509 & 510	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	secreted
	Seq ID 511 & 512	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	intracell
	Seq ID 513	431989	AW972870	Hs.291069	ESTs	
30	Seq ID 514	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	
	Seq ID 515 & 516	409178	BE393948	Hs.50915	kallikrein 5	secreted
	Seq ID 517 & 518	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	secreted
	Seq ID 519 & 520	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 521 & 522	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
35	Seq ID 523 & 524	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 525 & 526	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 527 & 528	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (secreted
	Seq ID 529 & 530	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	secreted
	Seq ID 531 & 532	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	plasma membrane
40	Seq ID 533 & 534	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	plasma membrane
	Seq ID 535 & 536	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 537 & 538	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 539 & 540	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	secreted
	Seq ID 541 & 542	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	secreted
45	Seq ID 543 & 544	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	plasma membrane
	Seq ID 545 & 546	452792	AB037765	Hs.30652	KIAA1344 protein	plasma membrane
	Seq ID 547 & 548	400294	N95796	Hs.278695	Homo sapiens prolein mRNA, complete cds	plasma membrane
	Seq ID 549 & 550	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 551 & 552	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
50	Seq ID 553 & 554	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 555 & 556	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 557 & 558	400290	H18836	Hs.31608	hypothetical protein FLJ20041	plasma membrane
	Seq ID 559 & 560	410001	AB041036	Hs.57771	kallikrein 11	secreted
	Seq ID 561 & 562	418396	AI765805	Hs.26691	ESTs	plasma membrane
55	Seq ID 563 & 564	451027	AW519204	Hs.40808	ESTs	plasma membrane
	Seq ID 565 & 566	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	plasma membrane
	Seq ID 567 & 568	433466	AA508353	Hs.105314	relaxin 1 (H1)	secreted
	Seq ID 569 & 570	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 571 & 572	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
60	Seq ID 573 & 574	414569	AF109298	Hs.118258	prostate cancer associated protein 1	plasma membrane
	Seq ID 575 & 576	413435	X51405	Hs.75360	carboxypeptidase E	secreted
	Seq ID 577 & 578	426501	AW043782	Hs.293616	ESTs	plasma membrane
	Seq ID 579 & 580	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	plasma membrane
	Seq ID 581 & 582	408369	R38438	Hs.182575	solute carrier family 15 (H???) transport	plasma membrane
65	Seq ID 583 & 584	412628	AI972402	Hs.306051	hypothetical protein MGC2648	secreted
	Seq ID 585 & 586	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
	Seq ID 587 & 588	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
	Seq ID 589 & 590	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	plasma membrane
	Seq ID 591 & 592	445413	AA151342	Hs.12677	CGI-147 protein	secreted
70	Seq ID 593 & 594	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	intracell
	Seq ID 595 & 596	427958	AA418000	Hs.98280	potassium intermediate/small conductance	plasma membrane
	Seq ID 597 & 598	421887	AW161450	Hs.109201	CGI-86 protein	plasma membrane
	Seq ID 599 & 600	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	secreted
	Seq ID 601 & 602	432101	AI918950	Hs.123642	EphA3	plasma membrane
75	Seq ID 603 & 604	407786	AA687538	Hs.38972	tetraspan 1	plasma membrane
	Seq ID 605 & 606	416836	D54745	Hs.80247	cholecystokinin	secreted
	Seq ID 607 & 608	416539	Y07909	Hs.79368	epithelial membrane protein 1	plasma membrane
	Seq ID 609 & 610	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 611 & 612	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
80	Seq ID 613 & 614	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 615 & 616	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 617 & 618	422424	AI186431	Hs.296638	prostate differentiation factor	secreted
	Seq ID 619 & 620	428970	BE276891	Hs.194691	retinoic acid induced 3	plasma membrane
	Seq ID 621 & 622	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	secreted
	Seq ID 623 & 624	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 625 & 626	420610	AI683183	Hs.99348	distal-less homeo box 5	intracell
	Seq ID 627 & 628	425723	NM_014420	Hs.159311	dickkopf (Xenopus laevis) homolog 4	secreted

Seq ID 629 & 630	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	intracell
Seq ID 631 & 632	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	secreted
Seq ID 633 & 634	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	intracell

Table 76B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
424399	238961_1	AI905687 AI905624 AI905837 AI905623 AA340069 R75793 W72837 BE074512 AI905633 W72838 BE092421 AI127172 BE186013 AW070916 AI139456 AW176044 AW291950
429220	301384_1	AW207206 AW341473 AA448195 AI951341
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

Table 76C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
403047	3540153	Minus	59793-59968
404029	7671252	Plus	108716-111112
404049	3688074	Minus	75765-78155
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404877	1519284	Plus	1095-2107
404977	3738341	Minus	43081-43229
405932	7767812	Minus	123525-123713
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 77 provides Pkey; Seq ID No; Disease Indications; and Preferred Utility for sequences in Table 78. Seq ID No links the information in Table 77 to Table 78.

5	Seq ID No:	Sequence ID No for sequences in table		
	Pkey:	Unique Eos probeset identifier number		
	Disease Indications:	Diseases designated for coverage as described in Table 1		
	Preferred Utility:	Preference of utility, based partly upon predicted localization (Ab is antibody; sm is small molecule target; CTL is vaccine target)		
	Seq ID No	Pkey	Disease Indications	Preferred Utility
10	Seq ID 1 & 2	425023	angiogenesis	Ab, sm, CTL, imaging
	Seq ID 3 & 4	424503	pancreas, prostate, angiogenesis, bladder, lung	Ab, sm, imaging
	Seq ID 5 & 6	429423	angiogenesis	Ab, sm
	Seq ID 7 & 8	400289	angiogenesis, bladder, lung, cervical, ovarian, head & neck	Ab, sm, CTL, diagnostic
15	Seq ID 9 & 10	419172	angiogenesis, renal	Ab, sm, CTL, imaging
	Seq ID 11 & 12	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 13 & 14	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 15 & 16	407836	angiogenesis	CTL
20	Seq ID 17 & 18	414577	angiogenesis	Ab, CTL, diagnostic
	Seq ID 19 & 20	418738	angiogenesis, lung, ovarian, bladder & stomach, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 21 & 22	428368	angiogenesis, head & neck, stomach	Ab, sm, diagnostic
	Seq ID 23 & 24	415138	angiogenesis, pancreas, stomach, lung, uterine	Ab, CTL, diagnostic
25	Seq ID 25 & 26	429276	angiogenesis, bladder, glioblastoma	Ab, sm, imaging
	Seq ID 27 & 28	418994	prostate, angiogenesis	Ab, CTL, imaging
	Seq ID 29 & 30	407975	angiogenesis, renal	Ab, CTL, diagnostic
	Seq ID 31 & 32	429113	angiogenesis, bladder and stomach	sm, CTL
30	Seq ID 33 & 34	418506	angiogenesis, ovarian, glioblastoma, uterine, lung, bladder, pancreas	Ab, sm, imaging
	Seq ID 35 & 36	423961	breast, colon, bladder, lung, fibrosis, pancreas, head and neck, ovarian	Ab, sm, diagnostic
	Seq ID 37 & 38	414812	breast, bladder, lung, Fibrosis, pancreas, colon, head and neck, cervical, stomach, renal, ovarian	Ab, CTL, diagnostic
	Seq ID 39 & 40	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
35	Seq ID 41 & 42	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
	Seq ID 43 & 44	424399	breast, uterine, head & neck	Ab, CTL, diagnostic
	Seq ID 45 & 46	422867	breast, ovarian, prostate, pancreas, lung, colon, uterine	Ab, CTL, diagnostic
	Seq ID 47 & 48	428227	breast, lung, bladder, ovarian, head & neck, fibrosis, colon, stomach, cervical	Ab, CTL, diagnostic
40	Seq ID 49 & 50	444381	breast, colon, bladder, lung, pancreas, head & neck, ovarian, stomach, uterine, renal, angiogenesis	Ab, CTL, diagnostic
	Seq ID 51 & 52	439569	breast, androgen withdrawal prostate, prostate, bladder	Ab, CTL, diagnostic
	Seq ID 53 & 54	411558	pancreas, prostate, stomach, breast, uterine, cervical, ovarian	Ab, sm, imaging
	Seq ID 55 & 56	400303	breast, ovarian, pros, stomach, uterine, bladder lung head & neck	Ab, sm, CTL, imaging
45	Seq ID 57 & 58	411789	pancreas, lung, breast, stomach, head & neck, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 59 & 60	428698	breast, colon, lung, pancreas, stomach, head & neck, ovarian	Ab, sm, imaging
	Seq ID 61 & 62	450098	breast, lung, stomach, uterine	CTL
	Seq ID 63 & 64	421552	breast, ovarian, pancreas, cervical, uterine, prostate, lung, stomach, head & neck	Ab, sm, CTL, diagnostic
50	Seq ID 65 & 66	452747	breast, bladder, lung, head & neck, ovarian, stomach, uterine, pancreas	Ab, imaging
	Seq ID 67 & 68	415539	breast, prostate, ovarian, cervical, uterine	Ab, sm, CTL, imaging
	Seq ID 69 & 70	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 71 & 72	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
55	Seq ID 73 & 74	409079	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 75 & 76	442082	breast, prostate, ovarian	Ab, imaging
	Seq ID 77 & 78	400297	breast, bladder, colon, prostate	Ab, sm, CTL, imaging
	Seq ID 79 & 80	451398	breast, ovarian	CTL
60	Seq ID 81 & 82	429220	breast, prostate, benign prostatic hyperplasia	Ab, CTL, imaging
	Seq ID 83 & 84	421524	breast	Ab, sm, CTL, imaging
	Seq ID 85 & 86	423242	breast, renal, ovarian, prostate, colon	Ab, CTL, imaging
	Seq ID 87 & 88	423242	breast, renal, ovarian, prostate, colon	CTL
65	Seq ID 89 & 90	423242	breast, renal, ovarian, prostate, colon	CTL
	Seq ID 91 & 92	452190	breast, stomach, pancreas	CTL
	Seq ID 93 & 94	452190	breast, stomach, pancreas	CTL
	Seq ID 95 & 96	325372	breast	CTL
70	Seq ID 97 & 98	450375	breast, ovarian, head & neck, pancreas, lung, colon	Ab, sm, CTL, imaging
	Seq ID 99 & 100	426215	breast, lung, renal, colon, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 101 & 102	425247	breast, ovarian, lung, colon, pancreas, head & neck, stomach, uterine, cervical, bladder	Ab, sm, CTL, diagnostic
	Seq ID 103 & 104	429353	breast, prostate	Ab, sm, CTL, imaging
75	Seq ID 105 & 106	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 107 & 108	432201	breast, colon, lung chemo, ovarian, stomach, pancreas, uterine, cervical	Ab, sm, CTL, imaging
	Seq ID 109 & 110	427585	breast, lung, head & neck, pancreas, stomach, colon, ovarian, cervical	CTL
	Seq ID 111 & 112	446163	breast, cervical, uterine	Ab, sm, imaging
80	Seq ID 113 & 114	442117	breast, lung, bladder, pancreas, head & neck, stomach, ovarian, prostate	Ab, CTL, imaging
	Seq ID 115 & 116	428179	breast	sm, CTL
	Seq ID 117 & 118	431211	colon, bladder, lung, pancreas, head & neck	Ab, sm, imaging
	Seq ID 119 & 120	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
75	Seq ID 121 & 122	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 123 & 124	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 125 & 126	115522	colon, lung, bladder, pancreas	CTL
	Seq ID 127 & 128	452679	prostate, colon, pancreas, Taxol prostate	Ab, CTL, imaging
80	Seq ID 129 & 130	446051	colon, breast	Ab, sm, CTL, imaging
	Seq ID 131 & 132	422048	colon, pancreas, prostate	diagnostic
	Seq ID 133 & 134	410418	colon, bladder, lung, ovarian, pancreas, head & neck	Ab, sm, CTL, imaging
	Seq ID 135 & 136	446342	uterine, colon, prostate	Ab, sm, CTL, imaging
80	Seq ID 137 & 138	422260	colon, ovarian mucinous	Ab, sm, CTL, diagnostic
	Seq ID 139 & 140	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 141 & 142	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 143 & 144	111929	colon, breast, fibrosis	Ab, sm, imaging
80	Seq ID 145 & 146	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 147 & 148	111929	colon, breast, fibrosis	Ab, sm, imaging

	Seq ID 149 & 150 104888	colon, stomach, uterine	Ab, imaging
	Seq ID 151 & 152 420159	bladder, stomach	Ab, sm, CTL, imaging
	Seq ID 153 & 154 422330	pancreas, colon, bladder	Ab, sm, CTL, imaging, diagnostic
5	Seq ID 155 & 156 452461	bladder, lung, head & neck, ovarian, glioblastoma, stomach, colon, cervical	CTL
	Seq ID 157 & 158 413324	bladder	Ab, sm, CTL, diagnostic
	Seq ID 159 & 160 412420	bladder, glioblastoma, lung, stomach	Ab, diagnostic
	Seq ID 161 & 162 416658	lung, ovarian, uterine, bladder	Ab, CTL, diagnostic
	Seq ID 163 & 164 407811	bladder, pancreas, stomach, uterine, lung	Ab, sm, diagnostic
10	Seq ID 165 402230	bladder	sm, CTL
	Seq ID 166 & 167 402230	bladder	sm, CTL
	Seq ID 168 & 169 432829	bladder	CTL
	Seq ID 170 & 171 425721	bladder	Ab, imaging
	Seq ID 172 & 173 420370	bladder	Ab, CTL, imaging
15	Seq ID 174 & 175 437852	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 176 & 177 402075	bladder, lung, head & neck, cervical	diagnostic
	Seq ID 178 & 179 421110	bladder, pancreas, stomach, ovarian, lung	Ab, sm, diagnostic
	Seq ID 180 & 181 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 182 & 183 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
20	Seq ID 184 & 185 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 186 & 187 408243	bladder, stomach, head & neck, cervical	Ab, diagnostic
	Seq ID 188 & 189 422282	bladder, lung, head & neck	CTL, diagnostic
	Seq ID 190 & 191 425852	bladder, lung, head & neck	Ab, sm, CTL, imaging
	Seq ID 192 & 193 439738	bladder, lung, cervical	Ab, sm, CTL, imaging
25	Seq ID 194 & 195 404875	bladder	sm, CTL
	Seq ID 196 & 197 425883	bladder, pancreas	Ab, CTL, imaging
	Seq ID 198 & 199 404977	bladder, ovarian	Ab, sm, CTL, diagnostic
	Seq ID 200 & 201 420876	pancreas, bladder	Ab, sm, CTL, imaging
	Seq ID 202 & 203 427747	bladder, lung, ovarian, stomach	sm, CTL
30	Seq ID 204 & 205 420281	lung, bladder, ovarian, pancreas	Ab, sm, imaging
	Seq ID 206 & 207 446673	bladder	sm, CTL
	Seq ID 208 437553	bladder	Ab, CTL, imaging
	Seq ID 209 & 210 437553	bladder	Ab, CTL, imaging
	Seq ID 211 & 212 437553	bladder	Ab, CTL, imaging
35	Seq ID 213 & 214 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 215 & 216 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 217 & 218 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 219 & 220 405932	bladder, lung, head & neck, cervical	sm
40	Seq ID 221 & 222 405932	bladder, lung, head & neck, cervical	sm
	Seq ID 223 & 224 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 225 & 226 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 227 & 228 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 229 & 230 444342	hepatitis C, lung, fibrosis, bladder	Ab, CTL, diagnostic
	Seq ID 231 & 232 421379	breast, pancreas, head & neck, lung, stomach, bladder, cervical, colon	Ab, CTL, diagnostic
45	Seq ID 233 & 234 417079	bladder, lung, head & neck, cervical	Ab, diagnostic
	Seq ID 235 & 236 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 237 & 238 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 239 & 240 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 241 & 242 447072	glioblastoma, pancreas	sm, CTL
50	Seq ID 243 & 244 419723	glioblastoma	Ab, CTL, diagnostic
	Seq ID 245 & 246 419723	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 247 & 248 430890	glioblastoma, lung, cervical, bladder	Ab, CTL, imaging, diagnostic
	Seq ID 249 & 250 456759	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 251 429466	glioblastoma, uterine	
55	Seq ID 252 429466	glioblastoma, uterine	
	Seq ID 253 & 254 419721	glioblastoma, lung	Ab, sm, CTL, imaging
	Seq ID 255 & 256 407034	glioblastoma	Ab, CTL, diagnostic
	Seq ID 257 & 258 413472	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 259 & 260 438380	glioblastoma	Ab, CTL, diagnostic, imaging
60	Seq ID 261 & 262 426271	glioblastoma	Ab, CTL, diagnostic
	Seq ID 263 & 264 419704	glioblastoma	sm, CTL
	Seq ID 265 & 266 444471	glioblastoma, lung, colon	Ab, sm, CTL, imaging
	Seq ID 267 & 268 409395	glioblastoma	Ab, CTL, diagnostic
	Seq ID 269 & 270 413063	glioblastoma, ovarian, bladder, lung	Ab, CTL, diagnostic
65	Seq ID 271 & 272 433800	glioblastoma, lung	Ab, CTL, imaging
	Seq ID 273 458435	glioblastoma	
	Seq ID 274 458435	glioblastoma	
	Seq ID 275 & 276 424343	glioblastoma, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 277 & 278 424998	glioblastoma	Ab, CTL, diagnostic
70	Seq ID 279 & 280 412709	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 281 & 282 435615	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 283 & 284 404049	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 285 & 286 418932	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 287 & 288 404029	glioblastoma	Ab, sm, CTL, imaging
75	Seq ID 289 & 290 436480	glioblastoma	sm, CTL
	Seq ID 291 & 292 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 293 & 294 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 295 & 296 436895	breast, renal, ovarian, glioblastoma	Ab, sm, imaging
	Seq ID 297 & 298 421471	renal	Ab, sm, CTL, imaging
80	Seq ID 299 & 300 428296	renal	Ab, sm, CTL, imaging
	Seq ID 301 & 302 423508	renal, colon	Ab, CTL, imaging
	Seq ID 303 & 304 450001	renal, lung	Ab, sm, CTL, imaging
	Seq ID 305 & 306 410407	renal, lung, colon, stomach, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 307 & 308 453496	renal, prostate	Ab, sm, CTL, imaging

	Seq ID 309 & 310 420737	renal	Ab,sm, CTL, imaging
	Seq ID 311 & 312 309931	lung	Ab,sm, CTL, imaging
	Seq ID 313 & 314 412719	lung, head & neck, bladder, glioblastoma, cervical	CTL
5	Seq ID 315 & 316 417034	lung, head & neck, a couple cervical	Ab, CTL, diagnostic
	Seq ID 317 & 318 430486	lung, bladder, head & neck, cervical	Ab,sm, imaging
	Seq ID 319 & 320 413753	lung, bladder, head & neck, pancreas, cervical, colon	CTL, diagnostic
	Seq ID 321 & 322 425650	lung, head & neck, cervical, bladder	Ab, imaging
	Seq ID 323 & 324 423673	bladder, lung, head & neck, ovarian, pancreas, colon, stomach, uterine, cervical	Ab, CTL, diagnostic
10	Seq ID 325 & 326 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 327 & 328 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 329 & 330 429610	lung	CTL, diagnostic
	Seq ID 331 & 332 406690	lung, head & neck, pancreas, stomach, bladder, colon, cervical	Ab, imaging
	Seq ID 333 & 334 431846	lung, bladder, head & neck, uterine, cervical, stomach, ovarian	Ab, imaging
	Seq ID 335 & 336 422158	head & neck, bladder, lung, cervical, stomach	diagnostic
15	Seq ID 337 & 338 431958	lung, bladder, cervical, head & neck, ovarian, colon, prostate, pancreas, breast	Ab, CTL, imaging
	Seq ID 339 & 340 437044	head & neck, cervical, lung, bladder, breast, prostate, ovarian, stomach	Ab, imaging
	Seq ID 341 & 342 428484	lung, glioblastoma, bladder, head & neck, colon, cervical	Ab, sm, imaging
	Seq ID 343 & 344 429211	lung, bladder, head & neck, cervical, stomach	Ab, imaging
20	Seq ID 345 & 346 417389	ovarian, lung, bladder, uterine, cervical, pancreas, stomach	Ab, diagnostic
	Seq ID 347 & 348 431009	lung, bladder, head & neck	Ab, sm, imaging
	Seq ID 349 & 350 417542	lung	CTL, diagnostic
	Seq ID 351 & 352 449230	lung, cervical, head & neck, bladder, ovarian, colon	Ab, imaging
	Seq ID 353 & 354 410555	lung	Ab, sm, imaging
25	Seq ID 355 & 356 410555	lung	Ab, sm, imaging
	Seq ID 357 & 358 424687	head & neck, pancreas, lung, uterine, cervical, colon, stomach	Ab, sm, diagnostic
	Seq ID 359 & 360 418462	lung, bladder	Ab, imaging
	Seq ID 361 & 362 410274	lung, renal	diagnostic
	Seq ID 363 & 364 439606	lung, bladder, head & neck, cervical	Ab,sm, imaging
30	Seq ID 365 & 366 404877	lung, bladder	CTL
	Seq ID 367 & 368 444781	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 369 & 370 109424	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 371 & 372 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 373 & 374 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
35	Seq ID 375 & 376 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 377 & 378 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 379 & 380 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 381 & 382 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 383 & 384 421817	lung, cervical, head & neck & bladder	CTL
40	Seq ID 385 & 386 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL, diagnostic
	Seq ID 387 & 388 418678	lung, bladder, stomach, ovarian, pancreas & cervical	Ab, sm, imaging
	Seq ID 389 & 390 409420	lung, head & neck, pancreas, stomach, cervical, bladder	Ab, sm, imaging
	Seq ID 391 & 392 332180	lung	Ab,sm, CTL, imaging
	Seq ID 393 & 394 408790	lung	Ab,sm, CTL, imaging
45	Seq ID 395 & 396 408790	lung	Ab, CTL, imaging
	Seq ID 397 & 398 439223	lung, head & neck, cervical, bladder & colon	Ab, CTL, diagnostic
	Seq ID 399 & 400 409757	pancreas, stomach, lung, bladder, stomach	Ab, CTL, diagnostic
	Seq ID 401 & 402 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 403 & 404 428969	lung, cervical	Ab, CTL, diagnostic
50	Seq ID 405 & 406 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 407 & 408 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 409 & 410 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 411 & 412 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 413 & 414 414774	lung, bladder, head & neck, pancreas, stomach, ovarian	Ab, sm, diagnostic
55	Seq ID 415 & 416 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 417 & 418 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 419 & 420 428486	pancreas	Ab, CTL, diagnostic
	Seq ID 421 & 422 457489	pancreas, prostate, lung	Ab, CTL, diagnostic
	Seq ID 423 & 424 432874	pancreas, stomach	Ab, CTL, diagnostic
60	Seq ID 425 & 426 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 427 & 428 445891	stomach, pancreas, ovarian	Ab, CTL, diagnostic
	Seq ID 429 & 430 404682	pancreas	Ab, CTL, imaging
	Seq ID 431 & 432 429547	pancreas, head & neck, lung, ovarian	Ab, CTL, diagnostic
	Seq ID 433 & 434 425921	stomach, pancreas	Ab,sm, CTL, imaging
65	Seq ID 435 & 436 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 437 & 438 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 439 & 440 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 441 & 442 432596	pancreas, breast	CTL
	Seq ID 443 & 444 444006	pancreas, colon, lung, ovarian & cervical	Ab, CTL, imaging
	Seq ID 445 & 446 423685	pancreas, uterine, colon	CTL
70	Seq ID 447 & 448 428392	pancreas	Ab, CTL, diagnostic
	Seq ID 449 & 450 429597	pancreas, colon, stomach, lung	Ab,sm, CTL, imaging
	Seq ID 451 & 452 448030	pancreas, renal and stomach,	Ab,sm, imaging
	Seq ID 453 & 454 422109	pancreas, lung, colon	Ab, CTL, diagnostic
	Seq ID 455 & 456 419235	pancreas, fibrosis, head & neck & lung	Ab, CTL, imaging
75	Seq ID 457 & 458 449048	pancreas, ovarian, uterine, glioblastoma, head & neck & lung	Ab, CTL, imaging
	Seq ID 459 & 460 427333	pancreas, colon	Ab, sm, imaging
	Seq ID 461 & 462 417931	ovarian, pancreas, stomach, colon, uterine, prostate	Ab, diagnostic
	Seq ID 463 & 464 419216	pancreas, lung, stomach, cervical, prostate, head & neck	Ab, CTL, diagnostic
80	Seq ID 465 & 466 431629	pancreas, uterine, cervical, stomach	Ab, CTL, diagnostic
	Seq ID 467 & 468 413554	pancreas, glioblastoma	Ab, CTL, diagnostic
	Seq ID 469 & 470 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 471 & 472 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 473 & 474 426322	pancreas, bladder, stomach	Ab, diagnostic

	Seq ID 475 & 476 429010	pancreas	sm, CTL
	Seq ID 477 & 478 431462	pancreas, lung, glioblastoma	Ab, diagnostic
	Seq ID 479 & 480 448243	ovarian, uterine, lung, stomach, head & neck, glioblastoma, pancreas	Ab, sm, imaging
5	Seq ID 481 & 482 426427	ovarian, lung, head & neck, cervical, colon, uterine, stomach	sm, CTL
	Seq ID 483 & 484 428187	ovarian, uterine, colon, stomach	Ab, sm, CTL, imaging
	Seq ID 485 & 486 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 487 & 488 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 489 & 490 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
10	Seq ID 491 & 492 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 493 & 494 445537	ovarian, bladder, uterine, breast, lung, head & neck, renal, fibrosis, pancreas, cervical	Ab, CTL, diagnostic
	Seq ID 495 & 496 422278	ovarian, head & neck, bladder, cervical, lung	Ab, sm, imaging
	Seq ID 497 & 498 424620	ovarian	Ab, CTL, diagnostic
	Seq ID 499 & 500 406400	ovarian, uterine	Ab, CTL, diagnostic
15	Seq ID 501 & 502 431130	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 503 & 504 420440	ovarian, uterine, cervical	Ab, CTL, diagnostic
	Seq ID 505 & 506 428450	ovarian, cervical, pancreas, lung	sm
	Seq ID 507 & 508 446619	ovarian, fibrosis, pancreas, head & neck, lung, colon	Ab, diagnostic
	Seq ID 509 & 510 436982	ovarian, fibrosis	Ab, CTL, diagnostic
20	Seq ID 511 & 512 453392	ovarian, lung, glioblastoma	CTL
	Seq ID 513 431989	ovarian	
	Seq ID 514 439820	ovarian, uterine, cervical, breast, prostate	
	Seq ID 515 & 516 409178	ovarian, breast	Ab, CTL, diagnostic
	Seq ID 517 & 518 426514	ovarian, colon, bladder, lung, cervical	Ab, CTL, diagnostic
25	Seq ID 519 & 520 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 521 & 522 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 523 & 524 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 525 & 526 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 527 & 528 452097	ovarian	Ab, sm, diagnostic
30	Seq ID 529 & 530 416530	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 531 & 532 431515	ovarian, prostate, lung	Ab, sm, CTL, imaging
	Seq ID 533 & 534 419452	ovarian, prostate, lung, breast, uterine	Ab, sm, CTL, imaging
	Seq ID 535 & 536 412078	ovarian	CTL
	Seq ID 537 & 538 412078	ovarian	CTL
35	Seq ID 539 & 540 411773	ovarian	Ab, sm, CTL, diagnostic
	Seq ID 541 & 542 407792	ovarian, uterine, cervical, pancreas	Ab, CTL, diagnostic
	Seq ID 543 & 544 431616	prostate, pancreas, colon	Ab, sm, CTL, imaging
	Seq ID 545 & 546 452792	prostate, uterine, breast	Ab, CTL, imaging
	Seq ID 547 & 548 400294	prostate, taxol prostate	Ab, sm, CTL, imaging
40	Seq ID 549 & 550 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 551 & 552 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 553 & 554 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 555 & 556 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 557 & 558 400290	prostate, colon	Ab, sm, CTL, imaging
45	Seq ID 559 & 560 410001	ovarian, prostate, uterine, cervical, lung	Ab, CTL, diagnostic
	Seq ID 561 & 562 418396	prostate	Ab, sm, CTL, imaging
	Seq ID 563 & 564 451027	prostate, uterine, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 565 & 566 446057	prostate	Ab, sm, CTL, imaging
	Seq ID 567 & 568 433466	prostate	Ab, CTL, diagnostic
50	Seq ID 569 & 570 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 571 & 572 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 573 & 574 414569	prostate	Ab, sm, CTL, imaging
	Seq ID 575 & 576 413435	prostate, glioblastoma, pancreas	Ab, sm, diagnostic
	Seq ID 577 & 578 426501	prostate, breast, glioblastoma, lung	Ab, CTL, imaging
55	Seq ID 579 & 580 448999	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 581 & 582 408369	prostate, lung, fibrosis, uterine, glioblastoma, cervical, ovarian	Ab, sm, CTL, imaging
	Seq ID 583 & 584 412628	prostate	Ab, CTL, diagnostic
	Seq ID 585 & 586 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
	Seq ID 587 & 588 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
60	Seq ID 589 & 590 408430	prostate	Ab, sm, CTL, imaging
	Seq ID 591 & 592 445413	prostate, colon, uterine, ovarian, lung, pancreas	diagnostic
	Seq ID 593 & 594 451982	prostate, bladder	CTL
	Seq ID 595 & 596 427958	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 597 & 598 421887	prostate	Ab, CTL, imaging
65	Seq ID 599 & 600 425071	prostate, colon, stomach, uterine, cervical, head & neck, pancreas	Ab, diagnostic
	Seq ID 601 & 602 432101	prostate, pancreas	Ab, sm, imaging
	Seq ID 603 & 604 407786	prostate, colon, uterine, stomach, inflammatory bowel disease, ovarian	Ab, sm, imaging
	Seq ID 605 & 606 416836	Prostate, Ewing, glioblastoma	Ab, CTL, diagnostic
	Seq ID 607 & 608 416539	ZD1839 resistant cancers, head & neck	Ab, sm, CTL, imaging
70	Seq ID 609 & 610 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 611 & 612 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 613 & 614 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 615 & 616 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 617 & 618 422424	bladder, pancreas, prostate, angiogenesis, colon, stomach, lung	Ab, CTL, diagnostic
	Seq ID 619 & 620 428970	stomach, pancreas, colon	Ab, sm, imaging
75	Seq ID 621 & 622 428330	uterine, ovarian, fibrosis, prostate, pancreas, lung, bladder, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 623 & 624 439018	uterine, stomach, prostate	Ab, sm, CTL, imaging
	Seq ID 625 & 626 420610	uterine, ovarian endometrioid, lung	CTL
	Seq ID 627 & 628 425723	ovarian endometrioid, uterine, colon	Ab, CTL, diagnostic
80	Seq ID 629 & 630 456662	uterine, ovarian	CTL
	Seq ID 631 & 632 418281	uterine, ovarian	Ab, CTL, diagnostic
	Seq ID 633 & 634 429903	lung	sm

Table 78

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001400
Coding sequence: 251..1399

	1	11	21	31	41	51	
10	TCTAAAGGTC	GGGGGCGAGCA	GCAAGATGCG	AAGCGAGCCG	TACAGATCCC	GGGCTCTCCG	60
	AAAGCTACAC	AAAAAGCCTG	GATCACTCAT	CGAACCACCC	CTGAAGCCAG	TGAAGGCTCT	120
	CTCGCCTCGC	CCTCTAGCGT	TCGCTGAGAG	TAGCGCCACC	CCGGCTTCCT	GGGGACACAG	180
	GGTTGGCACC	ATGGGGCCCA	CCAGCGTCCC	GCTGGTCAAG	GCCCACGCCA	GCTCGGTCTC	240
15	TGACTACGTC	AACATATGATA	TCATCGTCCG	GCATTACAAC	TACACGGGAA	AGCTGAATAT	300
	CAGCGCGGAC	AAGGAGAACA	GCATTAAACT	GACCTCGGTG	GTGTTTCATT	TCATCTGCTG	360
	CTTTATCATC	CTGGAGAACA	TCTTTGTCTT	GCTGACCATT	TGGAAAACCA	AGAAATTCCA	420
	CCGACCCATG	TACTATTTTA	TTGGCAATCT	GGCCCTCTCA	GACCTGTGTG	CAGGAGTAGC	480
	CTACACAGCT	AACCTGCTCT	TGTCTGGGGC	CACCACCTAC	AAGCTCACTC	CCGCCCAGTG	540
20	GTTTCTGCGG	GAAGGGAGTA	TGTTTGTGGC	CCTGTCAGCC	TCCGTGTTC	GTCTCTCTCG	600
	CATCGGCATT	GAGCGGTATA	TCACAATGCT	GAAAAATGAAA	CTCCACAACG	GGAGCAATAA	660
	CTTCCGCCTC	TTCCGTCTAA	TCAGCGCCTG	CTGGGTCTATC	TCCCTCATCC	TGGGTGGCCT	720
	GCCTATCATG	GGCTGGAACT	GCATCAGTGC	GCTGTCCAGC	TGCTCCACCG	TGCTGCCGCT	780
	CTACCAACAG	CACATATATCC	TCTTCTGCAC	CACGGTCTTC	ACTCTGCTTC	TGCTCTCCAT	840
25	CGTCATTCTG	TACTGCAGAA	TCTACTCCTT	GGTCAGGACT	CGGAGCCGCC	GCCTGACGTT	900
	CCGCAAGAAC	ATTTCACAGG	CCAGCCGCAG	CTCTGAGAAG	TGCTGGCGC	TGCTCAAGAC	960
	CGTAATTATC	GTCTGAGCG	TCTTCATCGC	CTGCTGGGCA	CCGCTCTTCA	TCTGCTCCT	1020
	GCTGGATGTG	GGCTGCAAGG	TGAAGACCTG	TGACATCCTC	TTCAGAGCGG	AGTACTTCCT	1080
	GGTGTAGTAG	GTGCTCAACT	CCGGCACCAA	CCCCATCATT	TACACTCTGA	CCAACAAGGA	1140
	GATGCGTCGG	GCCTTCATCC	GGATCATGTC	CTGCTGCAAG	TGCCGAGCG	GAGACTCTGC	1200
30	TGGCAAAATC	AAGCGACCCA	TCATCGCCGG	CATGGAATTC	AGCCGCAGCA	AATCGGACAA	1260
	TTCTCTCCAC	CCCCAGAAAG	ACGAAGGGGA	CAACCCAGAG	ACCATTATGT	CTTCTGGAAA	1320
	CGTCAACTCT	TCTTCCTAGA	ACTGGAAGCT	GTCCACCCAC	CGGAAGCGCT	CTTACTTGG	1380
	TCGCTGGCCA	CCCCAGTGTT	TGGAAAAAAA	TCTCTGGGCT	TGCACTGCTG	CCAGGGAGGA	1440
35	GCTGCTGCAA	GCCAGAGGGA	GGAAGGGGGA	GAATACGAAC	AGCCTGGTGG	TGTCGGGTGT	1500
	TGGTGGGTAG	AGTTAGTTCC	TGTGAACAAT	GCACTGGGAA	GGGTGGAGAT	CAGGTCCCGG	1560
	CCTGGAATAT	ATATTCTACC	CCCCTGAGGC	TTTGATTTTG	CAGTGGAGCA	AAGGTCTAGC	1620
	ATTGTCAAGC	TCCTAAAGGG	TTCAATTGGC	CCCTCTCAA	AGACTAATGT	CCCCATGTGA	1680
	AAGCGTCTCT	TTGTCTGGAG	CTTTGAGGAG	ATGTTTTCTT	TCATTTAGT	TTCAAACCCA	1740
40	AGTGAGTGTG	TGCACTTCTG	CTTCTTTAGG	GATGCCCTGT	ACATCCCACA	CCCCACCTTC	1800
	CCTTCCCTTC	ATACCCCTCC	TCAACGTTCT	TTTACTTTAT	ACTTTAAGTA	CCTGAGAGTT	1860
	ATCAGAGCTG	GGGTGTGGGA	ATGATCGATC	ATCTATAGCA	AATAGGCTAT	GTTGAGTACG	1920
	TAGGCTGTGG	GAAGATGAAG	ATGGTTTGGG	GGTGTAAAC	AATGTCCTTC	GCTGAGGCCA	1980
45	AAGTTTCCAT	GTAAGCGGGA	TCCGTTTTTT	GGAATTTGGT	TGAAGTCACT	TTGATTTCTT	2040
	TAAAAAATCT	CTTTTCAATG	AAATGTGTTA	CCATTTCATA	TCCATTGAAG	CCGAAATCTG	2100
	CATAAGGAAG	CCCCTTTTAT	CTAAATGATA	TTAGCCAGGA	TCCTTGGTGT	CCTAGGAGAA	2160
	ACAGACAAGC	AAAACAAAGT	GAAAACCGAA	TGGATTAACT	TTTGCAAACC	AAGGGAGATT	2220
	TCTTAGCAAA	TGAGTCTAAC	AAATATGACA	TCCGCTTTTC	CCACTTTTGT	TGATGTTTAT	2280
	TTCAGAACTC	TGTTGTGATT	ATTTCAAGCA	ACAACATGTT	GTATTTTGTG	GTGTTAAAG	2340
50	TACTTTTCTT	GATTTTGA	TGTATTTGTT	TCAGGAAGAA	GTCATTTTAT	GGATTTTCTT	2400
	AACCGTGTG	CACTTTTCTA	GAATCCACCC	TCTTGTGCC	TAAAGCATTA	CTTTAACTGG	2460
	TAGGGAACGC	CAGAACTTTT	AAGTCCAGCT	ATTCAATTGA	TAGTAATTGA	AGATATGTAT	2520
	AAATATTACA	AAGATAAAAA	ATATATTACT	GTCTCTTTAG	TATGTTTTC	AGTGCAATTA	2580
	AACCGAGAGA	TGCTCTGTTT	TTTTAAAAAG	AATAGTATTT	AATAGGTTTC	TGACTTTTGT	2640
55	GGATCATTTT	GCACATAGCT	TTATCAACTT	TAAACATTA	ATAAAGTAT	TTTTTTAAAG	2700

Seq ID NO: 2 Protein sequence
Protein Accession #: NP_001391

60	1	11	21	31	41	51	
	MGPTSVPLVK	AHRSSVSDYV	NYDIIVRHYN	YTGKLNISAD	KENSIKLTSV	VFILICCFII	60
	LENIFVLLTI	WTKKKEHRPM	YFIGNLALS	DLLAGVAYTA	NLLLSGATTY	KLTPAQWFLR	120
	EGSMFVALSA	SVFSLLAIAI	ERYITMLKMK	LHNGSNFRL	FLILISACWVI	SLILGGLPIM	180
65	GWNCISALSS	CSTVLPPLYHK	HYILFCTTVF	TLLLLLSIVIL	YCRIYSLVRT	RSRRLTFRKN	240
	ISKASRSSEK	SLALLKTVII	VLSVFIACWA	PLFILLLLDV	GCKVKTCIDIL	FRAEYFLVLA	300
	VLNSGTNPPI	YTLTNKEMRR	AFIRIMSCCK	CPSGDSAGKF	KRPPIAGMEF	SRSKSDNSSH	360
	PQKDEGDNPE	TIMSSGNVNS	SS				

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: NM_002205.1
Coding sequence: 1..3149

75	1	11	21	31	41	51	
	ATGGGGAGCC	GGACGCCAGA	GTCCCTCTCT	CAGCCCGTGC	AGCTGCGCTG	GGGCCCCCGG	60
	CGCCGACCCC	CGCTSSGTCC	GCTGCTGTTC	CTGCTSSGTC	CGCCGCCACC	CAGGGTCGGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGAGT'TTTA	CCGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
80	CCCAAGGCTA	ATACCAAGCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGCTCT	300
	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAAGG	CTCTCGGCTC	360
	CTGGAGTCCT	CACGTGTCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCTTGCAG	420
	TGGTTGGGG	CAACAGTTCT	AGCCCCATGG	TCCTCCATCT	TGGCATGCGC	TCCACTGTAC	480
	AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCCGCT	CAGATTTTCA	CTGGGCGACA	600

5 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCGAGTTCA CCAAGACTGG CCGTGTGGTT 660
 TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720
 ATTGCAGAAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
 CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTTGGTGAA 840
 10 TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAAGGGAA CCTCACTTAC 900
 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCGATCCC TCTACAACIT CTCAGGGGAA 960
 CAGATGGCCT CCTACTTTGG CTATGCAGTG GCCGCCACAG ACGTCAATGG GGACGGGCTG 1020
 GATGACTTGC TGGTGGGGGC ACCCCTGCTC ATGGATCGGA CCCCTGACGG GCGGGCTCAG 1080
 GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCACCC 1140
 15 CTTACCCCTA CTGGCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTGAC CCCCTGGGG 1200
 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCTTTTGG TGGGGAGACC 1260
 CAGCAGGGAG TAGTGTTTGT ATTTCTTGGG GGCCAGGAG GGTCTGGGCTC TAAGCCTTCC 1320
 CAGGTCTCTG AGCCCTGTG GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380
 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCTTTGGT 1440
 20 GTGGACAAGG CTGTGGTATA CAGGGGCCGC CCCATCGTGT CGCTAGTGC CTCCCTCACC 1500
 ATCTTCCCGG CCATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1560
 GCGCTGCATC ACCTTAGCTT CTGCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT 1620
 GGTTTACAG TGGAACTTCA GCTGGAATGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1680
 CTGTTCTCTG CCTCCAGGCA GGCAACCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAATT TCGAGACAAA 1800
 25 CTCTCGCCGA TTACCATCGC TCTCACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1860
 CACGGCCTCA GGCACGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920
 ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGT 1980
 GGGGAGCAGA ACCATGTGTA CTGGGTGAC AAGAATGCC TGAACCTCAC TTTCATGCC 2040
 30 CAGAATGTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCAACCC CCCTCCAGAG 2100
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2160
 TTTGCCGTGA ACCAGAGCCG CTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGCAGGA 2220
 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCGGGACAC TAAGAAAACC 2280
 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGACGTGGTT 2340
 35 TCCTTTCCGG TCTCCGTGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCCAAGCCT 2400
 GAGGCACTGC TATTCCAGT AAGCGACTGG CATCCCCGAG ACCAGCTCA GAAGGAGGAG 2460
 GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520
 AGCCAGGGTG TTGTGGAAT CAGCTGTCCC CAGGCTCTGG AAGGTGAGCA GCTCCTATAT 2580
 GTGACCAAG TTACCGGACT CAACTGCACC ACCAATCACC CCATTAACCC AAAGGGCCTG 2640
 40 GAGTTGATC CCGAGGGTTC CTGCAACCAC CAGCAAAAAC GGGAACTCC AAGCCGCAGC 2700
 TCTGCTTCCT CGGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGT 2760
 TGTGAGCTCG GGGCCCTGCA CCAACAAGAG AGCCAAGTC TGCAAGTGCA TTTCAGAGT 2820
 TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCCTGCAGTG TGAGGCTGTG 2880
 45 TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGCG AGTGCCCCA AAAAGAGCGT 2940
 CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGCGT CCCACTGTGG 3000
 ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060
 TACAAGCTTC GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG 3120
 CTCAGCCTC CAGCCACCTC TGATGCTCTGA

Seq ID NO: 4 Protein sequence
 Protein Accession #: NP_002196.1

50 1 11 21 31 41 51
 MGSRTPEPL HAVQLRWGPR RRPPLPLLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
 GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WGSPTQCTP IEFDSKGSRL 120
 LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPGVTCYLSL 180
 55 DNFTTRILEYA PCRSDFSWAA QGGYCCQGGFS AEFKTGRV LGGPGSYFWQ GQILSATQEQ 240
 IAESYYPEYL INLVQGLQT RQASSIYDDS YLGYSVAVGE FSGDDTDFV AGVPKGNLTY 300
 GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLVVGAPLL MDRTPDGRPQ 360
 EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGET 420
 60 QQGVVVFVPG GPGLGSKPS QVLQPLWAAS HTPDFFGSAL RGRDLDDNG YPDLIVGSFG 480
 VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
 GFTVELQLDW QKQKGGVRR LFLASRQATL TQTLTIQNGA REDCREMKIY LRNESEFRDK 600
 LSPHIALNLF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
 GEQNHVYLDG KNALNLTFAH QNVGEGGAYE AELRVTAPE AEYSGLVRHP GNFSLSLCDY 720
 65 FAVNQSRLLV CDLGNPMKAG ASLWGGRLFT VPHLRDTKKT IQDFDQILSK NLNNSQSDVV 780
 SFRLSVEAQA QVTILNGVSKP EAVLFVPSDW HPRDQPFKEE DLGPAVHHVY ELINQGPSSI 840
 SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLSHH QKREAPSR 900
 SASSGPQILK CPEABCFRLR CELGPLHQE SSQLHLFRV WAKTFLQREH QPFSLQCEAV 960
 70 YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFLGL LLLGLLIYIL 1020
 YKLGFPRSL PYGTAMEKAQ LKPPATSDA

Seq ID NO: 5 DNA sequence
 Nucleic Acid Accession #: NM_002211.1
 Coding sequence: 1..2397

75 1 11 21 31 41 51
 ATGAATTTAC AACCAATTTT CTGGATTGGA CTGATCAGTT CAGTTTGCTG TGTGTTTGCT 60
 CAAACAGATG AAAATAGATG TTTAAAAGCA AATGCCAAAT CATGTGGAGA ATGTATACAA 120
 GCAGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT 180
 80 TCTGCACGAT GTGATGATT AGAAGCCTTA AAAAAGAAGG GTTGCCCTCC AGATGACATA 240
 GAAAAATCCA GAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAACCAA CCGTAGCAAA 300
 GGAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCACA GCAGTTGGTT 360
 T2CGATTAA GATCAGGGCA GCCACAGACA TTTACATTAA AATTCAAGAG AGCTGAAGAC 420
 TATCCCATTG ACCTCTACTA CCTTATGGAC CTGTCTTACT CAATGAAAGA CGATTGGAG 480
 AATGTAAGAA GTCTTGAAC AGATCTGATG AATGAAATGA GGAGGATTAC TTCGACTTC 540

AGAATTGGAT TTGGCTCATT TGTGGAAAAG ACTGTGATGC CTTACATTAG CACAACACCA 600
 GCTAAGCTCA GGAACCCCTTG CACAAGTGAA CAGAAGTGCA CCAGCCCAT TAGCTACAAA 660
 AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTGG AAAACAGCGC 720
 ATATCTGGAA ATTTGGATTG TCCAGAAGGT GGTTCGATG CCATCATGCA AGTTGCAGTT 780
 TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTTC CACAGATGCC 840
 GGGTTTCACT TTGCTGGAGA TGGGAACTT GGTGGCATG TTTTACCAA TGATGGACAA 900
 TGTACCTGG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960
 CACCTTGTCC AGAAACTGAG TGAAAATAAT ATTCAGACAA TTTTGCAGT TACTGAAGAA 1020
 TTTACGCTG TTTCAAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
 TCTGCAAAAT CTAGCAATGT AATTCAAGTT ATCATTGATG CATACAATTC CCTTTCCTCA 1140
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 TGCAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCTA TATTCCATT 1260
 GGAGATGAGG TTCAATTTGA AATTAGCATA ACTTCAAATA AGTGTCCAAA AAAGGATTCT 1320
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 AATGGGACAT TTGAGTGTGG CGCGTGCAGG TGCAATGAAG GCGGTGTGG TAGACATTGT 1500
 GAATCAGACA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAA 1560
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 TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTTCT TGGATACTAG TACTTGTGAA 1800
 GCCAGCAACG GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTGGTGT CTGTAAGTGT 1860
 ACAGATCCGA AGTTTCAAG GCAAACGTGT GAGATGTGTC AGACCTGCTT TGGTGTCTGT 1920
 GCTGAGCATA TTGAGTGTGT TCAGTGCAGA GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980
 TGCAACACAG AATGTTCTTA TTTTAACATT ACCAAGGTAG AAAGTCGGGA CAAATTACCC 2040
 CAGCGGTGCC AACCTGATCC TGTGTCCCAT TGTAAGGAGA AGGATGTTGA CCACTGTTGG 2100
 TTCTATTTTA CATTATTCAGT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAAT 2160
 CCAGAGTGTG CCACCTGGTCC AGACATCAT CCAATTGTAG CTGGTGTGGT TGCTGGAATT 2220
 GTTCTTATTG GCCTTGCAAT ACTGCTGATA TGGAAAGCTT TAATGATAAT TCATGACAGA 2280
 AGGGAGTTTG CTAATTTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAT 2340
 CCTATTATA AGAGTGCCGT AACAACTGTG GTCAATCCGA AGTATGAGGG AAAATGA

Seq ID NO: 6 Protein sequence
 Protein Accession #: NP_002202.1

1 11 21 31 41 51
 MNLQPIFWIG LISSVCCVFA QDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60
 SARCDLEAL KKKGCPDDI ENPRGSKDIK KKNVNTNRSK GTAELKLPED ITQIQPQLV 120
 LRLRSGEPQT FTLKFKRAED YPIDLYLMD LSYMKDDLE NVKSLGTDLM NEMRRITSDF 180
 RIGFGSFVEK TUMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTKNGE VFNELVGKQR 240
 ISGNLDSPEG GFDAIMQVAV CGSLIGWRNV TRLLVFSSTA GFHFAGDGLK GGIVLPNDGQ 300
 CHLENNMYTM SHYVDYPSIA HLVQKLENN IQTIFAVTEE FQPVYKELKN LIPKSAVGT 360
 SANSSNVIQL IIDAYNSLSS EVILENGKLS EGVTSISKSY CKNGVNGTGE NGRKCSNISI 420
 GDEVQFEISI TSNKCPKIDS DSFKIRPLGF TEEVEVILQY ICECEQSGE IPESPKCHEG 480
 NGTFECGACR KNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCGQCVRCK 540
 RDNTNEYISY KFCECDNFNC DRNGLICGG NGVCKCRVCE CNPNYTGSA CDSLDTSTCE 600
 ASNGQICNGR GICEGVCKC TDPKFQGGTC EMCQTCLGVC AEHKECVQCR AFNKGEKKDT 660
 CTQECSYFNI TKVESRDKLP QVPQDPFVSH CKEKDVEDCW FYFTYSVNGN NEVMVHVVEN 720
 PECPGTGPDII PIVAGVVAGI VLIGLALLLI WKLLMIHHR REFAKFEKEK MNAKWDVTGEN 780
 PIKSAVTTV VNPKEGK

Seq ID NO: 7 DNA sequence
 Nucleic Acid Accession #: NM_002425
 Coding sequence: 26..1453

1 11 21 31 41 51
 AAAGAAGGTA AGGCGAGTGA GAATGATGCA TCTTGCAATC CTTGTGCTGT TGTGCTGCC 60
 AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
 TGCCCGACAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
 AAAGGACAGT AATCTCATG TTAATAAAAT CCAAGGAATG CAGAAGTCC TTGGGTTGGA 240
 GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
 TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
 TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT 420
 TGAGAAAGCT CTGAAAGTCT GGGAAAGAGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
 AGGAGAGGCT GATATAATGA TCTCTTTGCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
 TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
 TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCTT 660
 CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACCTGGAAGC 720
 TTTGATGTAC CCACCTCTACA ACTCATTCAC AGAGCTCGCC CAGTTCCGCC TTTGCAAGA 780
 TGATGTGAAT GGCATTCACT CTCTCTACGG ACCTCCCTCT GCCTCTACTG AGGAACCCCT 840
 GGTGCCACCA AAATCTGTTT CTTGCGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
 GTCCTTCGAT GCGCATCAGCA CTCGTAGGGG AGAATATCTG TTTCTTAAAG ACAGATATTT 960
 TTGGCGAAGA TCCCACTGAG ACCCTGAACC TGAATTTTCT TTTGATTTCT CATTGCGGCC 1020
 CTCTCTTCCA TCAATTTTGG ATGCTGCATA TGAAGTTAAC AGCAGGGACA CGGTTTTTAT 1080
 TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
 AGGCATCCAT ACCCTGGGTT TTCCTCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
 CAAGGAAAAG AAGAAAACAT ACTTCTTTCG AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
 TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
 GCCTAAGGTT GATGCTGTAT TACAGGCATT TGSATTTTTC TACTTCTTCA GTGGATCATC 1380
 ACAGTTTGTG TTTGACCCA ATGCCAGGAT GGTGACACAC ATATTAAGA GTAACAGCTG 1440
 GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
 ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAAATT TTCTGTCATG TTCTGTGACT 1560

GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTCTTC 1620
 ACTTGCTTTT GAATTGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
 ATGTATTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740
 CTT

Seq ID NO: 8 Protein sequence
 Protein Accession #: NP_002416

1 11 21 31 41 51
 | | | | |
 MHLAFLVLLC LPVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVQKF RPKDSNLIVK 60
 KIQGMQKFLG LEVTGKLDTD TLEVMRKPRC GVDPVGHFSS FPGMPKWRKT HLTIRIVNYT 120
 PDLPRDAVDS AIEKALKVWE EVTPLTFSRL YEGEADIMIS FAVKEHGDYF SFDGPGHSLA 180
 HAYPPGPGLY GDIHFDDDEK WTEDASGTNL FLVAAHELGH SLGLFHSANT EALMYPLVNS 240
 FTSLAQFRLS QDDVNGIQSL YGPPPAFSTEE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300
 RGEYLFFKDR YFWRSSHWNF BPEFHLISAF WPSLPSYLD AYEVSNSRDV FIFKGNFWSA 360
 IRGNEVQAGY PRGHTLGFPT PTIRKIDAAV SDKEKKKTYF FAADKYWRFD ENSQSMEQGF 420
 PRLIADDFPG VEPKVDVAVLQ AFGFFYFFSG SSQFEFDPNA RMVTHILKSN SWLHC

Seq ID NO: 9 DNA sequence
 Nucleic Acid Accession #: XM_058189.2
 Coding sequence: 169..774

1 11 21 31 41 51
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 GAAGACCAGC TCAGCTCTTC AGTTGTTGAT CATTGTCTAT TGTCTCTCAA ACAGTAAACC 60
 AGTATTTTAC ACTGAGATTG TCGGCTGCGG GTATATTCCA ATTCCTCCGTC TCCTCATGAA 120
 TATGAAGTGA AGGGCTCTGA CCTCGGAAGT GGTTCTAAGC AGGGCAAAAT GGGGTCTCGG 180
 AAGTGTGGAG GCTGCTAAG TGTGTTGCTG ATTCGCTTG CACTTTGGAG TATAATCGTG 240
 AACATATTAT TGTATTTCCC GAATGGGCAA ACTTCCTATG CATCCAGCAA TAAACTCACC 300
 AACTACGTGT GGTATTTTGA AGGAATCTGT TTCTCAGGCA TCATGATGCT TATAGTAACA 360
 ACAGTTCTTC TGGTACTGGA GAATAATAAC AACTATAAAT GTTGCCAGAG TGAAGAACTGC 420
 AGCAAAAAAT ATGTGACACT GCTGTCAATT ATCTTTTCTT CCTCGGAAT TGCTTTTCTT 480
 GGATACTGCC TGGTCACTTC TGCCCTGGGT CTGTGCTCAAG GGCCATATTG CCGCACCCCTT 540
 GATGGCTGGG AGTATGCTTT TGAAGGCACT GCTGGACGTT TCCTTACAGA TTCTAGCATA 600
 TGGATTTCAGT GCCTGGAACC TGCACATGTT GTGGAGTGGG ACATCATTTT ATTTTCCATT 660
 CTCATAACCC TCAGTGGGCT TCAAGTGATC ATCTGCCTCA TCAGAGTAGT CATGCAACTA 720
 TCCAGATATC TGTGTTGAAG CTATTGAGTG ATCTTCCAGC CTGGAATCAT TTGAATAAGG 780
 ACAAAATGTT TTCCATTATC AAGACATGGC CATCTATCTA AATATTATAT CAACGTGTGA 840
 GACTTGAGGG CAATATTGAA ATGATGGTGC TTTCTGCATT TGGTGTATAT TTGTAAAAAA 900
 TTTGCACTCC TCACTGCACA TGCAAGTATA CCACCCCTTC ATTTAGTATG TTTTAAAGT 960
 AATATGCATC AGAAACTTCA GAAATACTTC TGCCCTTTGA TCAACAAAT CCATTCCAA 1020
 GAATCTGTAC TAGGGAGTA AATAAGAAAT TGAGAGAAAC CTTTATGCAA ATATGTATAT 1080
 TGCAACATTA TTTAATATTC TGGAAAATTG GAAACACCCC AAAATTCTAA ACTCAGAGGA 1140
 AGGATTAAGT AAAGAGTGGT ACATACGTGA AATGTTTCTT GATATTAAAA AAAAAATTAA 1200
 ATAAAAAATA AAGAGTACTA CATGGTTGTA AAA

Seq ID NO: 10 Protein sequence
 Protein Accession #: XP_058189.1

1 11 21 31 41 51
 | | | | |
 MGSRRKCGCL SCILLIPLALW SIIVNILLYF PNGQTSYASS NKLTINYVWYF EGICFSGIMM 60
 LIVTTVLLVL ENNNNYKCCQ SENCSSKIVT LLSIIFSSLG IAFSGYCLVI SALGLVQGPY 120
 CRTLDGWEYA FEGTAGRFLT DSSIWIQCLE PAHVVEWNII LFSILITLSG LQVIICLIRV 180
 VMQLSKILCG SYSVIFQPGI I

Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

1 11 21 31 41 51
 | | | | |
 ATGCACAGCT TTCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC 60
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120
 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCACTG 180
 GTTGAAAAAT TGAAGCAATG GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCCAGT 240
 GCTGAAACCC TAGAAGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT 300
 GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT 360
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCTCACT 420
 TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTTGCTCATG CTTTCAACAT AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACCT 660
 GGCCATTCTC TTGCACTCTC CCACTTCTACT GATATCGGGG CTTTGAATGA CCTAGCTAC 720
 ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGGCCACAAA CCCCAGAAAGC ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CCGGGAGAAAG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCA TTCTGTTTTC 960
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCAAGGACA TCTACAGCTC CTTTGGCTTC CTTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260

GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTA TTTCTTTCAT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

5

Seq ID NO: 12 Protein sequence
 Protein Accession #: NP_002412.1

10 1 11 21 31 41 51
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDRQ VEKRRNSGPV 60
 VEKLRQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFOPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSLGLSHST DIGALMYPST 240
 15 TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
 FYMRTNPFYP EVELNFISVF WPQLPENGLEA AYEFAADRDEV RFPKGNKYWA VQGQNVLHGY 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRY DEYKRSMDDPG YPKMIAHDFP 420
 GIGHKVDVAVF MKDGGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

20

Seq ID NO: 13 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

25 1 11 21 31 41 51
 ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTG ACACAGCTTC 60
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120
 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCACTG 180
 GTTGAAAAAT TGAAGCAATC GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCCAGAT 240
 30 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT 300
 GTCTCTCATG CTTTTCAACC AGGCCAGGT ATTGGAGGGG ATGCTCATTI TGATGAAGAT 360
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACCTC 420
 TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 35 CTGTCTCATG CTTTTCAACC AGGCCAGGT ATTGGAGGGG ATGCTCATTI TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC 660
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
 ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCAAAA CCCCAGAAAGC ATGTGACAGT 840
 40 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCT TTCTGTTTTT 960
 TGGCCCAAC TGCCTAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 45 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGAGGATAT 1200
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT 1260
 GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTA TTTCTTTCAT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

50

Seq ID NO: 14 Protein sequence
 Protein Accession #: NP_002412.1

55 1 11 21 31 41 51
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDRQ VEKRRNSGPV 60
 VEKLRQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 60 LAHAFOPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHAL GHSLGLSHST DIGALMYPST 240
 TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
 FYMRTNPFYP EVELNFISVF WPQLPENGLEA AYEFAADRDEV RFPKGNKYWA VQGQNVLHGY 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRY DEYKRSMDDPG YPKMIAHDFP 420
 GIGHKVDVAVF MKDGGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

65

Seq ID NO: 15 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 141..1580

70 1 11 21 31 41 51
 TCTGCGTGTG CCGGGGCTAG GGGCTGGAAG TCCTGGCTCT AGTTGCACCT CGGAAGGAAA 60
 AGGCACACAG AGGAGGGGAG GCGTCTTAGG ACTGCCTGGA TCCAGAGCAC TTTCTCGGC 120
 75 CTCTACAGGC CTGTGTCGCT ATGGGTTCCC CCGCCGCCCC GGAGGGAGCG CTGGGCTACG 180
 TCCGCGAGTT CACTCGCCAC TCCTCCGACG TGCTGGGCAA CCTCAACGAG CTGCGCCTGC 240
 GCGGGATCCT CACTGACGTC ACGCTGCTGG TTGGCGGCA ACCCTCAGA GCACACAAGG 300
 CAGTTCTCAT GCCTGTCAGT GGCTTCTTCT ATTCAATTTT CCGGGGCCGT GCGGGAGTCG 360
 GGGTGGACGT GCTCTCTCTG CCGGGGGGTC CCGAAGCGAG AGGCTTCGCC CCTCTATTGG 420
 80 ACTTCATGTA CACTTCGCGC CTGCGCCTCT CTCAGCCAC TGCACACGCA GTCCTAGCGG 480
 CCGCCACCTA TTTGCAGATG GAGCAGCTGG TCCAGGCATG CCACCGCTTC ATCCAGGCCA 540
 GCTATGAACC TCTGGGCATC TCCCTGCGCC CCCTGGAAGC AGAACCCCCA ACACCCCAA 600
 CGGCCCTCC ACCAGGTAGT CCCAGCGCCT CCGAAGGACA CCCAGACCCA CCTACTGAAT 660
 CTCGAAGCTG CAGTCAAGGC CCCCCAGTC CAGCCAGCCC TGACCCCAAG GCCTCAACT 720
 GGAAGAGTA CAAGTACATC GTGCTAAACT CTCAGGCCTC CCAAGCAGGG AGCCTGGTCG 780

5	GGGAGAGAAG TTCTGGTCAA CCTTGCCCCC AAGCCAGGCT CCCCAGTGGG GACGAGGCCT 840
	CCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GTGAAGAAGG ACCCATTCCT GGTCCCCAGA 900
	GCAGGCTCTC TCCAACCTGCT GCCACTGTGC AGTTCAAATG TGGGGCTCCA GCCAGTACCC 960
	CCTACCTCCT CACATCCCAG GCTCAAGACA CCTCTGGATC ACCCTCTGAA CGGGCTCGTC 1020
	CACTACCGGG AAGTGAATTT TTCAGCTGCC AGAACTGTGA GGCTGTGGCA GGGTGTCTAT 1080
	CGGGGCTGGA CTCTTGGTTC CCTGGGACG AAGACAAACC CTATAAGTGT CAGCTGTGCC 1140
	GGTCTTCGTT CCGCTACAAG GGCAACCTTG CCAGTCATCG TACAGTGCAC ACAGGGGAAA 1200
	AGCCTTACCA CTGCTCAATC TGCAGGAGCC GTTTTAACCG GCCAGCAAAC CTGAAAACGC 1260
10	ACAGCCGCAT CCATTCCGGG GAGAAGCCGT ATAAGTGTGA GACGTGCGGC TCGCGCTTTG 1320
	TACAGGTGGC ACATCTGCGG GCGCACGTGC TGATCCACAC CGGGGAGAAG CCCTACCCCT 1380
	GCCCTACCTG CGGAACCCGC TTCCGCCACC TGCAGACCCT CAAGAGCCAC GTTCGCATCC 1440
	ACACCGGAGA GAAGCCTTAC CACTGCGACC CCTGTGSCCT GCATTTCGG CACAAGAGTC 1500
	AACTGCGGCT GCATCTGCGC CAGAAACACG GAGCTGTAC CAACACCAA GTGCACTACC 1560
15	ACATTCTCGG GGGGCCCTAG CTGAGCGCAG GCCCAGGCC CACTTGCTTC CTGCGGGTGG 1620
	GAAAGCTGCA GGGCCAGGCC TTGCTTCCCT ATCAGGCTTG GGCATAGGGG TGTGCCAGGC 1680
	CACCTTGGTA TCAGAAATTT CCACCCTCTT AATTTCTCAC TGGGGAGAGC AGGGGTGGCA 1740
	GATCTCGGCT AGATCTGCCT CTGTTTTGCT GGTCAAACCC TCTTCCCCAC AAGCCAGATT 1800
	GTCTTCTGAG AGAGAGCTAG CTAGGGGCTG GAAAGGGGA GAGATTGGAG TCTTGTCTCT 1860
20	CCTAAGGGAA TAGCCCTCCA CCTGTGGCCC CCATTGCATT CAGTTTATCT GTAAATATAA 1920
	TTTATTGAGG CCTTTGGGTG GCACCGGGGC CTTCATTGCA TTGCATTTC CACTCCCTCT 1980
	TTCCACAAGT TCAGATTAAA GTGACCAGAA ACACAGAAGG TGAGATCACA GCTCTGTGG 2040
	CAGAGATTAC TAGCCCTTGG CTCTCTCGTT TGGCTTGGGT ATTTTATATT ATTTCTGTCA 2100
	TAACTTTTAT CTTTAGAATT GTTCTTTCTC CTGTTTGTIT GCTTGTAGT TGTGTTAAAA 2160
25	TGGAAAAAGG GGTCTCTGTG GTTCTGCCCC TGTAAATCTA GGTCTGGAAC CTTTATTGTG 2220
	TCTAGGGCAG CTCTGGGAAC ATGCGGGATT GTGGAATTGG GTGAGGAACC CTCTCTGGTA 2280
	TTCTGGATGT TGTAGTTTCT CTAGCAGTCT AGAAATGGAT ACAGACATTT CTCTGTCTCT 2340
	CAAGGGTGAT AGGAACCATT ATGTTGAGCC CAAAATGGAA GTAATAATAA ATGCCCTCTG 2400
	GAGGCTGTGG GTGTGGGGGA TTCTGTATCT GGATTCCGTA TCACTCCAAC TGGAGGCTGT 2460
30	GGGTGTGGGG GATTCTGTAT CTGGATTCCG TATCACTCCA AGTGGAGGCT GGCAGGTTTT 2520
	TCTGCAAGAT GGTCCAGAAT CTAAATGTCT CCATTATCTT GGTCACTTGG GTTTGGCTCT 2580
	GCTGTATCCA TCTATAGTGG TAGAGACCCA CCAGGGCTCA AGTGGAGTCC ATCATCCTCC 2640
	CACGGGGGCC TGTCTTTAGC ACTGAGTTGA TCGCTCCATG GGGGAGAGAT CAGACATTCC 2700
	TTATCAGAGA TGATGTGACC TTTTCTGACT CTGCCCAGTC TCTATGAATG TTATGGCCTA 2760
35	GGGAAGAATC ATGAACCTCT TTAGCTTGA TTAGTGTAA ACAGTGTAA CCCATCCTTT 2820
	ACTACAGAGG CATATGGGTT TGAATGTTAC CTGGGGTCTC CTCTATTGAG TTGAGCCCTT 2880
	TCTTCTTTTA GTGGGTTTTG GACATCTTCT GGCAAGTGTC CAGATGCCAG AACCTTCTTT 2940
	TCCTCTAGAA GGGATGGTGC TTGGTAACCT TACCTTTTAA AAGCTGGGTC TGTGACCTGG 3000
	TCTTCCCATC CTGCAATTCC TGTCTGGAAC CAGTGAATGC ATTAGAACCT TCCATAGGAA 3060
40	AAGAAAAGGG GCTGAGTTTC ATTCTGGGTT TGTCTGAGTT TGGTTGGGAT TATTGTTGGC 3120
	ATTACAGATG TAAAAGATTG ACTAGCCCAT AGGCCAAAGG CCTGTTCTAG TTGACCAAGT 3180
	TTCAAGTAGG ATTAAGAGGT TGGTTGAGGG GTGCAAGTTC TGGTGTAGGC CAGGTAGGTA 3240
	GAAAGTGAGG AACAGGGTTG CCTCTTGGCT GGGTGGAGTC TCTGAAATGT TAGAAGAAGC 3300
	GCTGAAGCCT TGATTGATAG TTCTGCCCTT TGTGCCCCTG GGGCTTATCT GATTATGGGA 3360
45	CGAGGGTAGA AAGTAAGAAG CACTTTTGAA TTTGTGGGGT AGAAGTTCAA CAATAAGTCA 3420
	GTTCTAGTGG CTGTGCGCTG GGGACTAGTG AGAAAGCTAC TCTTCTCCCT CTCCCTCTCT 3480
	TCTCCCATG GCCCAGCTGC AGAATTAAAG AAGGAAGAAG GGAAGGCGGA GGAGTCTATA 3540
	AGAAGGAATC ATGATTTCTA TTTAGCAGAT TGGATGGGCA GGTGGAGAAT GCCTGGGGT 3600
50	AGAAATGTGA GATCTTGCAA CATCAGATCC TTGGAATAAA GAAGCCTCTC TGYGWRAAA 3660
	AAAAAAAAA AAAAAA

Seq ID NO: 16 Protein sequence
Protein Accession #: FGENESH predicted

55	1 11 21 31 41 51	MGSPAPEGA LGYVREFTRH SSDVLGNLNE LRLRGILTDV TLLVGGQPLR AHKAVLIACS 60
		GFFYSIFRGR AGVGVDFVLSL PGGPEARFPA PLDFMYTSR LRLSPATAPA VLAATYLMQ 120
		EHVVQACHRF IQASYEPLGI SLRPLEAEPF TPPTAPPPGS PRRSEGHDPF PTESRSCSQG 180
60		PPSPASPPDK ACNWKYKYI VLNSQASQAG SLVGERSSGQ PCPQARLPSG DEASSSSSSS 240
		SSSSEGPPI GPQSRSLPFA ATVQFKCAP ASTPYLLTSQ AQDTSGPSSE RARPLPGSEF 300
		FSCQNCEAVA GCSSGLDSLIV PGDEDKPYK QLCRSSFRYK GNLAHRTVH TGEKPYHCSI 360
		CGARENRPAN LKTHSRIHSG EKPYPKCTCG SRFVQVAHLR AHVLIHTGEK PYPCTCGTR 420
		FRHLQTLKSH VRIHTGEKPY HCDPCGLHFR HKSQRLRLHLR QKHGAATNTK VHYHILGGP

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: XM_039209
Coding sequence: 1..2049

70	1 11 21 31 41 51	ATGCTGAAGA TGCTCTCCTT TAAGTGCTG CTGCTGGCCG TGGCTCTGGG CTTCTTTGAA 60
		GGAGATGCTA AGTTTGGGGA AAGAAACGAA GGGAGCGGAG CAAGGAGGAG AAGGTGCCTG 120
		AATGGGAACC CCCCAGAGCG CCTGAAAAGG AGAGACAGGA GGATGATGTC CCAGCTGGAG 180
75		CTGCTGAGTG GGGAGAGAGAT GCTGTGCGGT GGCCTCTACC CTCGGCTGTC CTGCTGCCTG 240
		CGGAGTGACA GCGCGGGGCT AGGGCGCCTG GAGAATAAGA TATTTTCTGT TACCAACAAC 300
		ACAGAATGTG GGAAGTTACT GGAGGAAATC AAATGTGCAC TTTGCTCTCC ACATTCTCAA 360
		AGCCTGTTCC ACTCAGCTGA GAGAGAAGTC TTGGAAAGAG ACCTAGTACT TCCTCTGCTC 420
		TGCAAGACT ATTGCAAGA ATTCTTTTAC ACTTGCCGAG GCCATATTCC AGGTTTCTCT 480
80		CAAAACAACG CGGATGAGTT TTGCTTTTAC TATGCAAGAA AAGATGGTGG GTTGTGCTTT 540
		CCAGATTTTC CAAGAAAACA AGTCAGAGGA CCAGCATCTA ACTACTTGGA CCAGATGGAA 600
		GAATATGACA AAGTGGAAGA GATCAGCAGA AAGCACAAC ACAACTGCTT CTGTATTGAG 660
		GAGGTGTGTA GTGGCTGCGC GCAGCCCGTT GGTGCCCTGC ATAGTGGGGA TGGCTCGCAA 720
		CGTCTCTTCA TTCTGGAATA AGAAGGTTAT GTGAAGATAC TTACCCCTGA AGGAGAAATT 780
		TCAAGGAGC CTTATTGGA CATTACAAA CTTGTCTAAA GTGGAATAAA GGGAGGAGAT 840

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10
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GAAAGAGGAC TGCTAAGCCT CGCATTCAT CCCAATTACA AGAAAAATGG AAAGTTGTAT 900
GTGTCTTATA CCACCAACCA AGAACGGTGG GCTATCGGGC CTCATGACCA CATTCTTAGG 960
GTTGTGGAAT ACACAGTATC CAGAAAAAAT CCACACCAAG TTGATTGAG AACAGCCAGA 1020
GTCTTTCTTG AAGTTGCAGA ACTCCACAGA AAGCATCTGG GAGGACAACT GCTCTTTGGC 1080
CCTGACGGCT TTTTGTACAT CATTCTTGGT GATGGGATGA TTACACTGGA TGATATGGAA 1140
GAAATGGATG GGTTAAGTGA TTTCACAGGC TCAGTGCTAC GGCTGGATGT GGACACAGAC 1200
ATGTGTAACG TGCCTTATTC CATACCAAGG AGCAACCCAC ACTTCAACAG CACCAACCAG 1260
CCCCCGAAG TGTTCCTCA TGGGCTCCAC GATCCAGGCA GATGTGCTGT GGATAGACAT 1320
CCCACTGATA TAAACATCAA TTAAACGATA CTGTGTTTCA ACTCCAATGG AAAAAACAGA 1380
TCATCAGCCA GAATTCACCA GATAATAAAG GGGAAAGATT ATGAAAGTGA GCCATCACTT 1440
TTAGAATTCA AGCCATTTCAG TAATGGTCCT TTGGTTGGTG GATTGTGATA CCGGGGCTGC 1500
CAGTCAGAAA GATTGTATGG AAGCTACGTG TTGGGAGATC GTAATGGGAA TTTCTTAAT 1560
CTCCAGCAAA GTCCCTGTGAC AAAGCAGTGG CAAGAAAAAC CACTCTGTCT CGGCACTAGT 1620
GGGTCTGTGA GAGGCTACTT TTCCGGTCAC ATCTTGGGAT TTGGAGAAAG TGAAC TAGGT 1680
GAAGTTTACA TTTTATCAAG CAGTAAAGT ATGACCCAGA CTCACAATGG AAAACTCTAC 1740
AAAATTGTAG ATCCCAAAAG ACCTTTAATG CCTGAGGAAT GCAGAGCCAC GGTACAACT 1800
GCACAGACAC TGACTTCAGA GTGCTCCAGG CTCTGTGCGAA ACGGCTACTG CACCCCCACG 1860
GGAAAGTGCT GTCGCACTCC AGGCTGGGAG GGGGACTTCT GCAGAACTGC AAAATGTGAG 1920
CCAGCATGTC GTCATGGAGG TGCTGTGTT AGACCGAACA AGTGCCTCTG TAAAAAGGA 1980
TATCTTGGTC CTCAATGTGA ACAAGTGGAC AGAAACATCC GCAGAGTGAC CAGGGCAGAC 2040
ATCACCTAG

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Seq ID NO: 18 Protein sequence
Protein Accession #: XP_039209

30
35
40

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1 11 21 31 41 51
| | | | |
MLKMLSFKLL LLAVALGFFE GDAKFGERNE GSGARRRRCL NGNPPKRLKR RDRRMSQLE 60
LLSGGEMLCG GFYPRLSCLL RSDSPGLGRL ENKIFSVTNN TECGKLEEI KCALCSFHSQ 120
SLFHSPEREV LERDLVLPLL CKDYCKEFFY TCRGHIPGFL QTTADEFCFY YARKDGLCF 180
PDFPRKQVRG PASNYLDQME EYDKVEEISR KHKHNCFCIQ EVVSGLRQPV GALHSGDGSQ 240
RLFILEKEGY VKILTPEGEI FKEPYLDIHK LVQSGIKGGD ERLLSLAFH PNYKKNKLY 300
VSYTTNQERW AIGPHDHLR VVEYTVSRKN PHQVDLRTAR VFLEVAELHR KHLGGQLLF 360
PDGFLYIILG DGMITLDDME EMDGLSDFTG SVLRLDVDTD MCNVFYSIPR SNPHFNSTNQ 420
PPEVFAHGLH DPGRCVDRH PTDININLTI LCSDSNGKNR SSARILQIIK GKDYSEPSL 480
LEFKPFNSNG LVGGFVYRGC QSERLYGSYV FGDRNGNFLT LQSPVTKQW QEKPLCLGTS 540
GSCRGYFSGH ILFGFGEDELG EYVILSSSKS MTQTHNGKLY KIVDPKRPLM PEECRATVQP 600
AQTILTSECSR LCRNGYCTPT GKCCSPGWE GDFCRTAKCE PACRHGGVCV RPNKCLCKKG 660
YLGPOCEQVD RNIRRVTRAD IT

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Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: NM_014331.2
Coding sequence: 1..1506

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1 11 21 31 41 51
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GGAATCTTCA TCTCTCCTAA GGGCGTGCTC CAGAACACGG GCACGCTGGG CATGTCTCTG 240
ACCATCTGGA CGGTGTGTGG GGTCTGTGCA CTATTTGGAG CTTTGTCTTA TGCTGAATTG 300
GGAACAACATA TAAAGAAATC TGGAGGTGAT TACACATATA TTTTGGAAAT CTTTGGTCCA 360
TTACCACTCT TTGTACAGAT CTGGGTGGAA CTCCTCATAA TACGCCCTGC AGCTACTGCT 420
GTGATATCCT TGGCATTGGG ACGCTACATT CTGGAACCAT TTTTATTATC ATGTGAAATC 480
CCTGAACTTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTGAT GGTCTTAAT 540
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AACCTGAAA AAACCATTCG CCTTGCAATA TGTATATCCA TGGCCATTGT CACCATTGGC 840
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TTATTTCTATG TTGCGTCTCG AGAGGGTCAC CTTCCAGAAA TCCTCTCCAT GATTATGCTC 1080
CGCAAGCACA CTCCTCTACC AGCTGTTATT GTTTTGCAAC CTTTGACAAT GATAATGCTC 1140
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GTCCCTGGCT ATTAATCTCT TATTATATGG GACAAGAAAC CCAGGTGGTT TAGAATAATG 1440
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GCTTTAATGG ATTAATACCA GAGCACTTTG AACAAAGGTC AGTGGGGATT GTTGAATACA 2100
TTAAAGAGAA GTTTCTAGGG GCTACTGTTT ATGAGACACA TCCAGGAGTT ATGTTTAAAT 2160
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5 TTAATCTGTCA TTTTITTTTT TCACATCAGT TTGATCAGGA AAGTGTATAA CACATCTTAG 2280
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 CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCACAT 3000
 15 GCTGGTAATC TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGCG 3060
 GAGGTTGACG TGAGCCAAGA TTGCACCACT GTACTCCAGC CTGGGTGACA AAGTCAGACT 3120
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Seq ID NO: 20 Protein sequence
 Protein Accession #: NP_055146.1

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 25 GIFISPKGVL QNTGVSVMGL TIWTVCGVLS LFGALSYAEL GTTIKSGGH YTYILEVFGP 120
 LPAFVRVWVE LLIIIRPAATA VISLAFGRYI LEPPFIQCEI PELAIKLITA VGITVVMVLN 180
 SMSVSWASRI QIFLTFCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRPLAFY 240
 YGMYAYAGWF YLNFVTEEEVE NPEKTIPLAI CISMATITGV YVLTNVAYFT TINAEELLS 300
 NAVAVTFSSR LLGNFLSLAV IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV 360
 30 RKHTPLPAVI VLHPLNLMIML FSGDLDSLNL FLSFARWLFI GLAVAGLIYL RYKCPDMHRP 420
 FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM 480
 SEKITRTLQI ILEVVPEDDK L

35 Seq ID NO: 21 DNA sequence
 Nucleic Acid Accession #: NM_002422.2
 Coding sequence: 64..1497

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 TTGGATGGAG CTCGAAGGGG TGAGGACACC AGCATGAACC TTGTTAGAA ATATCTAGAA 180
 AACTACTACG ACCTCAAAAA AGATGTGAAA CAGTTTGTTA GGAGAAAGGA CAGTGGTCCT 240
 45 GTTGTAAAAA AAATCCGAGA AATGCAGAAAG TTCTTGGAT TGGAGGTGAC GGGGAAGCTG 300
 GACTCCGACA CTCGTGAGGT GATGCGCAAG CCCAGGTGTG GAGTTCTGA TGTGTGTAC 360
 TTCAAGACCT TTCTTGGCAT CCGAAGTGG AGGAAAACCC ACCTTACATA CAGGATTGTG 420
 AATTATACAC CAGATTGGCC AAAAGATGCT GTTGATTCTG CTGTTGAGAA AGCTCTGAAA 480
 GTCTGGGAAG AGGTGATCC ACTCACATTC TCCAGGCTGT ATGAAGGAGA GGTGATATA 540
 50 ATGATCTCTT TTGCAGTTAG AGAACATGGA GACTTTTACC CTTTGTATGG ACCTGGAAAT 600
 GTTTTGGCCC ATGCTATGAC CCCTGGGCCA GGGATTAATG GAGATGCCCA CTTGTATGAT 660
 GATGAACAAT GGACAAAGGA TACAACAGGG ACCAATTAT TTCTCGTTC TGCTCATGAA 720
 ATTTGGCCACT CCCTGGGTCT CTITCACTCA GCCAACACTG AAGCTTTGAT GTACCCACTC 780
 TATCACTCAC TCACAGACCT GACTCGGTTT CGCTGTCTC AAGATGATAT AAATGGCATT 840
 55 CAGTCCCTCT ATGACCTCC CCCTGACTCC CCTGAGACCC CCTTGGTACC CACGGAACCT 900
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 AGCACTCTGA GGGGAGAAAT CCTGATCTTT AAAGACAGGC ACTTTTGGCG CAAATCCCTC 1020
 AGGAAGCTTG AACCTGAATT GCATTGTATC TCTTCATTTT GGCCATCTCT TCCTTCAGGC 1080
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 60 TTCTGGGCCA TCAGAGGAAA TGAGGTACGA GCTGGATACC CAAGAGGCAT CCACACCCTA 1200
 GGTTCCTCTC CAACCGTGAG GAAAAATCGAT GCAGCCATTT CTGATAAGGA AAAGAACAAA 1260
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 GTTTTGAAG AAFTTGGGTT CTTTATTTC TTTACTGGAT CTTACAGTT GGAGTTTGA 1440
 65 CCAATGCAA AGAAAGTGAC ACACACTTTG AAGAGTAACA GCTGGCTTAA TTGTTGAAAG 1500
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 GGAACCTGAG CGTGAATCTG TATCTTGCCG GTCATTTTAA TGTATTACA GGCATTCAA 1680
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 70 AGCACTCGTG TGCAACAGAC AAGTGACTGT ATCTGTGTAG ACTATTGTCT TATTTAATAA 1800
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Seq ID NO: 22 Protein sequence
 Protein Accession #: NP_002413

75 1 11 21 31 41 51
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 VKKIREMQKF LGLEVTGKLD SDTLEVMRKP RCGVPDVGHF RTFPGIPKWR KTHLTYRIVN 120
 80 YTPDLKDAV DSAVEKALKV WEEVTPLTFS RLYEGEADIM ISFAVREHGD FYPFDGPGNV 180
 LAHAYAPGPG INGDAHFDDE EQWTKDITGT NLFLVAHEI GHSLGLFHSA NTEALMYPLY 240
 HSLTDLTRFR LSQDDINGIQ SLYGPPDPSP ETPLVPTEPV PEPGTPANC DPALSFDVA 300
 TLRGELIFK DRHFWRKSLR KLEPELHLIS SFWPSLPSPV DAAYEVTSKD LVFIFKGNQF 360
 WAIRGNVEVA GYPRGIHTLG FPPTVRKIDA AISDKEKNKT YFFVEDKYWR FDEKRNMEP 420
 GFFPKIAEDF PGIDSKIDAV FEEFGFFYFF TGSSQLEFDP NAKKVIHTLK SNSWLNC

Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

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GCGATGCTGC	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCCTG	CCCCTAGACT	180
ACGGAACCTG	CCGGGCCCTA	CTTCTCCGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
GCCAGTTCTT	GTACGGGGGC	TGCGAGGGCA	ACGCCAACAA	TTTCTACACC	TGGGAGGCTT	300
GCGACGATGC	TTGCTGGAGG	ATAGAAAAAG	TTCCCAAAGT	TTGCCGGCTG	CAAGTGAGTG	360
TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTTCTT	TAATCTAAGT	TCCATGACAT	420
GTGAAAAATT	CTTTTCCGGT	GGGTGTCACC	GGAACCGGAT	TGAGAACAGG	TTTCCAGATG	480
AAGCTACTTG	TATGGGCTTC	TGCGCACCAA	AGAAAATTCC	ATCATTTTGC	TACAGTCCAA	540
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CCTGTGATGC	TTTACCTTAT	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660
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GCTTTGCCAG	TAGAATCCGG	AAAATTCGGA	AGAAGCAATT	TAAACATTC	TAAATATGTC	780
ATCTTGTTTG	TCTTTATGGC	TTATTTGCCT	TTATGTTTGT	ATCTGAAGAA	TAATATGACA	840
GCATGAGGAA	ACAAATCATT	GGTGATTAT	TCACCAGTTT	TTATTAATAC	AAGTCACTTT	900
TTCAAAAAAT	TGGATTTTTT	TATATATAAC	TAGCTGCTAT	TCAAATGTGA	GTCCTACCATT	960
TTTAATTAT	GGTTCACCTG	TTTGTGAGAC	GAATTCCTGC	AATGCATAAG	ATATAAAAGC	1020
AAATATGACT	CACTCATTTT	TTGGGGTCGT	ATTCCTGATT	TCAGAAGAGG	ATCATAACTG	1080
AAACAACATA	AGACAATATA	ATCATGTGCT	TTTAACATAT	TTGAGAATAA	AAAGGACTAG	1140
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Seq ID NO: 24 Protein sequence
Protein Accession #: NP_006519

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TCEKFFSGGC	HRNRLENRFP	DEATCMGFCA	PKKIPSFYCS	PKDEGLCSAN	VTRYFFNPRY	180
RTCDAFYTYG	CGGNDNNFVS	REDCKRACAK	ALKKKKKMPK	LRFASRIRKI	RKKQF	

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: NM_005458.1
Coding sequence: 1..2825

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GGCTGGGCGC	GGGGCGCCCC	CGGGCGGCGG	CCCAGCAGCC	CGCCGCTCTC	CATCATGGGC	180
CTCATGCCCG	TCACCAAGGA	GGTGGCCAAG	GGCAGCATCG	GGCGCGGTGT	GCTCCCCGCC	240
GTGGAAGTGG	CCATCGAGCA	GATCCGCAAC	GAGTCACTCC	TGCGCCCCTA	CTTCTCTGAC	300
CTGCGGCTCT	ATGACACGGA	GTGCGACAAC	GCAAAAGGGT	TGAAAGCCTT	CTACGATGCA	360
ATAAAATACG	GGCCGAACCA	CTTGATGGTG	TTTGGAGGCG	TCTGTCCATC	CGTCACATCC	420
ATCATGTGCA	AGTCCCTCCA	AGGCTGGAAT	CTGGTGCAGC	TTTCTTTTGC	TGCAACCACG	480
CCTGTCTTAG	CCGATAAGAA	AAAATACCCT	TATTTCTTTC	GGACCGTCCC	ATCAGACAAT	540
GCGGTGAATC	CAGCCATTCT	GAAGTTGCTC	AAGCACTACC	AGTGGAAAGC	CGTGGGCACG	600
CTGACGCAAG	ACGTTTCAGAG	GTTCCTGTAG	GTGCGGAATG	ACCTGACTGG	AGTTCTGTAT	660
GGCGAGGACA	TGAGATTTC	AGACACCGAG	AGCTTCTCCA	ACGATCCCTG	TACCAAGTGC	720
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GCAAAAGTGT	TCTGTGTGTC	ATACGAGGAG	AACATGTATG	GTAGTAAATA	TCAGTGGATC	840
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CGCTGCCTCC	GGAGAATCT	GCTTGTCTGC	ATGGAGGGCT	ACATTGGCGT	GGATTTCGAG	960
CCCCTGAGCT	CCAAGCAGAT	CAAGACCATC	TCAGGAAAGA	CTCCACAGCA	GTATGAGAGA	1020
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GGCATCTGGG	TCATCGCCAA	GACACTGCAG	AGGGCCATGG	AGACACTGCA	TGCCAGCAGC	1140
CGGCACCAGC	GGATCCAGGA	CTTCAACTAC	ACGGACCACA	CGCTGGGCAG	GATCATCCTC	1200
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GAGTACAACG	CTGTGGCCGA	CACACTGGAG	ATCATCAATG	ACACCATCAG	GTTCCTAAGGA	1380
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GGATCCTTTG	TCTCTGAAAA	GACCTTTGAA	ACACTTTGCA	CCGTCAAGAC	CTGGATTCTC	1680
ACCGTGGGCT	ACACGACCGC	TTTTGGGGCC	ATGTTTGCAA	AGACCTGGAG	AGTCCACGCC	1740
ATCTTCAAAA	ATGTGAAAAA	GAAGAAGAAG	ATCATCAAGG	ACCAGAAACT	GCTTGTGATC	1800
GTGGGGGGCA	TGCTGTCTGAT	CGACCTGTGT	ATCCTGATCT	GCTGGCAGGC	TGTGGACCCC	1860
CTCGGAAGGA	CAGTGGAGAA	GTACAGCATG	GAGCCGGACC	CAGCAGGACG	GGATATCTCC	1920
ATCCGCCCTC	TCTTGAGAGCA	CTGTGAGAAC	ACCCATATGA	CCATCTGGCT	TGGCATCGTC	1980
TATGCCCTACA	AGGGCACTTCT	CATGTTGTTC	GGTGTGTTCT	TAGCTTGGGA	GACCCGCAAC	2040
GTCAGCATCC	CCGCACTCAA	CGACAGCAAG	TACATCGGGA	TGAGTGTCTA	CAACGTGGGG	2100
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TTCTGCATCG	TGGCTCTGGT	CATCATCTTC	TGCAGCACCA	TCACCCTCTG	CTTGGTATTCT	2220
GTGCCGAAGC	TCATCACCCCT	GAGAACAAC	CCAGATGCAG	CAACGCAGAA	CAGGCGATTTC	2280
CAGTTCACTC	AGAATCAGAA	GAAAGAAGAT	TCTAAAACGT	CCACCTCGGT	CACCACTGTC	2340
AACCAAGCCA	GCACATCCCG	CCTGGAGGGC	CTACAGTCAG	AAAACCATCG	CCTGCGAATG	2400

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 GGAAACTTCA CTGAGAGCAC AGATGGAGGA AAGGCCATT TAAAAATCA CCTCGATCAA 2580
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 CACGCCTACC TCCCATCCAT CGGAGGCGTG GACGCCAGCT GTGTCAGCCC CTGCGTCAGC 2760
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 CTGTAA

Seq ID NO: 26 Protein sequence
 Protein Accession #: NP_005449.1

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 IKYGNHLMV FGGVCPVSTS IIAESLQGNW LVQLSFAATT PVLADKKKYP YFFRTVPSDN 180
 AVNPAILKLL KHYQWKRVGT LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SFSNDPCTSV 240
 KKLKGNVRI ILQFDQDMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWV EQVHTEANSS 300
 RCLRKNLAA MEGYIGVDFE PLSSKQIKTI SGKTPQYER EYNMKRSGVG PSKFHGYAYD 360
 GIWVIKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRIL NAMNETNFFG VTGQVVRNG 420
 ERMGTIKFTQ FQDSREKVG EYNAVADTLE IINDTIRFQG SEPPKDKTII LEQLRKISLP 480
 LYSILSALTI LGMIMASAFI FFIKNRNQK LKMSSPYMN NLIIILGMLS YASIFLFLGD 540
 GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IFKNVKMKKK IKDQKLLVI 600
 VGGMLLIDL ILICWQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLGI 660
 YAYKGLMLF GCFLAWETRN VSIPALNDSK YIGMSVYNVG IMCLIGAAVS FLTRDQPNVQ 720
 FCIVALVIF CSTITLCLVF VPKLITLRTN PDAATQNRFF QFTQNKKEK SKTSTSVTSV 780
 NQASTSRLEG LQSENHRLRM KITELDKDLE EVTMQLQDTP EKTYYIKQNH YQELNDILNL 840
 GNFTSTDDG KAILKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLPI 900
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Seq ID NO: 27 DNA sequence
 Nucleic Acid Accession #: NM_000450.1
 Coding sequence: 117..1949

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 GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT TATTGTGACG 240
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 TCTGGGTAGG AACCCAGAAA CCTCTGACAG AAGAAGCCAA GAACCTGGCT CCAGGTGAAC 420
 CCAACAATAG GCAAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG 480
 TGGGCATGTG GAATGATGAG AGGTGCAGCA AGAAGAAGCT TGCCCTATGC TACACAGCTG 540
 CCTGTACCAA TACATCCTGC AGTGGCCACG GTGAATGTGT AGAGACCATC AATAATTACA 600
 CTTGCAAGTG TGACCTGGC TTCAGTGGAC TCAAGTGTGA GCAAAATTGT AACTGTACAG 660
 CCCTGGAATC CCCTGAGCAT GGAAGCCTGG TTTGCACTCA CCCACTGGGA AACTTCAGCT 720
 ACAATTCTTC CTGCTCTATC AGCTGTGATA GGGGTACCT GCCAAGCAGC ATGGAGACCA 780
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 CAGAAGAGGT TCCTTCTGTC CAAGTGGTAA AATGTTCAAG CCTGGCAGTT CCGGGAAGA 1620
 TCAACATGAG CTGCAGTGGG GAGCCCTGTG TTGGCACTGT GTGCAGTTTC GCCTGTCCCTG 1680
 AAGGATGGAC GCTCAATGGC TCTGCAGCTC GGACATGTGG AGCCACAGGA CACTGGTCTG 1740
 GCCTGTCTAC TACCTGTGAA GCTCCCACTG AGTCCAACAT TCCCTTGSTA GCTGGACTTT 1800
 CTGCTGCTGG ACTCTCCCTC CTGACATTAG CACCATTCTT CCTCTGGCTT CGGAAATGCT 1860
 TACGGAAAGC AAAGAAATTT GTTCTGCGCA GCAGCTGCCA AAGCCTTGAA TCAGACGGAA 1920
 GCTACCAAAA GCCTTCTTAC ATCCTTTAAG TTCAAAGAA TCAGAAACAG GTGCATCTGG 1980
 GGAACATGAG GGATACAGT AAGTTAACAG AGACAGATAA CTCTCTCGG GTCTCTGGCC 2040
 CTCTCTGCTT ACTATGCCAG ATGCCTTTAT GGCTGAAACC GCAACACCCA TCACCACCTT 2100
 AATAGATCAA AGTCCAGCAG GCAAGGACGG CCTTCAACTG AAAAGACTCA GTGTTCCCTT 2160
 TCTACTCTC AGGATCAAGA AAGTGTGGC TAATGAAGGG AAAGGATATT TTCTTCCAAG 2220
 CAAAGGTGAA GAGACCAAGA CTCTGAAATC TCAGAATTCC TTTTCTAACT CTCCTTGCT 2280
 CGCTGTAAAA TCTTGGCACA GAAACACAAT ATTTTGTGGC TTTCTTTCTT TTGCCCTTCA 2340
 CAGTGTTCG ACAGCTGATT ACACAGTTGC TGTCAATAA ATGAATAATA ATTATCCAGA 2400
 GTTTAGAGGA AAAAAATGAC TAAAAATATT ATAACCTAAA AAAATGACAG ATGTTGAATG 2460
 CCCACAGGCA AATGCAATGGA GGGTTGTAA TGGTGCAAAT CCTACTGAAT GCTCTGTGCG 2520
 AGGGTTACTA TGCACAATTT AATCACTTTC ATCCCTATGG GATTCACTGC TTCTTAAAGA 2580
 GTTCTTAAAG ATTGTGATAT TTTTACTTGC ATTGAATATA TTATAATCTT CCATACTTCT 2640
 TCATTCAATA CAGTGTGGT AGGGACTTAA AAAACTGTGA AATGCTGTCA ACTATGATAT 2700
 GGTAAAAAGT ACTTATTTCTA GATTACCCCT TCATTGTTTA TTAACAAATT ATGTTACATC 2760
 TGTTTTAAAT TTATTTTCAA AAGGGAAACT ATTGTCCCTT AGCAAGGCAT GATGTTAACC 2820

AGAATAAAGT TCTGAGTGT TTTACTACAG TTGTTTTTG AAAACATGGT AGAATTGGAG 2880
 AGTAAAAACT GAATGGAAGG TTTGTATATT GTCAGATATT TTTTCAGAAA TATGTGGTTT 2940
 CCACGATGAA AAACCTCCAT GAGGCCAAAC GTTTTGAAC TATAAAGCA TAAATGCAAA 3000
 CACACAAAGG TATAATTTTA TGAATGTCTT TGTTGGAAAA GAATACAGAA AGATGGATGT 3060
 5 GCTTTGCATT CCTACAAAGA TGTTTGTGAG ATGTGATATG TAAACATAAT TCTTGTATAT 3120
 TATGGAAGAT TTTAAATTCA CAATAGAAAC TCACCATGTA AAAGAGTCAT CTGGTAGATT 3180
 TTTAACGAAT GAAGATGTCT AATAGTTTAT CCCTATTTGT TTTCTTCTGT ATGTTAGGGT 3240
 10 GCTCTGGAAG AGAGGAATGC CTGTGTGAGC AAGCATTAT GTTTATTAT AAGCAGATT 3300
 AACAAATCCA AAGGAATCTC CAGTTTTCAG TTGATCACTG GCAATGAAAA ATTCTCAGTC 3360
 AGTAATTGCC AAAGCTGCTC TAGCCTTGAG GAGTGTGAGA ATCAAAACTC TCCTACACTT 3420
 CCATTAACCT AGCATGTGTT GAAAAAAGAA GTTTCAGAGA AGTTCTGGCT GAACACTGGC 3480
 AACGACAAAG CCAACAGTCA AAACAGAGAT GTGATAAGGA TCAGAACAGC AGAGGTTCTT 3540
 15 TTAAAGGGGC AGAAAACTC TGGGAAATAA GAGAGAACAA CTACTGTGAT CAGGCTATGT 3600
 ATGGAATACA GTGTTATTTT CTTTGAATTT GTTTAAGTGT TGTAAATATT TATGTAAACT 3660
 GCATTAGAAA TTAGCTGTGT GAAATACCAG TGTGGTTTGT GTTTGAGTTT TATTGAGAAAT 3720
 TTTAAATTAT AACTTAAAT ATTTTATAAT TTTTAAAGTA TATATTATTT TAAGCTTATG 3780
 TCAGACCTAT TTGACATAAC ACTATAAAGG TTGACAATAA ATGTGCTTAT GTTT

Seq ID NO: 28 Protein sequence
 Protein Accession #: NP_000441.1

1 11 21 31 41 51
 MIAOQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRVTHLVAI QNKKEIEYLN 60
 25 SILSYSPSY WIGIRKVMNV WVVVGTKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120
 DVGMMWDERC SKKKLALCYT AACTNTSCSG HGECVETINN YTKCDPFGFS GLKCEQIVNC 180
 TALESEPHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
 ECDAVTNPAN GFVECFQNGF SFPWNTCTCF DCEEGFELMG AQSLQCTSSG NWDNEKPTCK 300
 AVTCRAVRQP QNGSVRCSSHS PAGEFTFKSS CNFTCEEGFM LQGPQVVECT TQGWQIQIP 360
 30 VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGFTGEWEN 420
 EKPTCEAVRC DAVHQPFKGL VRCASPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
 WTTEEVPSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
 SGLLPTECAP TESNIPLVAG LSAAGLSLLT LAFPLLWLRL CLRKAKEFVP ASSCQSLESD 600
 35 GSYQKPSYIL

Seq ID NO: 29 DNA sequence
 Nucleic Acid Accession #: NM_007036
 Coding sequence: 56..610

1 11 21 31 41 51
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 45 TAATTATGCG CTGGACTGCC CTCAACACTG TGACAGCAGT GAGTGCAAAA GCAGCCCGCG 180
 CTGCAAGAGG ACAGTGTCTG ACAGCTGTGG CTGCTGCCGA GTGTGCGCTG CAGGGCGGGG 240
 AGAACTTGC TACCGCACAG TCTCAGGCAT GGATGGCATG AAGTGTGGCC CGGGGCTGAG 300
 GTGTCAGCCT TCTAATGGGG AGGATCCTTT TGGTGAAGAG TTTGGTATCT GCAAGACTG 360
 TCCTACGGC ACCTTCGGGA TGGATTGCAG AGAGACCTGC AACTGCCAGT CAGGCATCTG 420
 50 TGACAGGGGG ACCGGAATAA GCCTGAAATT CCCCTTCTTC CAATATTTCAG TAACCAAGTC 480
 TTCCAACAGA TTTGTTTCTC TCACGGAGCA TGACATGGCA TCTGGAGATG GCAATATTGT 540
 GAGAGAAGAA GTTGTGAAG AGAATGCTGC CGGCTCTCCC GTAATGAGGA AATGGTTAAA 600
 TCCACGCTGA TCCCGGCTGT GATTCTGAG AGAAGGCTCT ATTTTCGTGA TTTTCAACA 660
 CACAGCCAAC ATTTTAGGAA CTTTCTAGAT ATAGCATAAG TACATGTAAT TTTTGAAGAT 720
 55 CCAAATTGTG ATGCATGGTG GATCCAGAAA ACAAAGTA GGATACTTAC AATCCATAAC 780
 ATCCATATGA CTGAACACTT GTATGTGTTT GTTAAATATT CGAATGCATG TAGATTTGTT 840
 AAATGTGTGT GTATAGTAAC ACTGAAGAAC TAAAAATGCA ATTTAGGTAA TCTTACATGG 900
 AGACAGGCTA ACCAAGAGG GAGCTAGGCA AAGCTGAAGA CCGCAGTGAG TCAAAATTAG 960
 TCTTTGACTT TGATGTACAT TAATGTTGGG ATATGGAATG AAGACTTAAG AGCAGGAGAA 1020
 60 GATGGGGAGG GGGTGGGAGT GGGAAATAAA ATATTAGGCC CTTCTTGGT AGGTAGCTTC 1080
 TCTAGAAATT AATGTGCTT TTTTTTTTT TTTGGCTTGG GGAAGTCA AAAATAAACA 1140
 ACCAGAAAAC CCCTGAAGGA AGTAAGATGT TTGAAGCTTA TGGAAATTG AGTAACAAAC 1200
 AGCTTTGAAC TGAGAGCAAT TTCAAAGGC TGCTGATGTA GTTCCCGGGT TACCTGTATC 1260
 TGAAGGACGG TCTGGGGCA TAGGAAACAC ATACACTTCC ATAAATAGCT TTAACGTATG 1320
 65 CCACCTCAGA GATAAATCTA AGAAGTATTT TACCCACTGG TGGTTTGTGT GTGTATGAAG 1380
 GTAATATTTT ATATATTTT ATAAATAAAT GTGTAGTGC AAGTCATCTT CCCTACCCAT 1440
 ATTTATCATC CTCTGAGGA AGAAATCTA GTATTATTGT TTGAAATGG TTAGAATAAA 1500
 AACCTATGAC TCTATAAGGT TTTCAAACAT CTGAGGCATG ATAAATTTAT TATCCATAAT 1560
 TATAGGAGTC ACTCTGGATT TCAAAAAATG TCAAAAAATG AGCAACAGAG GGACCTTATT 1620
 70 TAAACATAAG TGCTGTGACT TCGGTGAATT TCAATTTAA GGTATGAAAA TAAGTTTTTA 1680
 GGAGGTTTGT AAAAGAAGAA TCAATTTTCA GCAGAAAAA TGTCAACTTT AAAATATAGG 1740
 TGGAAATTAG AGTATATTG AAAGAATCTT AGCACAACA GGAAGTGTGT ACTAGATGTT 1800
 CTTAGGAAAT ATCTCAGAAG TATTTTATTT GAAGTGAAGA ACTTATTTAA GAATTATTTT 1860
 AGTATTTACC TGTATTTTAT TCTTGAAGTT GGCCAACAGA GTTGTGAATG TGTGTGGAAG 1920
 75 GCCTTTGAAT GTAAAGCTGC ATAAGCTGTT AGGTTTGTGT TAAAAGGAC ATGTTTATTA 1980
 TTGTTCAATA AAAAGAACA AGATAC

Seq ID NO: 30 Protein sequence
 Protein Accession #: NP_008967.1

1 11 21 31 41 51
 MKSVLLLTLL LVPALHVAW SNNYAVDCPQ HCDSECKSS PRCKRTVLDD CGCCRVCAAG 60
 RGETCYRTVS GMDGMKCGPG LRCQPSNGED PFGEFEGICK DCPYGTFGMD CRETNCQSG 120
 ICDRGTGKCL KFPFFQYSVT KSSNRFVSLT EHDMAAGDGN IVREEVVKEN AAGSPVMRKW 180

LNPR

Seq ID NO: 31 DNA sequence

Nucleic Acid Accession #: NM_000963

Coding sequence: 135..1949

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	CAATTGTCAT	ACGACTTGCA	GTGAGCGTCA	GGAGCACGTC	CAGGAAGTCC	TCAGCAGCGC	60
	CTCCTTCAGC	TCCACAGCCA	GACGCCCTCA	GACAGCAAAG	CCTACCCCGG	CGCCGCGCCC	120
5	TGCCGCGCGC	TGGATGCTC	GCCCGCGCCC	TGCTGCTGTG	CGCGGTCCCTG	GCGCTCAGCC	180
	ATACAGCAAA	TCCTTGCTGT	TCCCACCCAT	GTCAAAACCG	AGGTGTATGT	ATGAGTGTGG	240
10	GATTTGACCA	GTATAAGTGC	GATTGTACCC	GGACAGGATT	CTATGGAGAA	AAGTGTCTAA	300
	CACCGGAATT	TTTGACAAGA	ATAAAATAT	TTCTGAAACC	CAGTCCAAAC	ACAGTGCAGT	360
	ACATACCTAC	CCACTTCAAG	GGATTTTGA	ACGTTGTGAA	TAACATTCCT	TTCTTCGAA	420
15	ATGCAATTAT	GAGTTATGTC	TTGACATCCA	GATCACATTT	GATTGACAGT	CCACCAACTT	480
	ACAATGCTGA	CTATGGCTAC	AAAAGCTGGG	AAGCCTTCTC	TAACCTCTCC	TATTATACTA	540
	GAGCCCTTCC	TCCTTGTCCT	GATGATTGCC	CGACTCCCTT	GGGTGTCAAA	GGTAAAAAGC	600
	AGCTTCTCTG	TCTCAATGAG	ATTGTGGAAA	AATTGCTTCT	AAGAAAGAA	TTTATCCCTG	660
20	ATCCCCAGGG	CTCAACATG	ATGTTTGCAT	TCCTTGCCCA	GCCTTCACG	CATCAGTTTT	720
	TCAAGACAGA	TCATAAGCGA	GGGCCAGCTT	TCACCAACGG	GCTGGGCCAT	GGGGTGGAGT	780
	TAAATCATAT	TATCGGTGAA	ACTCTGGCTA	GACAGCGTAA	ACTGCGCCTT	TTCAAGGATG	840
	GAAAAATGAA	ATATCAGATA	ATTGATGGAG	AGATGTATCC	TCCCACAGTC	AAAGATACTC	900
	AGGCAGAGAT	GATCTACCTT	CCTCAAGTCC	CTGAGCATCT	ACGGTTTGTCT	GTGGGGCAGG	960
25	AGGTCTTTGG	TCTGGTGCCT	GGTCTGATGA	TGTATGCCAC	AATCTGGCTG	CGGGAACACA	1020
	ACAGAGTATG	CGATGTGCTT	AAACAGGAGC	ATCCTGAATG	GGGTGATGAG	CAGTTGTTCC	1080
	AGACAAGCAG	GCTAAATACT	ATAGGAGAGA	CTATTAAGAT	TGTGATTGAA	GATTATGTGC	1140
	AACACTTGAG	TGGCTATCAC	TTCAAAGTGA	AATTTGACCC	AGAACTACTT	TTCAACAAAC	1200
	AATTTCCAGTA	CCAAAAATCGT	ATTGCTGCTG	AATTTAAGCC	CCTCTATCAC	TGGCATCCCC	1260
30	TTCTGCTGTA	CACCTTTCAA	ATTCTGACCC	AGAAATACAA	CTATCAACAG	TTTATCTACA	1320
	ACAACCTCAT	ATTGCTGGAA	CATGGAATTA	CCCAAGTTGT	TGAATCATTC	ACCAGGCAAA	1380
	TTGCTGGCAG	GGTTGCTGGT	GGTAGGAATG	TTCCACCCGC	AGTACAGAAA	GTATCACAGG	1440
	CTTCCATTGA	CCAGAGCAGG	CAGATGAAAT	ACCAGTCTTT	TAATGAGTAC	CGCAAAACGCT	1500
	TTATGCTGAA	GCCTATGAA	TCATTTGAAG	AACTTACAGG	AGAAAAGGAA	ATGCTGTCAG	1560
35	AGTTGGAAGC	ACTCTATGGT	GACATCGATG	CTGTGGAGCT	GTATCCTGCC	CTTCTGGTAG	1620
	AAAAGCCTCG	GCCAGATGCC	ATCTTTGGTG	AAACCATGGT	AGAAGTTGGA	GCACCATCTT	1680
	CCTTGAAAGG	ACTTATGGGT	AATGTTATAT	GTCTCTCTGC	CTACTGGAAG	CCAAGCACTT	1740
	TTGGTGGAGA	AGTGGGTGTT	CAAAATCATCA	ACACTGCCTC	AATTCAGTCT	CTCATCTGCA	1800
	ATAACGTGAA	GGGCTGTCCC	TTTACTTCAT	TCAGTGTTC	AGATCCAGAG	CTCATTAAAA	1860
40	CAGTCACCAT	CAATGCCAAT	TCTTCCCGCT	CCGACTAGA	TGATATCAAT	CCACAGTAC	1920
	TACTAAAAGA	ACGTTTCGACT	GAAGTGTAGA	AGTCTAATGA	TCATATTTAT	TTATTTATAT	1980
	GAACCATGTC	TATTAATTTA	ATTATTTAAT	AATATTTATA	TTAACTCCTT	TATGTTACTT	2040
	AACATCTTCT	GTACAGAAAG	TCAGTACTCC	TGTTGCGGAG	AAAGGAGTCA	TACTTTGTGA	2100
	GACTTTTATG	TCACTACTCT	AAAGATTTTG	CTGTTGCTGT	TAAGTTTGGG	AAACAGTTTT	2160
45	TATTTCTGTT	TATAAACCCAG	AGAGAAATGA	GTTTTGACGT	CTTTTACTTT	GAATTTCAAC	2220
	TTATATTATA	AGAAGCAAA	TAAAGATGTT	TGAATACTTA	AACACTATCA	CAAGATGGCA	2280
	AAATGCTGAA	AGTTTATACA	CTGTGATGTT	TTCCAATGCA	TCTTCCATGA	TGCATTAGAA	2340
	GTAACATAAT	TTTGAAATTT	TAAAGTACTT	TTGTTATTTT	TTCTGTATCT	AAACAAAAAC	2400
	AGGTATCAGT	GCATTATTTA	ATGAATATTT	AAATTAGACA	TTACCAGTAA	TTTCATGTCT	2460
50	ACTTTTAAAA	ATCAGCAATG	AAACAATAAT	TTGAAATTTT	TAAATTCATA	GGGTAGAAATC	2520
	ACCTGTAAAA	GCTTGTGTTG	TTTCTTAAAG	TTATTAAGCT	TGTACATATA	CCAAAAAGAA	2580
	GCTGTCTTGG	ATTTAAATCT	GTAAATCAG	ATGAAATTTT	ACTACAATTG	CTTGTAAAAA	2640
	TATTTTATAA	GTGATGTTCC	TTTTTCACCA	AGAGTATAAA	CCTTTTATAGT	GTGACTGTTA	2700
	AAACCTTCCT	TTAAATCAAA	ATGCCAAATT	TATTAAGGTG	GTGGAGCCAC	TGCAGTGTTA	2760
55	TCTCAAAATA	AGAATATTTT	GTTGAGATAT	TCCAGAAATT	GTTTATATGG	CTGGTAACAT	2820
	GTAAATCTTA	TATCAGCAAA	AGGGTCTACC	TTTAAATATA	GCAATAACAA	AGAAGAAAAA	2880
	CAAATTAATT	TTCAAATTTA	GGTTTAAACT	TTTGAAGCAA	ACTTTTTTTT	ATCCTTGTGC	2940
	ACTGCAGGCC	TGGTACTCAG	ATTTTGCTAT	GAGGTTAATG	AAGTACCAGG	CTGTGCTTGA	3000
	ATAACGATAT	GTTTCTCTAG	ATTTTCTGTT	GTACAGTTTA	ATTTAGCAGT	CCATATCACA	3060
60	TTGCAAAAGT	AGCAATGACC	TCATAAAATA	CCTCTTCAAA	ATGCTTAAAT	TCATTTCACA	3120
	CATTAAATTT	ATCTCAGTCT	TGAAGCCAAT	TCAGTAGGTG	CATTGGAATC	AAGCCTGGCT	3180
	ACCTGCATGC	TGTTCTCTTT	CTTTCTCTCT	TTTAGCCATT	TTGCTAAGAG	ACACAGTCTT	3240
	CTCATCACTT	CGTTTCTCCT	ATTTTGTTTT	ACTAGTTTTA	AGATCAGAGT	TCATTTCTTT	3300
	TGGACTCTGC	CTATATTTTC	TTACCTGAAC	TTTTGCAAGT	TTTCAGGTAA	ACCTCAGCTC	3360
65	AGGACTGCTA	TTTAGCTCCT	CTTAAGAAGA	TTAAAGAGAA	AAAAAAAGG	CCCTTTTAAA	3420
	AATAGTATAC	ACTTATTTTA	AGTGAAAAGC	AGAGAATTTT	ATTTATAGCT	AATTTTAGCT	3480
	ATCTGTAACC	AAGATGGATG	CAAGAGGGCT	AGTGCCCTAG	AGAGAAGTGT	ACGGGGTTTG	3540
	TGACTGGAAA	AAGTTACGTT	CCCATTTCTA	TTAATGCCCT	TTCTTATTTA	AAAACAAAAC	3600
	CAATGATAT	CTAAGTAGTT	CTCAGCAATA	ATAATAATGA	CGATAATACT	TCTTTTCCAC	3660
70	ATCTCATTGT	CACTGACATT	TAATGGTACT	GTATATTACT	TAATTTATTT	AAGATTATTA	3720
	TTTATGCTCT	ATTAGGACAC	TATGGTTATA	AACGTGTTTT	AAGCCTACAA	TCATTGATTT	3780
	TTTTTTGTTA	TGTCACAAAT	AGTATATTTT	CTTTGGGGTT	ACCTCTCTGA	ATATTATGTA	3840
	AACAATCCAA	AGAAATGATT	GTATTAAAGT	TTGTGAATAA	ATTTTATAGG	ATCTGATTGG	3900
	CATATTGAGA	TATTTAAGGT	TGAATGTTTG	TCCTTAGGAT	AGGCCATAGT	GCTAGCCAC	3960
75	AAAGATAAT	GTCTCATTTG	CCTGAATGTG	CCATAAGACT	GACCTTTTAA	AATGTTTGA	4020
	GGGATCTGTG	GATGCTTCTG	TAATTTGTTT	AGCCCAAAAT	TATTGAGAAA	ATATTCTGTG	4080
	TCAAGCAGTG	TGGGTTTTAA	TATTTTAA	TCAAACGCTG	ATTACAGATA	ATAGTATTTA	4140
	TATAAATAAT	TGAAAAAAT	TTTCTTTTGG	GAAGAGGGAG	AAAAATGAAT	AAATATCATT	4200
	AAAGATAACT	CAGGAGAAAT	TTCTTTACAA	TTTACGTTT	AGAATGTTTA	AGGTTAAGAA	4260
80	AGAAATAGTC	AATATGCTTG	TATAAAACAC	TGTTCACTGT	TTTTTTTAAA	AAAAAACTT	4320
	GATTTGTTAT	TAACATTGAT	CTGCTGACAA	AACCTGGGAA	TTTGGGTTGT	GTATGCGAAT	4380
	GTTCAGTGC	CTCAGACAAA	TGTGTATTTA	ACTTATGTAA	AAGATAAGTC	TGGAATAAAA	4440
	TGTCGTTTAA	TTTTGTACT	ATTTA				

Seq ID NO: 32 Protein sequence
Protein Accession #: NP_000954

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MLARALLCA VLALSHATNP CCSHPCQNRG VCMSSVGFDQY KDCDTRTGFY GENCSSTPEFL 60
      TRIKLFLEKPT PNTVHYILTH FKGFVNWVNM IPFLRNAIMS YVLTSRSHLI DSPPTYNADY 120
      GYKSWAEAFSN LSYVTRALPP VPDDCPTPLG VKGKKQLPDS NEIVEKLLLR RKFIIDPPQGS 180
10     NMMFAFFAQH FTHQFFKTDH KRGPATFNGL GHGVDLNHIY GETLARQRKL RLFKDGKMKY 240
      QIIDGEMVFP TVKDTQAEMI YPPQVPEHLR FAVGQEVFGL VPGLMMYATI WLREHNRVCD 300
      VLKQEHPEWG DEQLPQTSRL ILIGETIKIV IEDYVQHLGS YHFKLKFDPE LLFNKQFQYQ 360
      NRIAAEFNTL YHWHPLLPDT FQIHDQKYNQ QQFIYNNISIL LEHGITQFVE SFTRQIAGRV 420
      AGGRNVPPAV QKVSQASIDQ SRQMKYQSFN EYRKRFLMKP YESFEELTGE KEMSAELEAL 480
15     YGDI DAVELY PALLVEKPRP DAIFGETMVE VGAPPSLKGL MGNVICSPAY WKPSTFGGEV 540
      GFQIINTASI QSLICNNVKG CPFTSFSVPD PELIKTVTIN ASSRSRGLDD INPTVLLKER 600
      STEL

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Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: NM_001508.1
Coding sequence: 1..1361

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20     1      11      21      31      41      51
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      CCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGTA CCTGATCATC 120
      TTCTGATGG GCCTTCTGGG GAACAGCGTC ACCATTCCGG TCACCCAGGT GCTGCAGAAG 180
      AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC 240
      TTGGTGTTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTTGACC 300
      ACGTCCAGCT ACACCTGTCT CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
30     GCTACGCTGC TGCACGTGCT GACGCTCAGC TTGAGCGCT ACATCGCCAT CTGTCAACCC 420
      TTCAGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
      GTCACCTCCG CCTTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTTG 540
      GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG 600
      CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660
35     CAGTCCAGCA TCTTCGGCGC CTTCTGGTGC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720
      ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 780
      ACGCGGCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCCG CAGGAGGCAG 840
      ACCATCATCT TCTCTGAGGT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCCAG 900
      ATTCGGAGGA TCATGGCTGC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTCCCG 960
40     GCGTACATGA TCCTCTCTCC CTTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCAACAAC 1020
      CCGCTCCTGT ACACGCTGTC CTGCGAGCAG TTTCGGCGGG TGTTCTGTGA GGTGCTGTGC 1080
      TGCCGCTGTG CGCTGCAGCA CGCCAACCC GAGAAGCGCC TGGCGGTACA TGGCACTCC 1140
      ACCACCGACA GCGCCGCTT TGTGCAGCGC CCGTTGCTCT TCGCTCCCG GCGCCAGTCC 1200
      TCTGCAAGGA GAAGTGAAG GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
45     TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGCGCG GAAACAGGCC 1320
      AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

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Seq ID NO: 34 Protein sequence
Protein Accession #: NP_001499.1

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50     1      11      21      31      41      51
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      MASPSLPDSD CSQIIDHSHV PEFVATWIK ITLILVYLII FVMGLLNSV TIRVTQVLQK 60
      KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120
55     ATLLHLVTLF FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL 180
      VNVPSHRLGT CNRSSTRHHE QPETSNMISIC TNLSSRWTVF QSSIFGAFVY YLVVLLSVAF 240
      MCWMMQVLM KSKQKSLAGG TRPPQLRKSE SEESRTARRQ TIIIFLRILIV TLAVCWMPNQ 300
      IRRIMAAAKP KHDWTRSYFR AYMILLFPSE TFFYLSSVIN PLYTVSSQQ FRRVFVQVLC 360
60     CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARTEKIFL STFQSEABPQ 420
      SKSQSLSLES LEPNSGAKPA NSAAENGFOE HEV

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Seq ID NO: 35 DNA sequence
Nucleic Acid Accession #: NM_006475.1
Coding sequence: 28..2538

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      TTGCTGCTTA TTGTTAAACC TATAAACGCC AACAAATCATT ATGACAAGAT CTGGGCTCAT 120
70     AGTCGTATCA GGGGTCGGGA CCAAGGCCCA AATGTCTGTG CCCTTCAACA GATTTTGGGC 180
      ACCAAAAAGA AATACTTCAG CACTGTGAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
      AAAACGACTG TTTTATATGA ATGTTGCCCT GGTATATAGA GAATGGAAGG AATGAAAGGC 300
      TGCCAGCAGC TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC 360
75     ACAACGCAGC GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC 420
      TTCATTACT TTGACCCGAG TAATGAGGCT TGGGCAACT TGGATTCTGA TATCGGTAGA 480
      GGTTTGGAGA GCAACGTGAA TGTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
      AAGAGAATGT TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCCTTCAAT GTATAACAAT 600
      TTGGGGCTTT TCATTAAACA TTATCCTAAT GGGGTGTGCA CTGTTAATTG TGCTCGAATC 660
80     ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGTCCATG TCATTGACCG TGTGCTTACA 720
      CAAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
      GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGA GAGACGGTCA CTTCACTC 840
      TTTGTGCCA CCAATGAGGC TTTTGAGAAA CTTCCACGAG GTGTCCTAGA AAGGTTTCATG 900
      GGAGACAAAG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
      TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020

```

5 GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT 1080
 GTGACAAATA ATGGTGTGAT CCATTTGATT GATCAGGTCC TAATTCCTGA TTCTGCCAAA 1140
 CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGCCCAATTA 1200
 GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACC TGTGAATAAT 1260
 GCATTTCTCG ATGATACTCT CAGCATGGTT CAGCGCTCC TTAATAATAT TCTGCAGAA 1320
 CACATATTGA AAGTAAAGT TGGCCTTAAT GAGCTTTACA ACGGGCAAAT ACTGGAAACC 1380
 ATCGGAGGCA AACAGCTCAG AGTCTTCGTA TATCGTACAG CTGTCTGCAT TGAAAAATTC 1440
 10 TGCATGGAGA AAGGGAGTAA GCAAGGGAGA AACGGTGCAG TTCACATATT CCGCGAGATC 1500
 ATCAAGCCAG CAGAGAAATC CCTCCATGAA AAGTTAAAC AAGATAAGCG CTTTAGCACC 1560
 TTCTCTCAGC TACTTGAAGC TGCAGACTTG AAAGAGCTCC TGACACAACC TGGAGACTGG 1620
 ACATTATTGG TGCCAAACCA TGATGCTTTT AAGGGAATGA CTAGTGAAGA AAAAGAAATT 1680
 CTGATACGGG AAAAAAATGC TCTTCAAAAC ATCATTCTTT ATCACCTGAC ACCAGGAGTT 1740
 TTCAATTGGA AAGGATTTGA ACCTGGTGT ACTAACATT TAAAGACCAC ACAAGGAAGC 1800
 15 AAAATCTTTC TGAAGAAGT AARTGATACA CTTCTGGTGA ATGAATTGAA ATCAAAGAA 1860
 TCTGACATCA TGACAAACAA TGGTGTAATT CATGTTGTAG ATAACTCCT CTATCCAGCA 1920
 GACACACCTG TCGAAATGA TCAACTGCTG GAAATACTTA ATAAATTAAT CAAATACATC 1980
 CAAATTAAAT TGTTCGTGG TAGCACCTTC AAAGAAATCC CCGTGACTGT CTATACAACT 2040
 AAAATTATAA CCAAAGTTGT GGAACCAAAA ATTAAAGTGA TTGAAGCAG TCTTCAGCCT 2100
 ATTATCAAAA CTGAAGGACC CACACTAACA AAAGTCAAAA TTGAAGGTGA ACCTGAATT 2160
 20 AGACTGATTA AAGAAGGTGA AACAATAACT GAAGTGATCC ATGGAGAGCC AATTATTAAA 2220
 AAATACACCA AAATCATTTA TGGAGTGCTT GTGAAATAA CTGAAAAAGA GACACGAGAA 2280
 GAACGAATCA TTACAGGTCC TGAATAAAA TACACTAGGA TTTCTACTGG AGGTGGAGAA 2340
 ACAGAAGAAA CTCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTCAC CAAATTCTAT 2400
 GAAGGTGGTG ATGGTCATT ATTGAAGAT GAAGAAATTA AAAGACTGCT TCAGGGAGAC 2460
 25 ACACCCGTGA GGAAGTTGCA AGCCAACAAA AAAGTTCAAG GTTCTAGAAG ACGATTAAAG 2520
 GAAGGTCGTT CTCAGTGAAA ATCCAAAAAC CAGAAAAAAA TGTTTATACA ACCCTAAGTC 2580
 AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT TCAGGAACCTG AAACATCAGC 2640
 ACAAGAAGC AATCATCAAA TAATTCTGAA CACAAATTTA ATATTTTTTT TTCTGAATGA 2700
 GAAACATGAG GGAATTTGTG GAGTTAGCCT CCGTGGTAA AGGAAATTGA GAAATATAA 2760
 30 CACCTTACAC CCTTTTTCAT CTTGACATTA AAAGTTCTGG CTAACCTTGG AATCCATTAG 2820
 AGAAAAATCC TTGTCAACCAG ATTCATTACA ATTCAAATCG AAGAGTTGTG AACTGTTATC 2880
 CCATTGAAAA GACCGAGCCT TGTATGTATG TTATGGATAC ATAAATGCA CGCAAGCCAT 2940
 TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA 3000
 TCAAAAGGCT TTGCACATTT CTATATGAGT GGGTTTACTG GTAAATTATG TTATTTTTTA 3060
 35 CAACTAATTT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTAA 3120
 TCTCAACGTT TCAATATAAA CCATTTTTCG GATATAAAGA GAATTACTTC AAATTGAGTA 3180
 ATTCAGAAAA ACTCAAGATT TAAGTTAAAA AGTGGTTTGG ACTTGGGAA

Seq ID NO: 36 Protein sequence
 Protein Accession #: NP_006466.1

1 11 21 31 41 51
 | | | | |
 45 MIPFLPMFSL LLLLVNPNIN ANHYDKILA HSRIRGRDQG PNVCALQQIL GTKKKYFSTC 60
 KNWYKKSICG QKTTVLYECC PGYMRMEGMK GCPAVLPIDH VYGTGLGIVGA TTTQRYSDAS 120
 KLREEIEGKG SFTYFAPSNE AWDNLDSIR RGLSNVNVE LLNALHSHMI NKRMLTKDLK 180
 NGMIIPSMYN NLGLFINHPY NGVVTVNCAR IIHGNQIATN GVVHVIVDRVL TQIGTSIQDF 240
 IEAEDDLSSN RAAAITSDIL EALGRDGHFT LFPATNEAFE KLPRGVLERF MGDKVASEAL 300
 50 MKYHILNTLQ CSESIMGGAV FETLEGNTIE IGCDDGSITV NGIKMVNKKD IVTNNGVIHL 360
 IDQVLIPDSA GTVIELAGCK QTTPTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLMS 420
 VQRLKLILQ NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG 480
 RNGAIHIFRE IIKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTQPGD WTLFVPTNDA 540
 FKGMTSEEKE ILIRDKNALQ NIIYLHLPFG VFIKGFEPG VTNIILKTTQG SKIFLKEVND 600
 55 TLLVNLKSK ESDIMTTNGV IHVVDKLLYP ADTPVGNQDL LEILNKLKLY IQIKFVRGST 660
 FKEIPVTYVT TKIITKVVEP KIKVIEGSLQ PIKTEGPTL TKVKIEGEPE FRLIKEGETI 720
 TEVIHGEPII KKYTKIIDGV PVEITEKETR EERIITGPEI KYTRISTGGG ETEETLKKLL 780
 QEEVTKVTKF IEGGDGHLFE DBEIKRLLQG DTPVRKLQAN KKVQGSRRRL REGRSQ

Seq ID NO: 37 DNA sequence
 Nucleic Acid Accession #: NM_002416
 Coding sequence: 40..417

1 11 21 31 41 51
 | | | | |
 65 ATCCAATACA GGAGTGACTT GGAATCCAT TCTATCACTA TGAAGAAAAG TGGTGTCTT 60
 TTCCTCTTGG GCATCATCTT GCTGGTTCTG ATTGGAGTGC AAGGAACCCC AGTAGTGAGA 120
 AAGGGTCGCT GTTCTGTCAT CAGCACCAAC CAAGGAGCTA TCCACCTACA ATCCTTGAAA 180
 GACCTTAAAC AATTTGCCCC AAGCCCTTCC TCGAGAGAAA TTGAATCAT TGCTACACTG 240
 70 AAGAAATGAG TTCAAACATG TCTAAACCCA GATTGAGCAG ATGTGAAGGA ACTGATTAAA 300
 AAGTGGGATG AACAGGTGAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA 360
 AAGAAAGTTC TGAAGTTTCG AAAATCTCAA CGTTCTCGTC AAAAGAAAGAC TACATAAGAG 420
 ACCACTTCAC CAATAAGTAT TCTGTGTTAA AAATGTTCTA TTTTAATTAT ACCGCTATCA 480
 TTCCAAAGGA GGATGGCATA TAATACAAAG GCTTATTAAAT TTGACTAGAA AATTATAAAC 540
 75 ATTACTCTGA AATTGTAAGT AAAGTTAGAA AGTTGATTIT AAGAATCCAA ACGTTAAGAA 600
 TTGTTAAAGG CTATGATTGT CTTTGTCTT CTACACCCA CCAGTTGAAT TTCATCATGC 660
 TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTCACCCCA CCACATCCCA 720
 CTCAACACAG CTGCCCTGGA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCAGAGAG 780
 TATCTGAGGC ACATGTCAGC AAGTCCTAAG CCTGTTAGCA TGCTGGTGAG CCAAGCAGTT 840
 80 TGAATTTAG CTGACCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC 900
 CTACAGGCCT CACACACAAT GTGCTGAGG GATTGATGCT GATTGTTATT GGGTATCACC 960
 ACTGGAGATG ACCAGTGTGT GGCTTTTCAA GCCTCCTTTC TGGCTTTGGA AGCCATGTGA 1020
 TTCCATCTTG CCCGCTCAGG CTGACCACTT TATTTCTTTT TGTTCCTCTT TGCTTCATTC 1080
 AAGTCAGCTC TTCTCCATCC TACCACAAAG CAGTGCCTTT CTCTCTCTCA GTGCACCTGT 1140
 CATATGCTCT GATTTATCTG AGTCAACTCC TTTCTCATCT TGTCCCCAAC ACCCCACAGA 1200

5 AGTGCTTTCT TCTCCCAATT CATCCTCACT CAGTCCAGCT TAGTTCAGT CCTGCCTCTT 1260
 AAATAAACCT TTTTGGACAC ACAAAATTATC TTAAACTCC TGTTCACCTT GGTTCACTAC 1320
 CACATGGGTG AACACTCAAT GGTTAACTAA TTCTGGGTG TTTATCCTAT CTCTCCAACC 1380
 AGATTGTGAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC 1440
 CTAATAAATC TGTGGAACCTA GGTTTAAATA ATTTTAAAT TGATGTTGTT ATGGGCAGGA 1500
 TGGCAACCAG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560
 CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT 1620
 GATGCAACAT CCTTGTCTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680
 10 GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
 AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTC 1800
 CCAACCATAC AAAAAATCCCT TTTCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860
 TCTAAGATCT AACAAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAAATAG 1920
 AGTTTTATTG TCCGTTTACT TGTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980
 15 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040
 TAGTGGAAAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAAACC TCCTTCCAGG 2100
 GGAGGTTTCA TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160
 CTTTCCCAAA TTGAATCACT GCTCACTG CTGATGATT AGAGTGCTGT CCGGTGGAGA 2220
 TCCCACCGA ACGTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
 20 AAAAACTTAA GTGTTTCATA AATTTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
 GTAGACAGTA TATAACTAAC AACCAAGAC TACATATTGT CACTGACACA CACGTTATAA 2400
 TCATTTATCA TATATATACA TACATGCATA CACTCTCAA GCAAATAATT TTTCACTTCA 2460
 AAACAGTATT GACTTGTATA CCTTGTAAAT TGAAATATTT TCTTTGTTAA AATAGAATGG 2520
 TATCAATAAA TAGACCATTA ATCAG

Seq ID NO: 38 Protein sequence
 Protein Accession #: NP_002407

30 1 11 21 31 41 51
 MKKSGVFLFL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60
 IEIIATLKNQ VQTCNLNPSA DVKELIKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQRSR 120
 QKKT

Seq ID NO: 39 DNA sequence
 Nucleic Acid Accession #: NM_006670
 Coding sequence: 85..1347

40 1 11 21 31 41 51
 CCGGCTCGCG CCCTCCGGGC CCAGCCTCCC GAGCCTTCGG AGCGGGCGCC GTCCAGCCCC 60
 AGCTCCGGGG AAACGCGAGC CGCGATGCCT GGGGGGTGCT CCCGGGGCCC CGCCGCCGGG 120
 GACGGGGGTC TGGCGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCTCGTCT 180
 TCTCCACCT CCTCGGCATC CTCCTTCTCC TCCTCGGCGC CGTTCCTGGC TTCGCCGTG 240
 45 TCCGCCAGC CCCCGCTGCC GGACCACTGC CCGCGCTGT GCGAGTGCTC CGAGGCAGCG 300
 CGCACAGTCA AGTGCCTTAA CCGCAATCTG ACCGAGGTGC CCACGGACCT GCCCGCTAC 360
 GTGCGCAACC TCTTCTTAC CGGCAACCAG CTGGCCGTGC TCCTTGCCTG CGCCTTCGCC 420
 CGCCGGCCGC GCTGGCGGA GCTGGCCGCG CTCAACCTCA GCGGCGCCG CCTGGACGAG 480
 GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC 540
 50 CCCTGCGCG ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTGGGCCCCC 600
 AGTCCCTTGT TGGAACTGAT CCTGAACCAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660
 CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGCGCG GCCGTGCACT GCAGGGGCTC 720
 CGCGCCTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA 780
 CTGCCAGCC TCAGGCACCT GGACTTAAGT AATAATTGCG TGGTGAGCCT GACCTACGTG 840
 55 TCCTTCGCA ACCTGACACA TCTAGAAAGC CTCACCTGG AGGACAATGC CCTCAAGGTC 900
 CTTCAAAATG GCACCTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGCT TTTCTGGAC 960
 AACAAATCCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
 GAGGTAGTGC AGGGCAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
 GTCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG 1140
 60 CAAACCTCTT ATGCTTCTCT GGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200
 GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC 1260
 AGGGATCACA TGGAGGGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAAAC 1320
 AACCTCAGTT CTAACCTCGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACCTCG 1380
 CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
 65 TAGATACAAC GGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCTTGT TTATGTAAAG 1500
 TTTCTCGGTG TGTTCGTGTA ATGTAAGACG ATGAACAGTT GTGTATAGTG TTTTACCCTC 1560
 TTCTTTTCT TGGAACTCCT CAACACGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA 1620
 TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
 ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTCGAG AAAAATACTT TATTCATAAA 1740
 70 TATCAGTTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAAA AATTGCATCC TATAAACTGC 1800
 CTGCAGACGT TAGCAGGCTC TTCAAATAAA CTCCATGGTG CACAGGAGCA CCTGCATCCA 1860
 AGAGCATGCT TACATTTTAC TGTCTGTCAT ATTACAAAAA ATAACCTTGA ACTTCATAAC 1920
 TTCTTTGACA AAGTAAATTA CTTTTTGTAT TGCAGTTTAT ATGAAATGT ACTGATTTT 1980
 TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040
 ATTCTAAAAA GAA

Seq ID NO: 40 Protein sequence
 Protein Accession #: NP_006661

80 1 11 21 31 41 51
 MPGGCSRGA AGDGRRLRLR LALVLLGWVS SSSPTSSASS FSSSAFFLAS AVSAQPPLPD 60
 QCPALCECSE AARTVKCVNR NLTEVPTDLF AYVRNLPLTG NQLAVLPAGA FARRPPLAEL 120
 AALNLSGSR LDEVRAFAFEH LPSLRQLDLS HNPLADLSPF AFSGSNASVS APSPLVELIL 180
 NHIVPPEDER QNRSFEGMVV AALLAGRALQ GLRRLELASN HFLYLPRDVL AQLPSLRHLD 240

LSNNSLVSLT YVSRNLTHL ESHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWVDCD 300
 HMADMVTLWK ETEVVOGKDR LTCAYPEKMR NRVLLELNSA DLDCEPILPP SLQTSYVFLG 360
 IVLALIGAIF LLVLVLYLNRKG IKKWMHNIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

Seq ID NO: 41 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..927

1 11 21 31 41 51
 | | | | | |
 ATGCGTGGGG GGTGCTCCCG GGGCCCCGCC GCCGGGGACG GGCCTCTGCG GCTGGCGCGA 60
 CTAGCGCTGG TACTCTCTGG CTGGGTCTCC TCGTCTTCTC CCACCTCTCT GGCATCCTCC 120
 TTCTCCTCCT CGGCGCCGTT CCTGGCTTCC GCCGTGTCCG CCCAGCCCCC GCTGCCGGAC 180
 CAGTGCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240
 AATCTGACCG AGGTGCCACG GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300
 AACCAAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCC 360
 AGCCTCAGGC ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCCTGACCTA CGTGTCTCTC 420
 CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTCTCAC 480
 AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCCACATTA GGGTTTTCTT GGACAACAAT 540
 CCCTGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600
 GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAA AAATGAGGAA TCGGGTCTCT 660
 TTGGAACCTA ACAGTGCTGA CTGGAAGTGT GACCCGATTG TCCCCCATC CTGCAAAACC 720
 TCTTATGTCT TCCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCTT CCTGGTTTTG 780
 TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840
 CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900
 AGTTCTAACT CGGATGTCTT CGAGTGA

Seq ID NO: 42 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | | |
 MPGGCSRGA AGDGRLLRL LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD 60
 QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLELTG NQLASNHFLY LPRDVLAQLP 120
 SLRHLDSLNN SLVSLTYVSF RNLTHLESLH LEDNALKVLH NGTLAELQGL PHIRVFLDNN 180
 PWVCDCHMAD MVTWLKETEV VQKDRILTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT 240
 SYVFLGIVLA LIGAIPLVLV YLNRKGIKKW MHNIRDACRD HMEGYHYRYE INADPRLTNL 300
 SSNSDVLE

Seq ID NO: 43 DNA sequence
 Nucleic Acid Accession #: NM_058173
 Coding sequence: 68..340

1 11 21 31 41 51
 | | | | | |
 AGCGCCTTGC CTCTCTTAG GCCTTGAAGC ATTTTGTCT GTGCTCCCTG ATCTTCAGGT 60
 CACCACCATG AAGTCTTAG CAGTCTGGT ACTCTTGGGA GTTTCATCTT TTCTGGTCTC 120
 TGCCCAGAAT CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCTGTCTGA 180
 TGATGAAGCC CCGTATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC 240
 TACCACTGCA ACCACCGCTG CTCTACCAC TGCTCGTAAA GACATTCCAG TTTTACCRAA 300
 ATGGGTGGG GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAGTCT 360
 TCTGCAATTG GGTCACAACT ATTCATGCTT CCGTGTGATT CATCCAACCTA CTTACCTTGC 420
 CTACGATATC CCCTTTATCT CTAATCAGTT TATTTTCTTT CAAATAAAAA ATAACATATGA 480
 GCGAGCTAAC AT

Seq ID NO: 44 Protein sequence
 Protein Accession #: NP_477521

1 11 21 31 41 51
 | | | | | |
 MKFLAVLVLL GVSIFLVSAQ NPTTAAPADT YPATGPADDE APDAETATAA TTATTAAPT 60
 ATTAASTTAR KDIPVLPKWV GDLPNRVCV

Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_000095.1
 Coding sequence: 26..2299

1 11 21 31 41 51
 | | | | | |
 CAGCACCCAG CTCCTCCGCC CCGCATGGT CCGGACACC GCCTGCGTTC TTCTGCTCAC 60
 CCTGGCTGCC CTCGGCGCGT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC 120
 GCAGATGCTT CGGGAACATG AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180
 GCGGCAGCAG GTCAGGGAGA TCACGTTCTT GAAAAACACG GTGATGGAGT GTGACGCGTG 240
 CGGATGACAG CAGTCAAGTAC GCACCGGCTT ACCAGCGGTG CGGCCCCGTC TCCACTGCGC 300
 GCCCGGCTTC TGCTTCCCGG GCGTGGCTTG CATCCAGACG GAGAGCGGCG GCCGCTGCGG 360
 CCGCTGCCCG GCGGCTTCA CCGGCAACGG CTCGCACTGC ACCGACGTC ACGAGTGCAA 420
 CGCCACCCCC TGCTTCCCCG GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA 480
 GGCTTGCCCC CCGGGGTACA GCGGCCCCAC CCACCAGGGC GTGGGGCTGG CTTTCGCCAA 540
 GGCCAACAAG CAGTTTGTGA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAACCTGCT 600
 CCCCAACTCC GTGTGCATCA ACACCCGGGG CTCCTTCCAG TGCGGCCCCG GCCAGCCCGG 660
 CTTCGTGGGC GACCAGGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCGACGG 720
 CTCGCCAGC GAGTGCCACG AGCATGCAGA CTGCGTCTTA GAGCGCGATG GCTCGCGGTC 780
 GTGCGTGTGT CGCGTTGCTT GGGCCGGCAA CCGGATCCTC TGTGGTCGCG ACCTGACCT 840
 AGACGGCTTC CCGACGAGA AGCTGCGCTG CCGGAGCCG CAGTGCCGTA AGGACAACCT 900

CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCCTG 960
 CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAAG GACAACCTGCC CGCTGGTGCG 1020
 GAACCCAGAC CAGCGCAACA CCGACGAGGA CAAGTGGGGC GATGCGTGCG ACAACTGCCG 1080
 GTCCCAAGAG AACGACGACC AAAGAGACAC AGACCAGGAC GGCCGGGGCG ATGCGTGCGA 1140
 5 CGACGACATC GACGCGGACC GGAATCCGCA CCAGGCCGAC AACTGCCCTA GGTACCCAA 1200
 CTCAGACCAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA 1260
 GAAGAGCAAC CCGGATCAGG CCGATGTGGA CCACGACTTT TTGGGAGATG CTTGTGACAG 1320
 CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACCTGT CCACGGTGCC 1380
 10 TAACAGTGCC CAGGAGGACT CAGACCAGGA TGGCCAGGGT GATGCCTGCG ACACGACGGA 1440
 CGACAATGAC GGAGTCCCTG ACAGTCGGGA CAACTGCCCG CTGGTGCCCTA ACCCCGGCCA 1500
 GGAGGACGCG GACAGGGACG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
 GGTGGTAGAC AAGATCGACG TGTGTCCGGA GAACGCTGAA GTACACGCTCA CCGACTTCAG 1620
 GGCCTTCCAG ACAGTCGTGC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680
 15 GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT 1740
 GGGTTACACT GCCTTCAATG GCGTGGGACT CGAGGGCAGC TTCCATGTGA ACACGGTCAC 1800
 GGATGACGAC TATGCGGGT TCACTTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT 1860
 CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGCGGAAC CCCTTCCGTG CTGTGGCCGA 1920
 GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGCGGAA 1980
 20 CGCTCTGTGG CATAACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040
 AAACGTGGGT TGGAGGACA AGAAGTCCTA TCGTGTGGTTC CTGCAGCACC GGCCCCAAGT 2100
 GGGCTACATC AGGTGTGGAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
 CTTGGACACA ACCATGCGGG GTGGCCGCGT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
 CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
 25 TCAGCTGCGG CAAGCTAGG GACCAGGGTG AGGACCCGCC GGATGACAGC CACCTCACC 2340
 GCGGCTGGAT GGGGGCTCTG CACCAGCCC AAGGGGTGGC CGTCTGAGG GGAAGTGAG 2400
 AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGACGGG

Seq ID NO: 46 Protein sequence
 Protein Accession #: NP_000086.1

1 11 21 31 41 51
 | | | | |
 MVPDTACVLL LTLAALGASG QQSPLGSDL GPQMLRELQE TNAALQDVDR WLRQQVREIT 60
 35 FLKNTVMECD ACGMQSVRT GLPSVRPLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG 120
 NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
 INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH 240
 ADCVLERDGS RSCVCRVGWA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSGQ 300
 EDVDRDGIQD ACDPDAIDGDG VPNEKDNCPL VRNPDQRNTD EDKWDACDN CRSQKNDQDK 360
 40 DTDQDGRGDA CDDIDIDGRI RNQADNCPRV PNSDQKDSG DGIGDACDNC PQKSNPDQAD 420
 VDHDVFVGDA DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPS 480
 RDNCRVLPNP GQEDADRDGV GDVQCDDFDA DKVVDKIDVC PENAETVLT D FRAQTUVLLD 540
 PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600
 FGYQDSSSFY VVMWKQMEQT YWQANPFRV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT 660
 45 ESQVRLWLDK PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDLTMRG 720
 RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA

Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: NM_001565.1
 Coding sequence: 67..363

1 11 21 31 41 51
 | | | | |
 GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCAGTCTC 60
 55 AGCACCATGA ATCAAACTGC GATTCTGATT TGTCGCCTTA TCTTCTGAC TCTAAGTGGC 120
 ATTCAGGAGG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
 CCTGTTAATC CAAGGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
 CGTGTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
 TCGAAGGCCA TCAAGAATT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
 60 TAAACCAGGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
 CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTT TTAGTTTGCA 480
 GTTACTACTAA AAGGTGACCA ATGATGGTCA CCAAAATCAGC TGCTACTACT CCTGTAGGAA 540
 GGTAAATGTT CATCATCTTA AGCTATTTCAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
 GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTTCTGACC CTGCTTCAA TATTTCCTC 660
 65 ACCTTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTCTGCG TTTGGGGTTT ATCAGAATTC 720
 TCAGAATCTC AAATAACTAA AAGGTATGCA ATCAAACTCG CTTTTTAAAG AATGCTCTTT 780
 ACTTCATGGA CTTCCTCTGC CATCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840
 CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT 900
 CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT 960
 70 TTTCAAGTGA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
 TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
 TTTTCAAATA AAAATGAGGT ACTTCTCTGG AAATATTAAG

Seq ID NO: 48 Protein sequence
 Protein Accession #: NP_001556.1

1 11 21 31 41 51
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 MNQTAILICC LIFLTLSGIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV 60
 80 EIIATMKKKK EKRCINPESK AIKNLLKAVS KEMSKRSP

Seq ID NO: 49 DNA sequence
 Nucleic Acid Accession #: XM_057014
 Coding sequence: 143..874

1 11 21 31 41 51
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 5 CGTGCCCGG CAGCCGGGAG CCATGCGACC CCAGGCCCCC GCCGCCTCCC CGCAGCGGCT 180
 CCGCGCGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT 240
 CCCCAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
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 10 CATTCCGGGT ACACCTGGGA TCCCAGGTGCG GGATGGATTG AAAGGAGAAA AGGGGGAATG 420
 TCTGAGGGAA AGCTTTGAGG AGTCCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC 480
 ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
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 CTGTACGCGT TGGTATTTCA CATTCAATGG AGCTGAATGT TCAGGACCTC TCCCATTGA 660
 15 AGCTATAATT TATTGGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTTCATG 720
 CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGTG GGATTAGTGG ATGTTGCTAT 780
 CTGGGTTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
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 20 CATCTGAATG AAAAGCAAAG CTAATATATG TTACAGACCA AAGTGTGATT TCACACTGTT 1020
 TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCATAT TTTTTTTAGT 1080
 TGGTTAGAAT ACTTTCTTCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140
 GGTCCTTTGT TTTTCTCTCT AGTATAGCAT TTTTAAAAA ATATAAAAGC TACCAATCTT 1200
 TGTACAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
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Seq ID NO: 50 Protein sequence
 Protein Accession #: XP_057014

1 11 21 31 41 51
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 GVPGRDGPNG ANGIPGTPGI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
 GKIAECTFTK MRSNSALRLV FSGSLRLKCR NACCQRWYFT FNGAECSEPL PIEAIYLDQ 180
 35 GSPENNSTIN IHRITSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240
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Seq ID NO: 51 DNA sequence
 Nucleic Acid Accession #: NM_020974
 Coding sequence: 81..3080

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 CCGGTGCGGG CCGTGCCTGCG GGGCCGCGAGG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240
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 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAATGAGC 360
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 GCAAGGAGGG GTTTTTCTCT AGTGACAATC AGCACACCTG CATTCACCGC TCGGAAGAGG 600
 GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660
 GCAGCGTGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720
 55 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780
 GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840
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 60 ACCGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGTCCTGTT GGATTCACCTC 1020
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 65 CCCTGTATGG CTTACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320
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 ACTTTGATGG CTCCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGAGCTGG 2520

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 CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGGCTGGCT GAGCTGGACT 3360
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 TGTAGTGGAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACTTCAGC TTCCTCTAGC 3480
 CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGCAGG CTCTGACAGC GCAGAACAGG 3540
 CAAGAGGGGA GGGAGGGAGA CCCCTGCAGG CTCCTCCAC CCACCTTGAG ACCTGGGAGG 3600
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACITG 3660
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 AGCACTTCTG GAGACAT

Seq ID NO: 52 Protein sequence
 Protein Accession #: NP_066025

1 11 21 31 41 51
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 LGVAGRNRPG AAWAVLLLLL LLPLLLLLAG AVPPGRGRRA GPQEDVDECA QGLDDCHADA 60
 LCQNTPTSYK CSCKFGYQGE GRQCEDIDEC GNELNGGCVH DCLNIPGNR CTCFDGFMFLA 120
 HDGHNCLDVD ECLENNGGCG HTCVNMVMSY ECCCCKEGFPL SDNQHTCIHR SEEGLSMCMNK 180
 DHGCSHICKE APRGSVACBC RPFELAKNQ RDCILTCNHG NGGCQHSCHD TADGPECSCH 240
 PQYKMTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCRTCKDT 300
 STGVHCSCPV GFTLLQDQKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK 360
 SQQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCQVVCVN 420
 TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVS LH CGKSGGGDGC FLRCHSGIHL 480
 SSDVTITRTS VTFKLNEGKC SLKNAELFPE GLRPLALPEKH SSVKESFRYV NLTCSSGKQV 540
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600
 FHLQLSGMNL DVAKKPPRTS ERQAESCQVG QGHAENQCVS CRAGTYIDGA RERCILCPNG 660
 TFQNEEGQMT CEPCCPRPGNS GALKTPEAWN MSECGLCQFP GEYSADGFAP QQLCALGTFO 720
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHFY NTTTHRCIRC PVGTYPBEPG 780
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 PPPKRRLIV VPEIFLPIED DCGDYLVMRK TSSNSVTTYI ETCQTYERPI AFTSRSKLW 900
 IQFKSNEGNS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLIALKFDV 960
 LAHPQNYFKY TAQESREMF FRSFIRLLRSK VSRFLRPHY

Seq ID NO: 53 DNA sequence
 Nucleic Acid Accession #: NM_014211
 Coding sequence: 157..1479

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 CCTACTTCAG CCCTTGGTG TGAGCAGCTT CTCAACATGA ACTACAGCCT CCATCTGGCC 180
 TTCGTGTGTG TGAGTCTCTT CACTGAGAGG ATGTGCATCC AGGGGAGTCA GTTCAACGTC 240
 GAGGTGCGCA GAAGTGACAA GCTTTCCTTG CTTGGCTTTG AGAACCTCAC AGCAGGATAT 300
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 ATTGCAAGTA TCTCTAGCAT TTCAGAGAGT AACATGGACT ACACAGCCAC CATATACCCT 420
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 GCCCGCCTCG TGGAGTTCCT CTGGGTGCCA GATACTTACA TTGTGGAGTC CAAGAAGTCC 540
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 CTGTATGCCC TCAGAATCAC GACAACGTGT GCATGTAAAC TGGATCTGTC TAAATACCCC 660
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 GCCAATGTAT TTTACTGGG ATACTACATG TATTTTGGAG TCAATGTAA ATTCTTGCA 1500
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 TATGAGCCAA TCATATTGTT GATTTTTTAA AAAAAGTTTA AAAGGAAATA TCTGTTCTGA 3180
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Seq ID NO: 54 Protein sequence
 Protein Accession #: NP_055026

1 11 21 31 41 51
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 YIVESKSKSPL HEVTVGNRLI RLFSNGTVLY ALRITTTVAC NMDLSKYPMD TQTKQLQLES 180
 WGYDGNDFEF TWLRGNDVSF GLEHLRLAQY TIERYFTLVT RSQQETGNYT RLVLQFELRR 240
 NVLYFILETY VPSTFLVLVS WVSFWISLDS VPARTCIGVT TVLSMTTLM I GSRTSLPNTN 300
 CFKAIADVYL GICFSEVFGA LLEYAVAHYS SLQQMAAKDR GTTKEVEEVS ITNIINSSIS 360
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Seq ID NO: 55 DNA sequence
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Seq ID NO: 56 Protein sequence
 Protein Accession #: XP_084007

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Seq ID NO: 57 DNA sequence
 Nucleic Acid Accession #: NM_015419.1
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Seq ID NO: 58 Protein sequence
Protein Accession #: NP_056234.1

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	RLSTIRHLYL	AENMVRTLPA	SMLRNMPLLE	NLYLQGNPWT	CDCEMRWFLE	WDAKSRGILK	240
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	VRAQILAEPE	WVMQPSIDIQ	LNRRQSTAKK	VLLSYTYQYS	QTISTKDRTP	ARGRSWVMIE	480
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	SSADVPLLGE	EEHVLGTISS	ASMGLEHNHN	GVILVEPEVT	STPLEEVVDD	LSEKTEEITS	900
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	NPSRTAQPR	LQTDIPVTTT	GENLTDPPLL	KELEDVDFTS	EFLSSLTVST	PFHQEEAGSS	1440
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	PSIPSKFTDR	RTDQFNGYSK	VFGNNNIEPA	RNPVGKPPSP	RIPHYSNRGL	PPFTNKTLSP	1740
	PQLGVTRRRQ	IPTSAPVVMR	ERKVIKPSYN	RIHSHSTFHL	DFGPPAPPLL	HTPQTGSPS	1800
	TNLQNIPTMS	STQSSISFTI	SSVQSSGSFH	QSSSKFFAGG	PPASKFWSLG	EKPQILTKSP	1860
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	VFPNGTLYIR	NLAPKDSGRY	ECVAANLVGS	ARRTVQLNVQ	RAAANARITG	TSPRRTDVRY	2160
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	DGSLVNSFMQ	SDDSGGRTKY	YVVFNNGTLY	FNEVGMREBG	DYTCFAENQV	GKDEMVRVQD	2340
	VVTAPATIRN	KTYLAVQVFP	GDVTVVACEA	KGEPMKVTW	LSPTNKVIPT	SSEKYQIYVD	2400
	GTLILQKAQR	SDSGNYTCLV	RNSAGEDRKT	VWIHVNQVPP	KINGNFNPIT	TVREIAAGGS	2460
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Protein Accession #: Eos sequence

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 ATTTTATACC CACAAGAGAG GTATGCTACT CATCTTACTT CCCAGGACAT CCACCTGAG 2160
 AATAATTTGA CAAGCTTAAA AATGGCCTTC ATGTGAGTGC CAAATTTTGT TTTTCTTCAT 2220
 TTAATATTT TCTTTGCTCA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG 2280
 AAAGTTGAGT TCCACTCTG AATGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA 2340
 AAAAAGAAT TATTTGCAGC ATTTTATCAA CAAATTTTCT AATTGTGGAC AATTGGAGGC 2400
 ATTTATTTTA AAAACAAT TTATTGGCCT TTGCTAACA CAGTAAGCAT GTATTTTATA 2460
 AGGCATTCAA TAAATGCACA ACGCCCAAAG GAAATAAAT CCTATCTAAT CCTACTCTCC 2520
 ACTACACAGA GGTATCACT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580
 GCACTTATGA AATGATTTGA ACAAATAAAA CTAGGAACCT GTATACATGT GTTTCATAAC 2640
 CTGCTCTCTT TGCTTGGCCC TTTATTGAGA TAAGTTTTCC TGTCAAGAAA GCAGAAACCA 2700
 TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760
 TATTGGATAC TTAGGTGGTT TCTTCACTGA CAATCTGAA TAAACATCTC ACCGGAATTC

Seq ID NO: 64 Protein sequence
 Protein Accession #: NP_003005.1

1 11 21 31 41 51

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MPLSILVALC	LWLHLALGVR	GAPCEAVRIP	MCRHMPWNIT	RMPNHLHHST	QENAILAIEQ	60
YEELVDVNC	AVLRRFFCAM	YAPICTLEFL	HDPIKPCKSV	CQRARDCEP	LMKMYNHSWP	120
ESLACDELIV	YDRGVCISPE	AIVTDLPELV	KWIDITPDM	VQERPLDVDC	KRLSPDRCKC	180
KVKKPTLATY	LKKNYSYVIH	AKIKAVQRSG	CNEVTTVVDV	KEIFKSSSPI	PRTQVPLITN	240
SSCQCIPHILP	HQDVLIMCYE	WRSRMMLLEN	CLVEKWRDQL	SKRSIQWEER	LQEQRRIVQD	300
KKKTAGRTSR	SNPPKPKGKP	PAPKPASPKK	NIKTRSAQKR	TNPKRV		

Seq ID NO: 65 DNA sequence
 Nucleic Acid Accession #: BC010423
 Coding sequence: 248..1780

1
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CACAGCGTGG	GAAGCAGCTC	TGGGGGAGCT	CGGAGCTCCC	GATCACGGCT	TCTTGGGGGT	60
AGCTACGGCT	GGGTGTGTAG	AACGGGGCCG	GGGCTGGGGC	TGGGTCCCTT	AGTGGAGACC	120
CAAGTGCAGG	AGGCAAGAAG	TCTGCAGCTT	CCTGCCTTCT	GGGTCAAGTTC	CTTATTCAAG	180
CTGTGAGCCG	GCTCCAGGGG	AGATCTCGGT	GGAACCTTCAG	AAACGCTGGG	CAGTCTGCCT	240
TTCAACCATG	CCCCTGTCCC	TGGGAGCCGA	GATGTGGGGG	CCTGAGGCCT	GGCTGTCTGT	300
GCTGTACTGT	CTGGCATCAT	TTACAGGCCG	GTGCCCGCGG	GGTGAGCTGG	AGACCTCAGA	360
CGTGGTAAC	GTGGTGTCTG	GCCAGGACGC	AAAACCTGCC	TGCTTCTACC	GAGGGGACTC	420
CGGCGAGCAA	GTGGGGCAAG	TGGCATGGGC	TGGGTGGGAC	GCGGGCGAAG	GCGCCAGGA	480
ACTAGCGCTA	CTGCATCCCA	AATACGGGCT	TCACTGTAGC	CCGGCTTACG	AGGGCCCGCT	540
GGAGCAGCCG	CCGCCCCAC	GCAACCCCTT	GGACGGCTCA	GTGCTCCTGC	GCAACGCACT	600
GCAAGCGGAT	GAGGGCCGAG	ACGAGTGCCG	GGTCAGCACC	TTCCCGCCCG	GCACTTCCA	660
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ACTAGAAGAG	GGCCAGGGCC	TGACCTTGGC	AGCCTCCTGC	ACAGCTGAGG	GCAAGCCAGC	780
CCCCAGCGTG	ACCTGGGACA	CGGAGGTCAA	AGGCACAACG	TCCAGCCGTT	CCTTCAAGCA	840
CTCCCGCTCT	GCTGCGCTCA	CCTCAGAGTT	CCACTTGGTG	CCTAGCCGCA	GCATGAATGC	900
GCAGCCACTG	ACTTGTGTGG	TGTCCCATCC	TGGCTGTCTC	CAGGACCAAA	GGATCACCCA	960
CATCCTCCAC	GTGTCTTCC	TTGCTGAGGC	CTCTGTGAGG	GGCCTTGAAG	ACCAAAATCT	1020
GTGGCAGATT	GGCAGAGAAG	GAGCTATGCT	CAAGTGCTCT	AGTGAAGGGC	AGCCCCCTCC	1080
CTCATACAAC	TGGACACGGC	TGGATGGGCC	TCTGCCAGT	GGGTACGAG	TGGATGGGGA	1140
CACCTTGGCG	TTTCCCCAC	TGACCACTGA	GCACAGCGGC	ATCTACGCTC	GCCATGTCTC	1200
CAATGAGTTC	TCCTCAAGGG	ATTCTCAGGT	CACTGTGGAT	GTCTTGAACC	CCCAGGAAGA	1260
CTCTGGGAAG	CAGGTGTGAC	TAGTGTGAGC	CTCGGTGGTG	GTGGTGGGGT	TGATCGCCGC	1320
ACTCTTGTTC	TGCTTCTTGG	TGGTGGTGGT	GGTGTCTATG	TCCCGATACC	ATCGGCGCAA	1380
GGCCAGCAG	ATGACCCAGA	AATATGAGGA	GGAGCTGACC	CTGACCAAGG	AGAACTCCAT	1440
CCGGAGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CCGGAGGAGA	GTGTAGGGCT	1500
GAGAGCCGAG	GGCCACCTCG	ATAGTCTCAA	GGACAACAGT	AGTGCTCTGT	TGATGAGTGA	1560
AGAGCCCGAG	GGCCGCGAGT	ACTCCACGCT	GACCACGGTG	AGGAGATAG	AAACACAGAC	1620
TGAACTGCTG	TCTCCAGGCT	CTGGCGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCAT	1680
CAAAACAGCC	ATGAACCAAT	TTGTTCAGGA	GAATGGGACC	CTACGGGCCA	AGCCACGGGG	1740
CAATGGCATC	TACATCAATG	GGCGGGGACA	CCTGGTCTGA	CCCAGGCCTG	CCTCCCTTCC	1800
CTAGGCGCTG	CTCCTTCTGT	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GCCTCCTTAA	1860
ACACCCCATC	TTCTTGCGGA	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACCTCC	1920
AACCTTCTGT	TTCTATCGGA	GGGCTCCACC	AATTGAGTCT	CTCCACCAT	GCATGCAGGT	1980
CACCTGTGTG	GTGCTATGTT	GCCTGTGTGA	GTGTTGACTG	ACTGTGTGTG	TGTGGAGGGG	2040
TGACTGTCCG	TGGAGGGGTG	ACTGTGTCCG	TGGTGTGTAT	TATGCTGTCA	TATCAGAGTC	2100
AAGTGAAC	TGGTGTATGT	GCCACGGGAT	TTGAGTGGTT	GCGTGGGCAA	CACGTGCAGT	2160
GTTTGGCGTG	TGTGTCTATG	GGCTGTGTGT	GACCTCTGCC	TGAAAAGGCA	GGTATTTTCT	2220
CAGACCCAG	AGCAGTATTA	ATGATGCAGA	GGTTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
CAGACCCAG	TGTCCGGGCA	TAGCTGGAGC	TGGAATCTGC	CTCCGGTGTG	AGGGAACCTG	2340
TCTCTACAA	CTTGGAGGCC	ATGGGGGCAA	GTGTGAAGCA	GCCAGTCCCT	GGGTGAGCTA	2400
GAGGCTTGAA	CTGTAAACAGA	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGCATGT	2460
ACATATTTTC	TGTAAATATA	CATGCGCCGG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
ACTTTTAATT	TTTTTCTTTT	TTTTTCTTTG	CCCTTCTCAT	TAGTTGTATT	TTTTATTTAT	2580
TTTTATTTT	ATTTTCTTTT	AGAGTTTGAG	TCCAGCCTGG	ACGATATAGC	CAGACCTCTG	2640
CTGTAAAAAA	ACCAAAACCC	AAAAAATAAA	AAAAAATAAA			

Seq ID NO: 66 Protein sequence
 Protein Accession #: AAH10423

65
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MPLSLGAEMW	GPEAWLLLLL	LLASFTGRCP	AGELETSADV	TVVLGQDAKL	PCFYRGDSGE	60
QVQVAVARV	DAGEGAQELA	LLHSKYGLHV	SPAYEGRVEQ	PPPPRNPLDG	SVLLRNAVQA	120
DEGEYECRV	TFPAGSFQAR	LRLRLVLPPL	PSLNPGPALE	EGQGLTLAAS	CTAEGSPAPS	180
VTWDEVKGT	TSSRSFKHSR	SAAVTSEFHL	VPSRSMNGQP	LTCVVSHPLG	LQDQRITHIL	240
HVSFLAEASV	RGLEDQNLWH	IGREGAMLC	LSEGGPPPSY	NWTRLDGPLP	SGVRVDGDTL	300
GFPPLTTEHS	GIYVCHVSNE	FSSRDSQVT	DVLDPQEDSG	KQVDLVASV	VVVGIVIAALL	360
FCLLVVVVVL	MSRYHRRKAQ	QMTQKYEBEL	TLTRENSIRR	LHSHHTDPRS	QPEESVGLRA	420
EGHPDPLKDN	SSCSVMSEEP	EGRSYSTLT	VREIETQTEL	LSFGSGRAEE	EEDQDEGIKQ	480
AMNHVQENG	TLRAKPTGNG	IYINGRHLV				

Seq ID NO: 67 DNA sequence
 Nucleic Acid Accession #: NM_001203
 Coding sequence: 274..1782

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CGCGGGGCGC	GGAGTCGGCG	GGGCCTCGCG	GGACCGGGCG	AGTGGGAGA	CGCGGGCGCT	60
GAGGACGCGG	GAGCCGGGAG	CGCACGCGCG	GGGTGGAGTT	CAGCCTACTC	TTTCTTAGAT	120
GTGAAAGGAA	AGGAAGATCA	TTTCATGCC	TGTTGATAAA	GGTTCAGACT	TCTGCTGATT	180

CATAACCAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
 TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAATTA 300
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGG TCCAAAGGTC 360
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTGCTCTGT GGTCACTTCT 480
 GGTGCTCTAG GACTAGAAGG CTCAGATTTT CAGTGTCTGG ACCTCCCAT TCCTCATCAA 540
 AGAAGATCAA TTGAATGCTG CACGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600
 CTGCTCCCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660
 ATATCTGTGA CTGTCTGTAG TTTGCTCTGT GTCCCTATCA TATTATTTTG TTACTTCCGG 720
 TATAAAAGAC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780
 ATTCTCTCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
 TCAGGCTCC CTCTGCTGGT CCAAGGACT ATAGCTAAGC AGATTTCAGAT GGTGAAACAG 900
 ATTGGAAGAG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGGCGA AAAGGTAGCT 960
 GTGAAAGTGT TCTTACCAC AGAGGAAGCC AGCTGGTTC GAGAGACAGA AATATATCAG 1020
 ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080
 GGGTCTCTGA CCGAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
 TATCTGAAGT CCACACACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200
 AGTGGCTTAT GTCATTTACA CACGAAATC TTTAGTACTC AAGGCAACCC AGCAATTGCC 1260
 CATCGAGATC TGAAAGTAA AAAACATTCTG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320
 GACCTGGGCC TGGCTGTTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
 ACTCGAGTTG GCACCAACG CTATATGCCCT CCAGAAGTGT TGACGAGAG CTTGAACAGA 1440
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500
 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560
 CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620
 CGCCCTCAT TCCCAAAACG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAACTC 1680
 ATGACAGAA GCTGGGCTCA CAATCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740
 ACACCTGCCA AAATGTCAGA GTCCCAGGAC ATTAAACTCT GATAGGAGAG GAAAAGTAAG 1800
 CATCTCTGCA GAAAGCCAA AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860
 TAAGCATCCA CAGTCAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGT CAGACCTCAC 1920
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTTGTG GCGCGAGAAA CCGTTGGGTA ACTTGTTCAC GATATGATGC AT

Seq ID NO: 68 Protein sequence
 Protein Accession #: NP_001194

1 11 21 31 41 51
 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED 60
 DSGLPVVTSGLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120
 GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180
 EQSQSSGSGS GLPLLVQRTI AKQIQMVQKI GKGRYGEVWM GKWRGEKVAV KVFFTEEAS 240
 WPRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
 MLKLAYSSVS GLCHLHTEIF STQKGAIAH RDLKSKNIV KKNGTCCIA D LGLAVKFISD 360
 TNEVDIPPNT RVGTTRYMP EVLDESINRN HFQSYIMADM YSFGILLWEV ARRCVSGGIV 420
 EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSEPNRWSSD ECLRQMGKLM TECWAHPAS 480
 RLTAALRVKKT LAKMSESQDI KL

Seq ID NO: 69 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 166..1737

1 11 21 31 41 51
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 AGTGCAGTAG TGTGATCACT TCTTACTGCC GCCTCAAGCT TCCAGCTCA ACTCAAGCAA 120
 TCCTCCACAC TCAGCACCAC AAGTGGCTGG GACTACAGAT TAAGAATGAC CCAAAATAAA 180
 TTAAGACTTT GTTCCAAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240
 CCGGTAGCTG TTTCAATTTT CTTCTTCACT ACGGCATCAT CAAGACATTT 300
 GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360
 ATAATCTCAA TCTGTGTGTT TGTCTTAAAC TTTTCAGCTC CCCTCGCCAC AGTCCCTGAGC 420
 AATCGTTTCG GACACCGTCT GGTAGTGATG TTGGGGGGGC TACTTGTGCA CACCGGGATG 480
 GTGGCCGCTT CTTCTTACA AGAGGTTTCT CATATGTACG TCGCCATCGG CATCATCTCT 540
 GGTCTGGGAT ACTGCTTAG TTTTCTCCCA ACTGTAACCA TCCTATCACA ATATTTTGGC 600
 AAAAGACGTT CCATAGTCAC TGCAGTTGCT TCCACAGGAG AATGTTTCGC TGTGTTTGCT 660
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 GTGGGCTTAC TACAGTTAAA CATTGTATC TTCGGAGCAC TGCTCAGACC CATCTTTATC 780
 AGAGGACCAG CGTCACCGAA AATAGTCATC CAGGAAATC GGAAGAAGC GCAGTATATG 840
 CTTGAAAATG AGAAAACAG AACCTCAATA GACTCCATTG ACTCAGGAGT AGAACTAAT 900
 ACCTCACCTA AAAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCCGACATG 960
 CAGCAGGTCC TGGTGAAGAC CAGCCCCAGG CCAAGCGAAA AGAAAGCCCC GCTATTAGAC 1020
 TTCTCAATTT TGAAAGAGAA AAGTTTATTT TGTATGTCAT TATTGGTCT CTTTGAACA 1080
 CTGGGATTCT TTGCACCTTC CTTGTATATC ATTCTCTGG GCATTAGTCT GGGCATTGAC 1140
 CAGGACCGCG CTGCTTTTAT ATTATCTACG ATGGCCATTG CAGAAGTTT CGGAAGGATC 1200
 GGAGCTGGTT TTGTCTCTCA CAGGAGCCCC ATTCTGAAGA TTTACATTGA GTCATCTG 1260
 GTCATCTTAT TGACTGTGTC TCTGTTTGGC TTTACTTTTG CTACTGAATT CTGGGGTCTA 1320
 ATGTCATGCA GCATATTTT TGGGTTTATG GTTGAACAA TAGGAGGGAC TCACATTCCA 1380
 CTGCTTGCTG AGGATGATGT CGTGGGCATT GAGAAGATGT CTTCTGCAGC TGGGGTCTAC 1440
 ATCTTCATTC AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC 1500
 CAAAGTAAGA TCTACAGCAG GGCCTTCTAC TCTGCGCAG CTGGCATGGC CCGGCTGTCT 1560
 GTGTGCTCG CCCTGGTGAG ACCGTGTAA AGTGGACTGT GCCAGCATCA TCACTCAGGT 1620
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 GAAATGGATC TAGTCAAGAA TGAGCACAGA GTTCACGTGC AAAATGGAGCC GGTATGACAC 1740
 ACTTTCTTAC AACACAGCC ACTGTGTGG CTGGAGAGGG ATGGGGTGGG CCAACCGGG 1800
 ACACAGGAG GCAGAGGAGC TAACCCCTCT ACTCCACTTT CAAAATACA TTTTAAAGGG 1860

AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGTGT TGTTTTGTGT TGTTTTAAGC 1920
 TTTTGTGTGT TGTCTGTGTGT TAAAGCCAAA AAAAAAACA ACCAAGCACT CTCCATATA 1980
 TAAATCTGGC TGTATTCAGT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTCACA 2040
 TTCCGATATT AAAATAGTGA CATGAAGTGG CAAAGTGGTT TTTAAAGCTT TCACGTGGGA 2100
 TAAATGATT TCTTTTGTCT TTTTCTTTCT TCCTATGGTC TTGTCTGAAT AAACACTCT 2160
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Seq ID NO: 70 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 MTQNKLLKCS KANVYTEVPD GGWGWAVAVS FFFVEVFTYG IIKTFGVFFN DLMDSFNESN 60
 SRISWIISIC VFVLTFSAPL ATVLSNRFHG RLVVMLGGLL VSTGMVAASF SQEVSHMYVA 120
 IGIISGLGYC FSFLPTVTIL SQYFGKRRSI VTAVASTGEC FAVFAFAPAI MALKERIGWR 180
 YSLLFVGLLQ LNIIVFGALL RPIFIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240
 GVLELTSPKN VPHTHLELE PKADMQQVLV KTSRPPSEKK APLLDIFSILK EKSFCYALF 300
 GLFATLGGFA PSLYIIPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360
 IELICVILLT VSLFAFTFAT EFWGLMSCSI FFGFMVGTIG GTHIPLAED DVVGIEKMSS 420
 AAGVYIFIQS IAGLAGPFLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480
 HHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 71 DNA sequence
 Nucleic Acid Accession #: NM_004694
 Coding sequence: 166..1737

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 TCCTCCACAC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAATGAC CCAAAATAAA 180
 TTAAGAGCTTT GTTCCAAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240
 GCGGTAGCTG TTTTATTTTT CTTCTGTGAA GTCTTTCACCT ACGGCATCAT CAAGACATTT 300
 GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360
 ATAATCTCAA TCTGTGTGTT TGTCTTAACA TTTTCAGCTC CCCTCGCCAC AGTCTGAGC 420
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 GTGGCCGCCCT CCTTCTCACA AGAGGTTTCT CATATGTACG TCGCCATCGG CATCATCTCT 540
 GGTCTGGGAT ACTGCTTTAG TTTTCTCCCA ACTGTAACCA TCCTATCACA ATATTTTGGC 600
 AAAAGACGTT CCATAGTCAC TGCAGTTGCT TCCACAGGAG AATGTTTCGC TGTGTTTGCT 660
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 GTGGGCCCTAC TACAGTTAAA CATGTGCATC TTCGGAGCAC TGCTCAGACC CATCATTTATC 780
 AGAGGACCAG CGTACCACCA AATAGTCATC CAGGAAATC GGAAGAAGC GCAGTATATG 840
 CTTGAAAATG AGAAACACG AACCTCAATA GACTCCATTG ACTCAGGAGT AGAACTAACT 900
 ACCTCACCTA AAAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCCGACATG 960
 CAGCAGGTCC TGTGGAAGAC CAGCCCGAGG CCAAGCGAAA AGAAAGCCCC GTATTAGAC 1020
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 TGCTTGCTGA AGATGATGTC GTGGGCATTG CAGAAGATGT CTTCTGCAGC TGGGGTCTAC 1440
 ATCTTCATTG AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC 1500
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 GAAATGGATC TTGCAAAAAA TGAGCACAGA GTTCACGTGC AAATGGAGCC GGTATGACAC 1740
 ACTTTCTTAC AACACAGCC ACTGTGTTGG CTGGAGAGGG ATGGGGTGGG CCCAACGGGG 1800
 ACACAGGAGC GCAGAGGAGC TAACCCCTCT ACTCCACTTT CAAACTACA TTTTAAAGGG 1860
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 TTTTGTGTGT TGCTTGTGTT TAAAGCCAAA AAAAAAACA ACCAAGCACT CTCCATATA 1980
 TAAATCTGGC TGTATTCAGT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTCACA 2040
 TTCCGATATT AAAATAGTGA CATGAAGTGG CAAAGTGGTT TTTAAAGCTT TCACGTGGGA 2100
 TAAATGATT TCTTTTGTCT TTTTCTTTCT TCCTATGGTC TTGTCTGAAT AAACACTCT 2160
 CCTGAATAAA ACAACATCCA ACCCAGGTCA TTGAAATGAA ATTGCCAGT C

Seq ID NO: 72 Protein sequence
 Protein Accession #: NP_004685

1 11 21 31 41 51
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 SRISWIISIC VFVLTFSAPL ATVLSNRFHG RLVVMLGGLL VSTGMVAASF SQEVSHMYVA 120
 IGIISGLGYC FSFLPTVTIL SQYFGKRRSI VTAVASTGEC FAVFAFAPAI MALKERIGWR 180
 YSLLFVGLLQ LNIIVFGALL RPIIIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240
 GVLELTSPKN VPHTHLELE PKADMQQVLV KTSRPPSEKK APLLDIFSILK EKSFCYALF 300
 GLFATLGGFA PSLYIIPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360
 IELICVILLT VSLFAFTFAT EFWGLMSCSI FFGFMVGTIG GLTFHCLLM MSWALQKMSS 420
 AAGVYIFIQS IAGLAGPFLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480
 RHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 73 DNA sequence
 Nucleic Acid Accession #: NM_002184.1
 Coding sequence: 256..3012

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 AGACGCGGAG GGTGAGGCG GCGCGGCTCG AGTGAAACCC AATGGAAAAA GCATGACATT 180
 TAGAAGTAGA AGACTTAGCT TCAATCCCT ACTCCTTCC TACTAATTT TGTGATTTGG 240
 AAATATCCCG GCAAGATGTT GACGTTGCAG ACTTGGGTAG TGCAAGCCTT GTTTATTTC 300
 CTCACCACTG AATCTACAGG TGAACCTCTA GATCCATGTG GTTATATCAG TCCTGAATCT 360
 10 CAGGTGTGAC AACTTCATTC TAATTTCACT GCAGTTTGTG TGCTAAAGGA AAAATGTATG 420
 GATTATTTTC ATGTAATGTC TAATTACATT GTCTGGAAAA CAAACCATT TACTATTCT 480
 AAGGAGCAAT ATACTATCAT AAACAGAACA GCATCCAGTG TCACCTTTAC AGATATAGCT 540
 TCATTAAATA TTCAGCTCAC TTGCAACATT CTTACATTCG GACAGCTTGA ACAGAATGTT 600
 TATGGAATCA CAATAATTTC AGGCTTGCCCT CCAGAAAAAC CTAAAAATTT GAGTTGCATT 660
 15 GTGAACGAGG GGAAGAAAAAT GAGGTGTGAG TGGGATGGTG GAAGGGAAAC ACACCTGGAG 720
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Seq ID NO: 80 Protein sequence
 Protein Accession #: NP_057724.1

45 1 11 21 31 41 51
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Seq ID NO: 81 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..2070

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Seq ID NO: 82 Protein sequence
 Protein Accession #: FGENSEH predicted

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Seq ID NO: 84 Protein sequence
 Protein Accession #: NM_005264.1

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    YEPVNSRLSD IFRVVPFISD VFQQVEHIPK GNNCLDAAKA CNLDDICKKY RSAYITPCTT 180
    SVSNDV CNRR KCHKALRQFF DKVPAKHSYG MLFCSCRDIA CTERRRQTIV PVCSEEREK 240
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10 YIDSSSLVA PWDCSNSGN DLEECLKFLN FFKDNTCLKN AIQAFNGSD VTVWQPAFPV 360
    QTTTATTTTA LRVKNKPLGP AGSENEIPTH VLPPCANLQA QKLKSNVSGN THLCISNGNY 420
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Seq ID NO: 85 DNA sequence

Nucleic Acid Accession #: XM_027172.1

Coding sequence: 143..1405

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    TGAGAGCAGC CTCCATGAGG CCTCGGACCA GTGCATGACC GCCCTGGACC TCTTCTCAC 240
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30 GGACGAGAAC ATGGTGAGCT TCATCAAAGG CGGCATCAAA GTTCGAAACA GCTACCAGAC 720
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Seq ID NO: 86 Protein sequence
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	EVCYAECLLQ	RAALTFLQGS	SHGGAVRPRA	LHDPHSACSC	PPGPGRQHLF	LQDENMVSF	180
	IKGGIKVRNS	YQTYKELDSL	VQSSQYCKGE	NHPHFEGGVK	LGVAFNLTIL	SMLPTRLRL	240
50	LEFVGFSGNK	GTLLQLLEEG	ASGHSFRSVL	CVMLLLCYHT	FLTFVLGTGN	VNIEBAEKLL	300
	KPYLNRYPKG	ALFLFPAGRI	EVIKGNIDAV	SDGGPGRGWG	SLGVSQTSRK	SGTCDILRDR	360
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Seq ID NO: 87 DNA sequence
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	GTTGGCTTTG	GATTTCAGAG	GGATGGATTG	CAGTCCTAGC	TTGCCACTTA	TTAGGACTCC	180
	TGAGAGCAGC	CTCCATGAGG	CCCTGGACCA	GTGCATGACC	GCCCTGGACC	TCTTCCTCAC	240
	CAACCAGTTC	TCAGAAGCAC	TCAGCTACCT	CAAGCCGAGA	ACCAAGGAAA	GCATGTACCA	300
65	CTCACTGACA	TATGCCACCA	TCCTGGAGAT	GCAGGCCATG	ATGACCTTTG	ACCCTCAGGA	360
	CATCCTGCTT	GCCGGCAACA	TGATGAAGGA	GGCACAGATG	CTGTGTCAGA	GGCACCAGGAG	420
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	CACCTGAAGAG	GAAATCCACG	CTGAGGTCTG	CTATGCAGAG	TGCCTGCTGC	AGCGAGCAGC	540
	CCTGACCTTC	CTGCAGGGTT	CCTCACACGG	AGGGGCAGTC	AGGCCAGAG	CCTTGCAATGA	600
70	TCCCTCTCAC	GCCTGCAGCT	GCCCACCTGG	GCCAGGCCGT	CAGCATCTTT	TCTCCTCTGA	660
	GGACGAGAAC	ATGGTGAGCT	TCATCAAAGG	CGGCATCAAA	GTTGGAACA	GCTACCCAGAC	720
	CTACAAGGAG	CTGACAGGCC	TTGTTCAATC	CTCACAATAC	TGCAAGGGTG	AGAACCACCC	780
	GCACCTTGAA	GGAGGAGTGA	AGCTTGGTGT	AGGGGCCTTC	AACCTGACAC	TGTCCATGCT	840
	TCCTACTAGG	ATCCTGAGGC	TGTTGGAGTT	TGTGGGGTTT	TCAGGAAACA	AGGACTATGG	900
75	GCTGCTGAGC	CTGGAGGAGG	GAGCGTCAGG	GCACAGCTTC	CGCTCTGTGC	TCTGTGTCAT	960
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	CCTGTTCTTT	GCAGGGAGGA	TTGAAGTCAT	TAAAGGCAAC	ATTGATGCAG	TGAGTGATGG	1140
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80	ATGTGACATA	CTCAGGGACA	GGATAGACTG	GGGGCGGGGG	GGGGGGCCAA	GAGAGAACCA	1260
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	GGAGGAGAGT	GGAGGAGAGT	GCTTGAGGGA	GGCAGAGGTT	AGGAAAGCCC	ATCTGTTTAG	1440
	GGCATGACGA	TTAGGCTGGA	GTCTGGTACC	TCCCCTCCAT	TATAGCTCTC	TCCTGCTCTT	1500

5 TCATTTTGTGTT ACTAAAAACC AGAGTCCTAG GCGGGGGCTG TATTTGAGCC CAACGTCATG 1560
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 80 AGGCGGAGGT TGCAGTGAGC CGAGATCGCG CCATAGCACT CCAGCCTTAG CTTGGGCGAC 6240
 AGAGCGAGAC CACATC

Seq ID NO: 88 Protein sequence
 Protein Accession #: BAA32297.1

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    ILLAGNMMEK AQMLCQRHRR KSSVTSDFSS LVNRPTLGQF TEEBIHAEVC YAECLLQRAA 180
    LTFLLQSSSHG GAVRPRALHD PSHACSCPPG PGRQHLFLQ DENMVSFIKG GIKVRNSYQT 240
    YKELDSLVSQ S QYCKGENHP HFEGGVKLGV GAFNLTL SML PTRILRLLEF VGFSGNKDYG 300
    LLQLEEGASG HSFRSVLCVM LLLCYHTFLT FVLGTGNVNI EEAELKLPY LNRYPKGAIF 360
10  LFFAGRIEVI KGNIDAVSDG GPGRGWGSLG VSQTSRKSQT CDILRDRIDW GRGGGPRENQ 420
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Seq ID NO: 89 DNA sequence
 Nucleic Acid Accession #: AF007170
 Coding sequence: 73..1725

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    CTGGAGATGC AGGCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCACCATG 240
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    TTCAGCAGCC TGGTGAACCG CCCACGCTG GGCCAATTCA CTGAAGAAGA AATCCACGCT 360
25  GAGGTCTGCT ATGCAGAGTG CCTGCTGCAG CGAGCAGCCC TGACCTTCCT GCAGGACGAG 420
    AACATGGTGA GCTTCATCAA AGGCGGCATC AAAGTTCGAA ACAGCTACCA GACCTACAAG 480
    GAGCTGGACA GCCTTGTTCA GTCTCACA TACTGCAAGG GTGAGAACCA CCCGCACTTT 540
    GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCCTACT 600
    AGGATCTCTA GGCTGTGGGA GTTTGTGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660
30  CAGCTGGAGG AGGGAGCGTG AGGGCACAGC TTCCGCTCTG TGCTCTGTGT CATGCTCCTG 720
    CTGTGCTACC ACACCTTCCT CACCTTCGTG CTCGGTACTG GGAACGTCAA CATCGAGGAG 780
    GCCGAGAAGC TCTTGAAGCC CTACCTGAAC CGGTACCTTA AGGGTGCCAT CTTCTGTGTT 840
    TTTGCAGGGA GGATTTGAAG CATTAAAGGC AACATTGATG CAGCCATCCG GCGTTTCGAG 900
    GAGTGTCTGT AGGCCAGCA GCACCTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960
35  ATGTGGTGCT TCACCTACAA GGGCCAGTGG AAGATGTCCT ACTTCTACGC CGACCTGCTC 1020
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    GTGCCAGGCG TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200
    CGGAAGTCCC GGGCTACTT CTCTCCAA CCTATCTCGC TGCCAGTGCC TGCTCTGGAA 1260
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50  TGTATCCGCTG CAGAAGCCGA GCTGGCATT TCCAGTGT AGCCAAGGGC CTTTGCCAA 1920
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55  TCAGCAAGTT CTCAGCTTGT GTGACGGAAG GTCCTTCAGA GGACCTGAGG AATGCCTGGG 2220
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60  AAATTTGGGG GGCAGGAGA GGTCTCAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA 2520
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Seq ID NO: 90 Protein sequence
 Protein Accession #: AAC39582.1

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    EVCYAECLLQ RAALFQLQDE NMVSFIKGGI KVRNSYQTYK ELDSLVSQSSQ YCKGENHPHF 180
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    LCYHTFLFTV LGTGNVNIEE AEKLLKPYLN RYPKGAIPLF FAGRIEVIKG NIDAAIRFE 300
75  ECCEAQQHWK QFHHMCYWEI MWCFYKQGW KMSYFYADLL SKENCWSKAT YIYKMAAYLS 360
    MFGKEDHKPF GDDEVLFRA VPGLKLIAG KSLPTEKFAI RKSRRYFSSN PISLPVPALE 420
    MMYIWNQYAV IGKQPKLTDG ILEIITKABE MLEKGPENEY SVDDECLVKL LKGLCLKYLG 480
    RVQEAENFR SISANEKKIK YDHYLIPNAL LELALLLMEQ DRNEEAIKLL ESAKQNYKNY 540
    SMESRTHFRI QAATLQAKSS LENSRSRMSV SVSL

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Seq ID NO: 91 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 31..906

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	TCCCGCCAGC	CAATCTACAT	GAGTCTAGCA	GGCTGGACCT	GTCGGGACGA	CTGTAAGTAT	240
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	CATGGCAAGT	GGCCCTTCTC	CCGGTTCTCT	TTCTTTCAAG	AGCCGCGATC	GGCCGTGGCC	360
10	TCGTTTCTCA	ATGGCCTGGC	CAGCCTGGTG	ATGCTCTGCC	GCTACCGCAC	CTTCGTGCCA	420
	GCCTCTCTCC	CCATGTACCA	CACCTGTGTG	GCCTTCGCCT	GGGTGTCCCT	CAATGCATGG	480
	TTCTGGTCCA	CAGTYTTCCA	CACCAGGGAC	ACTGACCTCA	CAGAGAAAAA	GGACTACTTC	540
	TGTGCCTCCA	CTGTCACTCT	ACACTCAATC	TACCTGTGCT	GCGTCAGCCT	CATCCGCTTC	600
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20	CCCTTCTCCC	CTCAACCTTT	GAGATGATT	TCTCTTTTCA	ACTTCTTGAA	CTTGGACATG	1020
	AAGGATGTGG	GCCCAGAATC	ATGTGGCCAG	CCCACCCCTT	GTGGGCCCTC	ACCAGCCTTG	1080
	GAGTCTGTTC	TAGGGAAGGC	CTCCAGCAT	CTGGGACTCG	AGAGTGGGCA	GCCCTCTAC	1140
	CTCTCTGGAG	TGAAGTGGGG	TGGAAGTCTG	TGTGCTCTTA	GCTCTACCGG	GAGGACAGCT	1200
	GCCTGTCTTC	TCCCCTCAG	CCTCTCTCCC	ACATCCCCAG	CTGCCTGGCT	GGGTCTTGAA	1260
25	GCCCTCTGTC	TACCTGGGAG	ACCAGGGACC	ACAGGCCCTA	GGGATACAGG	GGGTCCCTTT	1320
	CTGTACACAC	CCCCACCTCT	CCTCCAGGAC	ACCACTAGGT	GGTGTCTGGT	GCTTGTCTCT	1380
	TGGCCAGCCA	AGGTTCTACGG	CGATTCTCCC	CATGGGATCT	TGAGGGACCA	AGCTGCTGGG	1440
	ATTGGGAAGG	AGTTTCAACC	TGACCRITGC	CCTAGCCAGG	TTCCCGAGAG	GCCTCACCAT	1500
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40	TTTGGGGAGG	AGGAAGGGGC	GATTTGAGGG	AGAAGGGGAG	AAAGCTTATG	GCTGGGTCTG	2220
	GTTTCTTCCC	TTCCAGAGGG	GTCTTACTGT	TCCAGGGTGG	CCCCAGGGCA	GGCAGGGGCC	2280
	ACACATATGCC	TGCGCCCTGG	TAAAGGTGAC	CCCTGCCATT	TACCAGCAGC	CCTGGCATGT	2340
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	TCCGTGGTTG	AAGCAGACTG	GATTTTGTCT	CTGCCCTTGA	CCCCCTTGTG	CTCTTTGAGG	2460
45	GAGGGGAGCT	ATGCTAGGAG	TCCAACCTCA	GGGACTCGGG	TGGCCTGCGC	TAGCTTCTTT	2520
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Seq ID NO: 92 Protein sequence
Protein Accession #: Eos sequence

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	MLCRYRTFVP	ASSPMYHTCV	AFANVSLNAW	FWSTVFHTRD	TDLTEKMDYF	CASTVILHSI	180
	YLCCVRTVGL	QHPAVVSFAF	ALLLLMLTVH	VSYLSLIRFD	YGYNLVANVA	IGLVNVVWWL	240
	AWCLWNQRR	PHVRKCVVVV	LLQLGLSLE	LLDFPPLFWV	LDHAIWHIS	TIPVHVLFFS	300
	FLEDDSLYLL	KESEDKFKLD					

Seq ID NO: 93 DNA sequence
Nucleic Acid Accession #: NM_033419.1
Coding sequence: 18..980

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	AGTGCGAAGA	GCAGAACTGC	TCTGGGGGCG	CTCTGAATCA	CTTCCGCTCC	CGCCAGCCAA	180
70	TCTACATGAG	TCTAGCAGGC	TGGACCTGTC	GGGACGACTG	TAAGTATGAG	TGTATGTGGG	240
	TCACCGTTGG	GCTCTACCTC	CAGGAAGGTC	ACAAAGTGCC	TCAGTTCCAT	GGCAAGTGGC	300
	CCTTCTCCCG	GTTCTGTTTC	TTTCAAGAGC	CGGCATCGGC	CGTGGCCTCG	TTTCTCAATG	360
	GCCTGGCCAG	CCTGGTGTATG	CTCTGCCGCT	ACCGCACCTT	CGTGCCAGCC	TCCTCCCCCA	420
	TGTACCACAC	CTGTGTGGCC	TTGCGCTGGG	TGTCCCTCAA	TGCATGGTTC	TGTTCCACAG	480
75	TTTTCCACAC	CAGGGACACT	GACCTCACAG	AGAAAATGGA	CTACTTCTGT	GCCTCCACTG	540
	TCATCCTTCA	CTCAATCTAC	CTGTGCTGCG	TCAGGACCGT	GGGGCTGCAG	CACCCAGCTG	600
	TGGTCAGTGC	CTTCGGGCTC	CTCCTGCTGC	TCATGCTGAC	CGTGCACGTC	TCCTACCTGA	660
	GCCTCATCCG	CTTCGACTAT	GGCTACAACC	TGGTGGCCAA	CGTGGCTATT	GGCCTGTGTC	720
	ACGTGGTGTG	GTGGCTGGCC	TGGTGCCTGT	GGAACACGCG	GCGGCTGCCT	CACGTGCGCA	780
80	AGTGCCTGGT	GGTGGTCTTG	CTGCTGCAGG	GGCTGTCCCT	GCTCGAGCTG	CTTGACTTCC	840
	CACGCTCTTT	CTGGGTCTCT	GATGCCCATG	CCATCTGGCA	CATCAGCACC	ATCCCTGTCC	900
	ACGTCTCTTT	TTTCAGCTTT	CTGGAAGATG	ACAGCCTGTA	CCTGCTGAAG	GAATCAGAGG	960
	ACAAGTTCAA	GCTGGACTGA	AGACCTTGGA	GCGAGTCTGC	CCCAGTGGGG	ATCCTGCCCC	1020
	CGCCTGCTG	GCCTCCCTTC	TCCCCTCAAC	CCTTGAGATG	ATTTTCTCTT	TTCAACTTCT	1080
	TGAACCTGGA	CATGAAGGAT	GTGGGCCAGG	AATCATGTGG	CCAGCCCAAC	CCCTGTTGGC	1140

5 CCTCACCAGC CTGGAGTCT GTTCTAGGGA AGGCCTCCCA GCATCTGGGA CTCGAGAGTG 1200
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 10 TGTGCTGCTG TCTGGTGTAG AGCCTGCCAC CGTGTGTGCG GAGTGTGGGC CAGGCTGAGT 1680
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 GGTGGGTGTG TTAGCTGGG TTAGGGGAAC GTGTGTGCGC GTGCTGGTGG GCATGTGAGA 1860
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 15 GTACCATCA ATAATCACTT GTGGAGCGCC AGCTCTGCC AAGGCGCCAC CTGGGCGGAC 1980
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 25 TCCCTCTTTG AGGGAGGGGA GCTATGCTAG GACTCCAACC TCAGGGACTC GGGTGGCCTG 2580
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 ATAAATCAAT TCCAAGCCTC AAAAAAAAAA AAAAAAAAAA AA

Seq ID NO: 94 Protein sequence
 Protein Accession #: NP_219487.1

30 1 11 21 31 41 51
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 35 LWPAPVHGDG PHGILRDQAA GIGKEFHDPD CPSQVPRRPH HTPFGQGSS KPRARILCCC 180
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Seq ID NO: 95 DNA sequence
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 45 TCCCTGGCAC AAGGCACAGG CTGCTCAGTG TGCTGGGAGG TGAACGGCCC AGGGTTGGAA 300
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 50 AACTCGCAG ATACTGACTG GGAACCTGAG GAGGACCAAG GAAGTCTAGA TTTCGCCGTG 420
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 55 CCGAGAGTAG ACGCGCCAGG CCGGCCCCC GGGCTGCGGA GCTCGGCAGC AGCCCTCAC 720
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 60 TGTGATCAAG AATCACCAGG TTCATTCCA ATAGGTTTAT GTAACAGAAC AGCTGAACCA 900
 TGTATCAAG GGGCTCTGGG TGTGGCTGCT GAAGCAGCAT TTCATTACA GTTTTCCAGT 960
 GAATGA

Seq ID NO: 96 Protein sequence
 Protein Accession #: XP_090469

65 1 11 21 31 41 51
 | | | | |
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 PPEVKMFGAS QGLLTMETNQ SLAQGTGCSV CWEVNGPGL MSLPGVLSAD AGQVEHRRQM 120
 70 NSADTDWTE EPGSLDFAV AAHQEDTFFL KDIKHTSTFR QSVQQNCIY SPREKPCGNV 180
 RAPCAPPRRE APLALSRPWR LSRSPAPSPR TPMAPPFTSD RELDAPGPPP GLRSSAAAPH 240
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 CIKALGVAA EAPFHLQFSS E

Seq ID NO: 97 DNA sequence
 Nucleic Acid Accession #: NM_003474.2
 Coding sequence: 37..3036

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 CTTTTTAAA AATGAAAGGC TAGAAGAGCT CAGCGCGCGC GCGGGCCGTG CGCGAGGGCT 180
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5 GCGACGATGG CAGCGCGCCC GCTGCCCCGTG TCCCCCGCCC GCGCCCTCCT GCTGCGCCTG 360
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 10 AGTGCACACA ACAGATACAA ACTCTTCCCA GCGAAGAAGC TGAAAGCGT CCGGGGATCA 840
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 15 ATCGTGTGG TAGGCGTGA AGTGTGGAAT GACATGGACA AATGCTCTGT AAGTCAGGAC 1140
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 40 CGTGGCTTCC AACCTGTCA GGCTCACCTC GGCCACCTTG GAAAAGGCC TATGAGGAAG 2640
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 80 AGATGCCCAA ATCCTTAGAT CTGGCATGTT AGCCCTTCT CCAATTATA GAGGATATGA 5040
 ACCAAAAAAA AAAAAAAA AA

Seq ID NO: 98 Protein sequence
 Protein Accession #: NP_003465

1 11 21 31 41 51
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 YGHVVRGYSY SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRGSCG 180
 SHHNTFNLAA KNVFPPPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLKVKQR 240
 LIEIANHVOK FYRPLNIRIV LVGVEVWDM DKCSVSQDFE TSLHEFLDWR KMKLLPRKSH 300
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 ACRDSSNSCD LBEFTGASG HCPANVYLHD GHSCQDVG DY CYNGICQTHE QQCVTWLGFG 540
 AKPAPGICFE RVNSAGDPYG NCGKVSXSSF AKCEMRDAKC GKIQCQGGAS RPYVIGTNAV 600
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 DSYPPKDNPR RLLQCQNDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP 840
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Seq ID NO: 99 DNA sequence
 Nucleic Acid Accession #: NM_003714
 Coding sequence: 135..1043

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 TGGCCACCTT TGACCCGGCG CGGGGGACCG ACGCCACCAA CCCACCCGAG GGTCCCAAG 240
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 GTTGTGTCAG CCGTGGCGAT GTGGGGTGTG GCGTGTGTA ATGTTTCGAG AACCACTCTT 360
 GTGAGATTCG GGGCTTACAT GGGATTGCA TGACTTTCT GCACAACGCT GGAATAATTG 420
 ATGCCACGGG CAAGTCATTC ATCAAAGACG CCTTGAATG TAAGGCCAC GCTCTGCGGC 480
 ACAGGTTCG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAATGGTG TCCAGTTGC 540
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 AGTGTGAGCA GAACCTGGGA AGCCTGTGCT CCATCTTGAG CTCTGCAACC TCGGCCATCC 780
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Seq ID NO: 100 Protein sequence
 Protein Accession #: NP_003705

1 11 21 31 41 51
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 ISRKCPAIRE MVSQQLRECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180
 CGEEVKEAIT HSVQVQCEQN WGSLSILSF CTSATQKPPT APPERQPVQD RTKLSSRAHHG 240
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Seq ID NO: 101 DNA sequence
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1 11 21 31 41 51

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 CCGACAGAAG AGGTTCTGTC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG 360
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 CGACTATGAT GAGACCTTGA CTATCGGGGA TGACCAGGGC ACAGACCTGC TGCAGGTGGC 660
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 CTGTGAGGCC TCCTTTGACG CGGTCTCCAC CATCCGAGGC GAGCTCTTT TCTCAAAGC 960
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 25 CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCCGTCTCGT 1440
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 TGAGCAACTG GGCTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCTGC 1980
 35 ATCTGTCTGC CTTCTGGCTG ACAATCTTGG AAATCTGTTC TCCAGAATCC AGGCCAAAAA 2040
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Seq ID NO: 102 Protein sequence

Protein Accession #: NP_005931

1 11 21 31 41 51
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Seq ID NO: 103 DNA sequence

Nucleic Acid Accession #: NM_033151.2

Coding sequence: 351..4499

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Seq ID NO: 104 Protein sequence
 Protein Accession #: NP_149163.2

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 SVHDASDNV QRLHRLWEEE VSRRIEIKAS VLLVMLRFQR TRLIIFDALLG ICFIASVLG 180
 PILIPKILE YSEEQLGNVV HGVGLCFALF LSECVKSLSF SSSWIINQRT AIRFRAAVSS 240
 70 FAPEKLIQFK SVIHITSGEA ISFFTGDVNY LFEGVICYGL VLITCASLVI CSISSYFIIG 300
 YFAFIALLCY LLVFPPLAVFM TRMAVKAQHH TSEVSDQIR VTSEVLTCIK LIKMYTWEKP 360
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 LSAVDHVGK HIFEICKKT LRKTVVLVT HQLQYLEFCG QIILLENGKI CENGTHSELM 720
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 80 RESNGTMADL GNIADNPQLS FYQLVYGLNA LLLICVGVCS SGIFTKVRK ASTALHNKLF 900
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 FISQFKRITD AQNNYLLFL SSTRWMALRL EIMTNLVTLA VALFVAFGIS STPYSFVKMA 1080
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Seq ID NO: 105 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..4043

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Seq ID NO: 106 Protein sequence

Protein Accession #: Eos sequence

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	SVHDASDKNV	QRLHRLWEEE	VSRRGIEKAS	VLLVMLRFQR	TRLIFDALLG	ICFCIASVLG	180
	PILIIIPKILE	YSEBQLGNV	HGVGLCFALF	LSECVKSLSP	SSSWIINQRT	AIRFRAAVSS	240
	FAFEKLIQFK	SVIHITSGEA	ISFFTGDVNY	LFEGVCYGPL	VLITCASLVI	CSISSYFIIG	300
	YTAFIAILCY	LLVPFLAVFM	TRMAVKAQHH	TSEVSDQRI	VTSEVLTCIK	LIKMYTWEKP	360
10	FAKIEGMES	LTFCCKPGDG	MAFSMLASLN	LLRLSVFFVP	IAVKGLTNSK	SAVMRFKKFF	420
	LQESPVFYVQ	TLQDPSKALV	FEEATLSWQQ	TCPGIVNGAL	ELERNGHASE	GMTRPDALG	480
	PEEEGNSLGP	ELHKINLVVS	KGMMLGVCGN	TGSGKSSLLS	AILEEMHLE	GSVGVQGSLS	540
	YVPQAWIVS	GNIRENLMG	GAYDKARYLQ	VLHCCSLNRD	LELLPFGDMT	BIGERGLNLS	600
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15	LEFCQGIILL	ENKICENG	HSELMQKKGK	YAQLIQKMHK	EATSDMLQDT	AKIAEKPVE	720
	SQALATSLEE	SLNGNAVPEH	QLTQEEEMEE	GSLSWRVYHH	YIQAAGGYMV	SCIIFFFVVL	780
	IVFLTIFSW	WLSYWLEQGS	GTNSSRESNG	TMADLGNAD	NPQLSFYQLV	YGLNALLLIC	840
	VGVCSGGIFT	KVTRKASTAL	HNKLPNKVFR	CPMSFFDTIP	IGRLNCFAG	DLEQLDQLLP	900
	IFSEQFLVLS	LMVIAVLIV	SVLSPIILM	GAIIMVICFI	YMMFKAIG	VFKRLENYSR	960
20	SPLFSHILNS	LQGLSSIHVY	GKTEDFISQF	KRLTDAQNNY	LLFLSSTRW	MALRLEIMTN	1020
	LVTLAVALFV	AFGISSTPYV	PKVMAVNIIVL	QLASSFQATA	RIGLETEAQF	TAVERILQYM	1080
	KMCVSEAPLH	MEGTSCPGQW	PQHGEIIFQD	YHMKYRDNT	TVLHGINTLI	RGHEVVGIVG	1140
	RTGSGKSSLG	MALFRLVEFM	AGRILIDGVD	ICSIGLEDLR	SKLSVIPQDP	VLLSGTIRFN	1200
	LDPFDRHTDQ	QIWDALERTF	LTKAISKFFK	KLHTDVVENG	GNFSVGERQL	LCIARAVLRN	1260
25	SKIIILIDEAT	ASIDMETDTL	IQRTIREAFQ	GCTVLVIAHR	VTTVLNCDHI	LVMGNGKVVE	1320
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Seq ID NO: 107 DNA sequence

Nucleic Acid Accession #: NM_024022

Coding sequence: 202..1563

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	CCATCTACAT	TTTTGGGACT	CGGGAATTAT	GAGGTAGAGG	TGGAGGCGGA	GCCGGATGTC	180
	AGAGGTCCTG	AAATAGTCAC	CATGGGGGAA	AATGATCCGC	CTGCTGTGA	AGCCCCCTTC	240
	TCATTCCGAT	CGCTTTTGG	CCTTGATGAT	TTGAAATATA	GTCTGTGTC	ACCAGATGCA	300
	GATGCTGTTG	CTGCACAGAT	CCTGTCACTG	CTGCCATTGA	AGTTTTTTC	AATCATCGTC	360
40	ATTGGGATCA	TGTCATTGAT	ATTAGCACTG	GCCATTGGTC	TGGGCATCCA	CTTCGACTGC	420
	TCAGGGAAGT	ACAGATGTCG	CTCATCTTTT	AAGTGTATCG	AGCTGATAGC	TCGATGTGAC	480
	GGAGTCTCGG	ATTGCAAGA	CGGGAGGAC	GAGTACCGCT	GTGTCCGGGT	GGTGGTCAG	540
	AATGCCGTGC	TCCAGGTGTT	CACAGCTGCT	TCGTGGAAGA	CCATGTGCTC	CGATGACTGG	600
	AAGGGTCACT	ACGCAATGAT	TGCTGTGCC	CAACTGGGTT	TCCCAAGCTA	TGTGAGTTCA	660
45	GATAACCTCA	GAGTGAGCTC	GCTGGAGGGG	CAGTTCGGG	AGGAGTTTGT	GTCCATCGAT	720
	CACCTCTTGC	CAGATGACAA	GGTGACTGCA	TTACACCACT	CAGTATATGT	GAGGGAGGGA	780
	TGTGCTCTG	GCCACGTGGT	TACCTTGACG	TGCACAGCCT	GTGGTCATAG	AAGGGGCTAC	840
	AGCTCAGCGA	TCGTGGGTGG	AAACATGTCC	TTGCTCTCGC	AGTGGCCCTG	GCAGGCCAGC	900
	CTTCAGTTCC	AGGGCTACCA	CCTGTGCGGG	GGCTCTGTCA	TACGCCCCCT	GTGGATCATC	960
50	ACTGCTGCAC	ACTGTGTTTA	TGACTTGTAC	CTCCCCAAGT	CATGGACCAT	CCAGGTGGGT	1020
	CTAGTTTCCC	TGTTGGACAA	TCCAGCCCCA	TCCCCTTGG	TGGAGAAGAT	TGTCTACCAC	1080
	AGCAAGTACA	ATGCCAAAGAG	GCTGGGCAAT	GACATCGCCC	TTATGAAGCT	GGCCGGGCCA	1140
	CTCAGTTTCA	ATGAAATGAT	CCAGCCTGTG	TGCCTGCCCA	ACTCTGAAGA	GAACCTTCCC	1200
	GATGGAAAAG	TGTGCTGGAC	GTCAGGATGG	GGGGCCACAG	AGGATGGAGG	TGACGCCCTC	1260
55	CCTGCTCTGA	ACCACGCGGC	CGTCCCTTTG	ATTTCACAAC	AGATCTGCAA	CCACAGGGAC	1320
	GTGTACGGTG	GCATCATCTC	CCCTCCATG	CTCTGCGCGG	GCTACCTGAC	GGGTGGCGTG	1380
	GACAGCTGCC	AGGGGGACAG	CGGGGGGCCC	CTGGTGTGTC	AAGAGAGGAG	GCTGTGGAAG	1440
	TTAGTGGGAG	CGACCAAGCT	TGGCATCGGC	TGCGCAGAGG	TGAACAAGCC	TGGGGTGTAT	1500
	ACCCGTGTCA	CCTCTTCTCT	GGACTGGATC	CACGAGCAGA	TGGAGAGAGA	CCTAAAAACC	1560
60	TGAAGAGGAA	GGGGACAAGT	AGCCACCTGA	GTTCTTGAGG	TGATGAAGAC	AGCCCCGATC	1620
	TCCCTTGAC	TCCCGTGTAG	GAACCTGCAC	ACGAGCAGAC	ACCCTTGGAG	CTCTGAGTTC	1680
	CGGCACCACT	AGCAGGCCCG	AAAGAGGCAC	CCTTCCATCT	GATTCCAGCA	CAACCTTCAA	1740
	GCTGCTTTTT	GTTTTTGTG	TTTTTGAGGT	GGAGTCTCGC	TCTGTGCCC	AGGCTGGAGT	1800
	GCAGTGGCGA	AATCCCTGCT	CACTGCAGCC	TCCGCTTCCC	TGGTTCAAGC	GATTCTCTTG	1860
65	CCTCAGCTTC	CCAGTAGCTG	GGGACCAAG	GTGCCGCCCA	CCACACCCAA	CTAATTTTGT	1920
	TATTTTGTAG	AGAGACAGGG	TTTACCATG	TTGGCCAGGC	TGCTCTCAA	CCCCTGACCT	1980
	CAAAATGATG	GCCTGCTTCA	GCCTCCACA	GTGCTGGGAT	TACAGGCATG	GGCCACCACG	2040
	CCTAGCCTCA	CGCTCCTTTC	TGATCTTAC	TAAGAACAAA	AGAAGCAGCA	ACTTGCAAGG	2100
70	GCGGCCTTTC	CCACTGGTCC	ATCTGGTTT	CTCTCCAGGG	GTCTTGCAA	ATTCCTGACG	2160
	AGATAAGCAG	TTATGTGACC	TCACTGCAA	AGCCACCAAC	AGCCACTCAG	AAAAGACGCA	2220
	CCAGCCCAGA	AGTGACAGAC	TGCAGTCACT	GCACGTTTTT	ATCTCTAGGG	ACCAGAACCA	2280
	AACCCACCTT	TTCTACTTCC	AAGACTTATT	TTCACATGTG	GGGAGGTTAA	TCTAGGAATG	2340
	ACTCGTTTAA	GGCCTATTTT	CATGATTTCT	TGTAGCATT	TGGTGCTTGA	CGTATTATTG	2400
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Seq ID NO: 108 Protein sequence

Protein Accession #: NP_076927

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	LALAIGLGIH	FDCSGKYRCR	SSEKCIELIA	RCDGVSDDCK	GEDEYRCVRV	GGQNAVQLQVF	120
	TAASWKTMC	DDWKGHYANV	ACAQLGFPSY	VSSDNLRVSS	LEGQFREEFV	SIDHLLPDDK	180
	VTALHHSVYV	REGCASGHVY	TLQCTACGHR	RGYSSRIVGG	NMSLLSQWPW	QASLQFQGYH	240

LCGGSVITPL WIITAACHVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSSE NFPDGVKVCWT SGWGATEDGG DASPVLNHAA 360
 VPLISNKICN HRDVVGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF 420
 GIGCAEVNKP GUYTRVTSFL DWIHEQMERD LKT

Seq ID NO: 109 DNA sequence
 Nucleic Acid Accession #: NM_000493.2
 Coding sequence: 97..2139

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 CTGCTAGTAT CCTTGAACCT GGTTCATGGA GTGTTTACG CTGAACGATA CCAATGCCCC 180
 ACAGGCATAA AAGGCCCACT ACCCAACACC AAGACACAGT TCTTCATTCC CTACACCATA 240
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 GGACTCCAAAG GAGAGCCAGG GTTGCCAGGA CCACCGGAC CATCAGCTGT AGGGAAACCA 420
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 CCCAGGGGCT TTCTTGAGGA AAAGGGTGCA CCAGGAGTCC CTGGTATGAA TGGACAGAAA 660
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 GCTGGAGCCC CAGGCCAGCC AGGGATTCCA GGAACAAAAG GTCTCCCTGG GGCTCCAGGA 960
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 GAAAGAGGAC CTGCTGGCCT TCCTGGGGGT CCAGGTGCCA AAGGGGAACA AGGGCCAGCA 1080
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 AAAGGCATCC CGGTATGCCA TGGTCTCCCA GGCCCTAAAG GTGAGACAGG GCCAGCTGGG 1200
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 GGTACTAGAG GCCCTATTGG GCCACAGGC ATTCCAGGAT TCCCTGGGTC TAAAGGGGAT 1500
 CCAGGAAGTC CCGGTCTCTC TGGCCAGCT GGCATAGCAA CTAAGGGCCT CAATGGACCC 1560
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 ACCAAAGGCT ACCTGGATCA GGCTTCAGGG AGTGCCATCA TCGATCTCAC AGAAATGAC 2040
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 AACAAACCTT CCCCCTGAAA AGTGAGCAGC AACGTAAAAA CGTATGTGAA GCCTCTCTTG 2340
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 CAAAGAGTCT CTGCTATGTT AAAAAACAAC AACAAAAAAC AAAGCAACAA AAAAAAAAT 2460
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 TGTATCCCCI AAAATATTTC TGATGGTGCA CTACTCTGAG GCCTGTATGG CCCCTTTCAT 2700
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 CCCAAATAT TGAAGTTCAT CTGAATGCA AGGTGCTTTC ATCAATGAAC CTTTTCAAAA 2820
 CTTTCTATG ATTGCAGAGA AGCTTTTTAT ATACCAGCA TAACTTGGAA ACAGGTATCT 2880
 GACCTATTCT TATTAGTTA ACACAAGTGT GATTAATTTG ATTTCTTTAA TTCTTATTG 2940
 AATCTTATGT GATATGATTT TCTGGATTGA CAGAACATTA GCACATGTAC CTGTGCTCTC 3000
 CCATTCAAGT GAAGTTATAA TTTACACTGA GGGTTTCAA ATTCTGACTAG AAGTGGAGAT 3060
 ATATTATTTA TTTATGCACT GTACTGTATT TTTATATTGC TGTTTAAAAA TTTTAAGCTG 3120
 TGCTCACTT ATTAAGACCA AAAATGTTTT ACCTACTCCT TATTTACGAC ACAATAAAAT 3180
 AACATCAATA GATTTTTAGG CTGAATTAAT TTGAAAGCAG CAATTTGCTG TTCTCAACCA 3240
 TTCTTTCAAG GCTTTTCATT CGACACAATA AAATAACATC AATAG

Seq ID NO: 110 Protein sequence
 Protein Accession #: NP_000484.2

1 11 21 31 41 51
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 MLPQIPFLLL VSLNLVHGVF YAERYQMPTG IKGPLPNTKT QFFIPYTIKS KGIHAVRGEQG 60
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 GPYGPKGDVG PAGLPGPRGP PGPPPIPGPA GISVPGKPGQ QGPTGAPGPR GPFGEKGAPG 180
 VPGMNGQKGE MGYGAPGRPG ERGLPGPQGP TGPSGPPGVG KRGENGVPGQ PGIKGDRGFP 240
 GEMGPIGPPG PQGPPEGERP EGIGKPGAAG APGQPGIPGT KGLPGAPGIA GPPGPPGFGK 300
 PGLPGLKGER GPAGLPGGPG AKGEQGPAGL PGKPLTGP GPNMGPQGPKG IPGSHGLPGP 360
 KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPLDGPKN GNPLPGPKG DPGVGGPPGL 420
 PGVPGPAGAK GPMGHNGEAG PRGAPGIPGT RGPIGPPGIP GPPGSKGDPG SPGPPGPAI 480
 ATKGLNGTGK PPGPPGPRGP SGEPGLGPGP GPPGPPGQAV MPEGFIKAGQ RPSLSGTPLV 540
 SANQGVGTMP VSAFTVILSK AYPAGTPIP FDKILYNRQO HYDPRTGIFT CQIPGIYFYS 600
 YHVHVKGTHV WVGLYKNTGP VMYTYDEYTK GYLDQASGSA IIDLTENDQV WLQLPNAESN 660
 GLYSSEYVHS SFGSLVAPM

Seq ID NO: 111 DNA sequence
Nucleic Acid Accession #: NM_000949
Coding sequence: 285..2153

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ATGTCTCTCGT	GCAGGAAGTA	CTCATCGACT	GATGTGGCAG	ACTTTGCTCC	CTGACAAAAAC	180
TAAAGAACTC	TCCTATTTCAT	GGAGGCGAAC	ACTGAGGATG	CTTTCCACAT	GAACCCCTGAA	240
GTGAACCTCT	GATACATTTT	CTGCAGCAAG	AGAAGGCAGC	CAACATGAAG	GAAAAATGTGG	300
CATCTGCAAC	CGTTTTCACT	CTGCTACTTT	TTCTCAACAC	CTGCCTTCTG	AATGGACAGT	360
TACCTCTCTGG	AAAACTGTAG	ATCTTTAAAT	GTCTTCTCC	CAATAAGGAA	ACATTCACTT	420
GCTGGTGGAG	GCTTGGGACA	GATGGAGGAC	TTCTACCAA	TTATTCCTG	ACTTACCACA	480
GGGAAGGAGA	GACACTCATG	CATGAATGTC	CAGACTACAT	AACCGGTGGC	CCCAACTCCT	540
GCCACTTTGG	CAAGCAGTAC	ACCTCCATGT	GGAGGACATA	CATCATGATG	GTCAATGCCA	600
CTAACAGAGT	GGGAAGCAGT	TTCTCGGATG	AACTTTATGT	GGACGTGACT	TACATAGTTC	660
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ACCTGTGGAT	TAAATGGTCT	CCACCTACCC	TGATTGACTT	AAAACTGGT	TGGTTCACGC	780
TCCTGTATGA	AATTCGATTA	AAACCCGAGA	AAGCAGCTGA	GTGGGAGATC	CATTTTGCTG	840
GGCAGCAAAAC	AGAGTTTAAAG	ATTCTCAGCC	TACATCCAGG	ACAGAAATAC	CTTGTCCAGG	900
TTCTGTGCAA	ACCAGACCAT	GGATACTGGA	GTGCATGGAG	TCCAGCGACC	TTCATTGAGA	960
TACCTAGTGA	CTTCACCATG	AATGATACAA	CCGTGTGGAT	CTCTGTGGCT	GTCTTTTCTG	1020
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GCATCTTTCC	GCCAGTTCCT	GGGCCAAAAA	TAAAAGGATT	TGATGCTCAT	CTGTTGGAGA	1140
AGGGCAAGTC	TGAAGAAGTA	CTGAGTGCTT	TGGGATGCCA	AGACTTTCTT	CCCCTTTCTG	1200
ACTATGAGGA	CTTGCTGGTG	GAGTATTTAG	AAGTAGATGA	TAGTGAGGAC	CAGCATCTAA	1260
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ACACTGACTC	AGGCGGGGGG	AGCTGTGACA	GCCCTTCCCT	TTTGTCTGAA	AAGTGTGAGG	1380
AACCCAGGCG	CAATCCCTCC	ACATTCTATG	ATCCTGAGGT	CATTGAGAAG	CCAGAGAATC	1440
CTGAAACAAC	CCACACCTGG	GACCCCCAGT	GCATAAGCAT	GGAAGGCCAA	ATCCCTTATT	1500
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AGTCTTAGAGA	AGAGGGAAG	GCAACCCAGC	AGAGGGAGGT	AGAAAGCTTC	CATTCTGAGA	1740
CTGACCAGGA	TACGCCCTGG	CTGCTGCCCC	AGGAGAAAAC	CCCCTTTGGC	TCCGCTAAAC	1800
CCTTGGATTA	TGTGTGAGATT	CACAAGGTCA	ACAAAGATGG	TGCATTATCA	TTGCTACCAA	1860
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ATGCCAAGGT	GTCCGGGGTC	ATGGATAACA	ACATCTGGT	GTGTGTGCCA	GATCCACATG	1980
CTAAAAACGT	GGCTTGCTTT	GAAGAATCAG	CCAAAGAGGC	CCCACCATCA	CTTGAACAGA	2040
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ACTAATGGAA	GATTGGTTTA	AAATGTGATT	TTCTTTCAGG	TAACACTACA	GAGTACGTGA	2220
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GCTTTCATGA	TTTGGCATGG	GACAGACGGA	AATGAAATTG	TCAAAATTGT	TTACCATAGA	2520
AAGATGACAA	AAGAAAATTT	TCCACATAGG	AAAATGCCAT	GAAAATTGCT	TTTGAAAAAC	2580
AACTGCATAA	CCTTTACACT	CCTCGTCCAT	TTTATTAGGA	TTACCCAAAT	ATAACCATTT	2640
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Seq ID NO: 112 Protein sequence
Protein Accession #: NP_000940

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VTYIVQDPDP	LELAVEVKQP	EDRKPYLWIK	WSPPTLIDLK	TGWFTLLYEI	RLKPEKAAEW	180
EIHFAQQTE	FKILSLHPGQ	KYLQVRCKP	DHGYWSAWSP	ATFIQIPSD	TMNDTTVWIS	240
VAVLSAVICL	IIVWAVALKG	YSMTVICFPP	VPGPKIKGFD	AHLLEKKGSE	ELLSALGCQD	300
FPPTSDYEDL	LVEYLEVDD	EDQHLMSVHS	KEHPSQGMKP	TYLDPDTS	RGSCDSPSLL	360
SEKCEEPQAN	PSTFYDPEVI	EKPENPETTH	TWDPQCISME	GKIPYFHAGG	SKCSTWPLPQ	420
PSQHNPRSSY	HNITDVCELA	VGPAGAPATL	LNEAGKDALK	SSQTIKSREE	GKATQQREVE	480
SFHSSETDQD	PWLLPQEKTP	FGSAKPLDYV	BIHKVNKDGA	LSLLPKQREN	SGKPKPKPTP	540
ENNKEYAKVS	GVMDDNIIVL	VPDPHAKNVA	CFEESAKEAP	PSLBQNAEK	ALANFTATSS	600
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Seq ID NO: 113 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

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TGGCTGGAGC	CGCAGGGCGT	CTGGCGCATC	GGCTTCCAGT	GTCCCGAGCG	CTTCGACGGC	180
GGCGACGCCA	CCATCTGCTG	CGGCAGCTGC	GCGTTGCGCT	ACTGCTGCTC	CAGCGCCGAG	240
GCGCGCCTGG	ACCAGGGCGG	CTGCGACAAT	GACCGCCAGC	AGGGCGCTGG	CGAGCCTGGC	300
CGGGCGGACA	AAGACGGCCC	CGACGGCTCG	GCAGTGCCCA	TCTACGTGCC	GTTCTTCATT	360
GTTGGCTCCG	TGTTTGTGCG	CTTTATCATC	TTGGGGTCCC	TGGTGGCAGC	CTGTTGCTGC	420

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 CCCACGAATT TCTCTGTGCT GAACTGTCAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720
 CAGTATCTGC ATCCCCCATA CGTGGGGTAC ACQGTGCAGC ACGACTCTGT GCCCATGACA 780
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Seq ID NO: 114 Protein sequence
 Protein Accession #: XP_062811

1 11 21 31 41 51
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 VGSVFVAFII LGSIVAACCC RCLRPKQDPQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ 180
 SSTAASSSS ANSGARAPPT RSQTNCLPE GTMNNVYNM PTNFSVLNCQ QATQIVPHQG 240
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 CAGAAAAAAA TAGTTCTCAA CAGAAAAGAG CAAAACATA TTATGGCTGA ACGTAATGTG 660
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 TTGGGTTACT TACATTCCAT CAAAATAGTA TACAGAGACT TGAACCCAGA AAATATTCCT 900
 TTGGATTAG TAGGACATGT TGTCTTAACA GATTTTGGGC TTTGTAAAGA AGGAATTGCT 960
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 AGTGTATTGG AGGCAGATGA TGCATTCGTT GGTTTCTCTT ATGCACCTCC TTCAGAAGAC 1500
 TTATTTTGTG GAGCAGTTTG CCATTAGAA ACCATTGAGC AAAATAAGTC TATAGATGGG 1560
 ACTGAACTTT CTATTGTGT GAATATATTC AAATATGTAT AACTAGTGCC TCATTTTAT 1620
 ATGTAATGAT GAAACTATG AAAAATGTA TTTTCTCTA TGTGCAAGAA AAATAGGGCA 1680
 TTTCAAAGAG CTGTTTGTAT TAAAATTTAT ATTCTGTGT AATAAGCTTA TTTTAAACA 1740
 ATTTAAAGC TATTATCTT AGCATTAAAC TATTTTAAA GAAACCTTT TTGCTATTGA 1800
 CTGTTTTTC CTCTAAGTT TACACTAACA TCTACCCAAG ATAGACTGTT TTTTAAACAG 1860
 CAATTTAGT TCAGCTAACA TATATTAATA CCTTTGTAAC TCITTTGCTAT GGCTTTGTG 1920
 ATCACACCAA AACTATGCAA TTGGTACATG GTTGTTAAG AAGAAACCGT ATTTTTCAT 1980
 GATAAATCAC TGTTTGAAAT ATTTGGTTCA TGGTATGATC GAAATGTAAA AGCATAATTA 2040
 ACACATTGGC TGCTAGTTAA CAATTGGAAT AACTTTATTC TGCAATCAT TTAAGAAGTA 2100
 ACAGGCCGGG CGCGGTGGCT CACGCTGTA ATCCAGCAC TTTGGGAGGC TGAGGCGGGC 2160
 AGATCACCTG AGGTACAGGAG TTGGAGACCA GCCTGACCAA CATGGACAAA CCCCGTCTCT 2220
 ACTAAAAATA CAAATTTGGC AGGGTGTGGT GGCACATGCC TATAATCCCA GCTACTTGGG 2280
 AGGCTAAGGC AGGAGAATCG CTTGAACCCG GGAGGCGGAG GTTGCAGTGA GCGGAGATCG 2340
 CACCATGCA CTCCTGCCTG GGCAACAAGA GTGAACTCC ATCTCCAAAA A

Seq ID NO: 116 Protein sequence
 Protein Accession #: NP_037389

1 11 21 31 41 51
 MALKIPAKRI FGDNFDPDFI KQRRAGLNEF IQNLVRYPEL YNHPDVRAFL QMDSFKHQSD 60
 PSEDEDERSS QKLHSTQNI NLGPSGNPFA KPTDFDFLKV IGKGSFGKVL LAKRKLDGKF 120
 YAVKVLQKKI VLNRKEQKHI MAERNVLLKN VKHPFLVGLH YSFQTEKLY FVLDFVNGGE 180
 LFPHLQRERS FPEHRARFYA AEIASALGYL HSIKIVYRDL KPENILLDSV GHVLTDFGL 240
 CKEGIAISDT TTTFCGTPEY LAPEVIRKQP YDNTVDWVCL GAVLYEMLYG LPPFYCRDVA 300
 EMYDNILHKP LSLRPGVSLT AWSILEELLE KDRQNRIGAK EDFLEIQNHP FFEISLWADL 360
 VQKKIPPPFN PNVAGPDDIR NFDATFTEET VPYSVCVSSD YSIVNASVLE ADDAFVGFYSY 420
 APPSEDLFL

Seq ID NO: 117 DNA sequence
 Nucleic Acid Accession #: NM_004004.1

Coding sequence: 1..681

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1      11      21      31      41      51
5      |      |      |      |      |
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GGAAAGATCT GGCTCACCGT CCTCTTCATT TTTCGCATTA TGATCCTCGT TGTGGCTGCA 120
AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCCCTGCA GCCAGGCTGC 180
AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACAC TCCGGCTATG GGCCCTGCAG 240
CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
GAGAAGAAGA GGAAGTTTCA CAAGGGGAG ATAAAGAGTG AATTAAAGGA CATCGAGGAG 360
ATCAAAACCC AGAAGGTTCC CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC 420
TTCTTCCGGG TCATCTTCGA AGCCGCTTC ATGTACGCTC TCTATGTCAT GTACGACGGC 480
TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
TTTGTGTCCC GGCCACCGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA 600
ATTGTGCATCC TGCTGAATGT CACTGAATTG TGTATTGTC TAATTAGATA TTGTTCTGGG 660
AAGTCAAAA AGCCAGTTTA A

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Seq ID NO: 118 Protein sequence
Protein Accession #: NP_003995.1

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1      11      21      31      41      51
25     |      |      |      |      |
MDWGLTQIL  GGVNKHSTSI  GKIWLTVLFI  FRIMILVVAA  KEVVGDEQAD  FVCNTLQPGC 60
KNVCYDHYFP ISHRLRLWALQ LIFVSSPALL  VAMHVAYRRH  EKRRKFIKGE  IKSEFKDIEE 120
IKTKQVRIEG SLWWTYTTSSI FFRVIFEAAF  MYVFVVMYDG  FSMQRLVKCN  AWPCNPNTVDC 180
FVSRPTEKTV FTFVMIASVG  ICILNVTTEL  CYLLIRYCSG  KSKKPV

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Seq ID NO: 119 DNA sequence
Nucleic Acid Accession #: XM_061091.1
Coding sequence: 1..2481

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1      11      21      31      41      51
35     |      |      |      |      |
ATGCCAAATA CTTACGGAAC AACCAGGATT GAAATTGGC TTCTCCAAGA GCCGCCCGGG 60
CACCGAGCGC TGGTCGCCGC TCTCCTCCG GTGAGTCCCA GCCCGAGTT GGCTCTGGCG 120
CCCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGCTCCCGAT GATTGGAGGT 180
CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTAA 240
GTTGGGAAGC ISHRLRLWALQ LIFVSSPALL  VAMHVAYRRH  EKRRKFIKGE  IKSEFKDIEE 300
ATTTACAGCTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTCTGTGTA 360
GATGGGTCTA ACAGCGTCCG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA 420
GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT 480
TCCACTCCTC ATCTGGAATT CCCTTGGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA 540
AGAATCAAGA GGATGTTTTC CAAAGGAGGG CGCACGGAGA CGGAACCTGC TCTGAAATAC 600
45     CTTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
GTCACGTATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720
GGTGTCACTG TGTTTGCTGT GGGGGTCAGG TTTCCAGGTT GGGAGGAGCT GCATGCACTG 780
GCCAGCGAGC CTAGAGGGCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
GGCCTCTTCA GCACCTTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC 900
50     CCGGAGCTTG TCTTCATGGA GCGGTTAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG 960
CAGCCCTGCC AGAATGAGAG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCCCTC 1020
TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
GTCGACCTCC TCTTCTGCTC GGACAGCTCT GCGGGCACC A CTCTGGACGG CTCTCTGCGG 1140
GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG GCGGTGCTGA GCGAGGACTC TCGGGCCCGA 1200
55     GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCTGTGGGG GGAGTACCAG 1260
GATGTGCTGG ACCTGGTCTG GAGCCTCGAT GGCATTCCCT TCCGTGGTGG CCCCACCTTG 1320
ACGGGCAGTG CCTTGCAGCA GCGGCGAGAG CGTGGCTTCG GGAGCGCCAC CAGGACAGGC 1380
CAGGACCGGC CACGTAGAGT GGTGGTTTTG CTCACTGAGT CACACTCCGA GGATGAGGTT 1440
GCGGGCCCGC CGCGTCACGC AAGGGCCGCA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG 1500
60     GCCGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
GATCCTCAGG ATCTGTTCAA CCAATCCCTT GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG 1620
CGGCCAGGGT GCCGACACA AGCCCTGGAC CTCGTCTTCA TGTGGACAC CTCTGCCTCA 1680
GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
GAGGTGAACC CTGACGTGAC ACAGGTCGGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT 1800
65     GCCTTCGGGC TGGACACCAA ACCCACCAGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
CCCTACCTAG GTGGGGTGGG CTCAGCCGGC ACCGCCCTGC TGCACATCTA TGACAAAGTG 1920
ATGACCGTCC AGAGGGGTGC CCGGCCTGGT GTCCCCAAG CTGTGGTGGT GCTCACAGGC 1980
GGGAGAGGCG CAGAGGATGC AGCCGTTTCT GCCCAGAAGC TGAGGAACAA TGGCATCTCT 2040
GTCTTGGTCG TGGGCGTGGG GCCTGTCTTA AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC 2100
70     CGGGATTCCC TGATCCACGT GGCAGCTTAC GCCGACCTGC GGTACCACCA GGAGCTGCTC 2160
ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCAGTCAACC TCTGCAAAAC CAGCCCGTGC 2220
ATGAATGAGG GCAGCTGCGT CCTGCAGAA TGGAGCTACC GCTGCAAGTG TCGGGATGGC 2280
TGGAGGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
75     GGATGGATTG TTGAGACGCC CCTGAGGCAC ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT 2400
ACCCCTCCCA GCAACTACAG AGAAGGCCCTG GGCACGTAAA TGGTGCCTAC CTTCTGGAAT 2460
GTCTGTGCCC CAGGTCCCTTA G

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Seq ID NO: 120 Protein sequence
Protein Accession #: XP_061091.1

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1      11      21      31      41      51
80     |      |      |      |      |
MPNTSGTTRI EIWLLQEPPE HRALVAALLP VSPSPALALA PGYPPVPAAD DRFTLPMIGG 60
QMHGEKVDLW SLGVLCYEFL V GKPPFEANE VHVSKETIGK ISAASKMMWC SAAVDIMFL 120

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DGSNSVKGKS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQQEVKA 180
 RIKRMVFKGG RTETELALKY LLHRLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240
 GVTVFAGVGR FPRWELHAL ASEPRGQHV LAEQVEDATN GLFSTLSSSA ICSSATPAGS 300
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR 360
 5 VDLLFLDSS AGTTLDGFLR AKVFKRFVR AVLSEDSRAR VGVATYSREL LVAVPVGEYQ 420
 DVPDLVWSLD GIPFRGGPTL TGSALRQAAE RGFGSATRTG QDRPRRVVVL LTESHSEDEV 480
 AGPARHARAR ELLLLGVGSE AVRAELEBIT GSPKHMVVS DPQDLFNQIP ELQGLKCSRQ 540
 RPGCRTQALD LVFMLDTSAS VGPENFAQMQ SFVRSALQF EVNPDVTQVQ LVVYGSQVQT 600
 10 AFGLDTKPTR AAMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660
 GRGAEDAAVP AQKLRNNGIS VLVVGVGPVL SEGLRRLAGP RDSLIHVAAY ADLRYHQDVL 720
 IEWLCEGAQK PYNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSO 780
 GWILETPLRH MAPVQEGSSR TTPSNYREGL GTEMVPTFWN VCAPGP

Seq ID NO: 121 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2424

1 11 21 31 41 51
 | | | | |
 20 ATGCCCCCTT TCCTGTGTCT GGAGGCCGTC TGTGTTTCC TGTTTTCCAG AGTGCCCCCA 60
 TCCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120
 AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTAGA TGGGTCTAAC 180
 AGCGTCGGGA AAGGGAGCTT TGAAGGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT 240
 25 CTGGACATCA GCCCCGAGAG GGTGAGAGTG GGAGCATTC AGTTCAGTTC CACTCCTCAT 300
 CTGGAATTCC CCTTGGATTG ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
 ATGTGTTTCA AAGGAGGGCG CACGGAGACG GAACCTGTCT TGAATACCT TCTGCACAGA 420
 GGGTTGCTGT GAGGCAGAAA TGCTTCTGTG CCCAGATCC TCATCATCGT CACTGATGGG 480
 AAGTCCGAGG GGGATGTGAA ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG 540
 30 TTTGCTGTGG GGGTCAGGTT TCCGAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
 AGAGGGCAGC ACCTGTCTGT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
 ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
 CCCTGTGAGC ACAGGACGCT GGAGATGGTG CGGGAGTTCG CTGGCAATGC CCCATGCTGG 780
 AGAGGATCGC GCGCGACCCT TCGCGTGCTG GCTGCACACT GTCCTTTCTA CAGCTGGAAG 840
 35 AGAGTGTTC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCCTGTGAC 900
 TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAA GACTGGACGG CTACCAGTGC 960
 CTCTGCCCCG TGGCCTTTGG AGGGGAGGCT AACTGTGCC TGAAGCTGAG CCTGGAATGC 1020
 AGGGTCGACC TCCTCTTCCT GCTGGACAGC TCTGCGGCA CCACTCTGGA CGGCTTCCTG 1080
 CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
 40 CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCCGTG GGGGGAGTAC 1200
 CAGGATGTGC CTGACCTGGT CTGGAGCCTC GATGGCATTC CCTTCCGTGG TGGCCCCACC 1260
 CTGACGGGCA GTGCCTTGGC GCAGCGCGCA GAGCGTGCT TCGGGAGCGC CACCAGACA 1320
 GGCCAGGACC GGCCACGTAG AGTGTGTGTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
 GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440
 GAGGCCGTGC GGGCAGAGGA TGAGGAGATC ACAGGAGGCC CAAAGCATGT GATGCTCTAC 1500
 45 TCGGATCCTC AGGATCTGTT CAACCAATC CCTGAGCTGC AGGGGAAGCT GTGCAAGCCG 1560
 CAGCGGCCAG GGTGCCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620
 TCAGTAGGCG CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
 TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG 1740
 ACTGCCTTCG GGCTGGACAC CAAACCCACC CGGGCTGCCA TGCTGCGGGC CATTAGCCAG 1800
 50 GCCCCTACCC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
 GTGATGACCG TCCAGAGGGG TGCCCGGCCCT GGTGTCCCCA AAGCTGTGGT GGTGCTCACA 1920
 GCGGGGAGAG GCGCAGAGGA TGCAGCCGTT CTGCCCCAGA AGCTGAGGAA CAATGGCATC 1980
 TCTGTCTTGG TCGTGGGCGT GGGGCTGTC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
 CCCCAGGATT CCCTGATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG 2100
 55 CTATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
 TGCATGAAT AGGGCAGCTG CTTCTGTCAG AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
 GGCTGGGAGG GCCCCACTG CGAGAACCGT GAGTGGAGCT CTGTCTCTGT ATGTGTGAGC 2280
 CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGCAGCAGC 2340
 60 CGTACCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG 2400
 AATGTCTGTG CCCAGGTCC TTAG

Seq ID NO: 122 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 65 MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
 SVKGGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
 70 MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180
 FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPPYSWK RVFLTHPATC YRTTCTPGPCD 300
 SQPCQNGGTC VPGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
 RAKVFKRFV RVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
 75 LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480
 EAVRAELEEI TGSPKHMVVS SDPQDLFNQI PELQGLKCSR QRPGCRTQAL DLVFMMLDTSA 540
 SVGPENFAQM QSFVRSALQ FEVNPDTQV GLVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLGGVGS A TALLHIYDK VMTVQRGARP GVPKAVVVLG GGRGAEDAAV PAQKLRNNGI 660
 SVLVVGVGPV LSEGLRRLAG PRDSLIHVA YADLRYHQDV LIEWLCEGAQ QPNLCKPSP 720
 80 CMNEGSCVLQ NGSYRCKCRD WEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAFGP

Seq ID NO: 123 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 89..2356

	1	11	21	31	41	51	
5	GCCCCCTGGC	CCGAGCCGCG	CCCGGGTCTG	TGAGTAGAGC	CGCCCCGGCA	CCGAGCGCTG	60
	GTCCGCGCTC	TCCCTCCGTT	ATATCAACAT	GCCCCCTTTC	CTGTTGCTGG	AAGCCGCTCTG	120
	TGTTTTCTCTG	TTTTCAGAG	TGCCCCCATC	TCTCCCTCTC	CAGGAAGTCC	ATGTAAGCAA	180
	AGAAACCATC	GGGAAGATTT	CAGCTGCCAG	CAAAATGATG	TGGTGCTCGG	CTGCAGTGGA	240
	CATCATGTTT	CTGTTAGATG	GGTCTAACAG	CGTCGGGAAA	GGGAGCTTTG	AAAGGTCCAA	300
10	GCACTTTGCC	ATCACAGTCT	GTGACGGTCT	GGACATCAGC	CCCGAGAGGG	TCAGAGTGGG	360
	AGCATTTCCAG	TTCAAGTTCCA	CTCCTCATCT	GGAAATCCCC	TTGGATTTCAT	TTTCAACCCA	420
	ACAGGAAGTG	AAGGCAAGAA	TCAAGAGGAT	GGTTTTTCAA	GAGGGGCGCA	CGGAGACGGA	480
	ACTTGCTCTG	AAATACCTTC	TGCACAGAGG	GTTGCCTGGA	GGCAGAAATG	CTTCTGTGCC	540
	CCAGATCCCTC	ATCATCGTCA	CTGATGGGAA	GTCCCAGGGG	GATGTGGCAC	TGCCATCCAA	600
15	GCAGCTGAAG	GAAAGGGGTG	TCACTGTGTT	TGCTGTGGGG	GTCAAGTTTC	CCAGGTGGGA	660
	GGAGCTGCAT	GCACTGGCCA	GCGAGCCTAG	AGGGCAGCAC	GTGCTGTTGG	CTGAGCAGGT	720
	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TCGGCCATCT	GCTCCAGCGC	780
	CACGCCAGAG	TGCAGGGTCG	AGGCTCACCC	CTGTGAGCAC	AGGACGCTGG	AGATGGTCCG	840
	GGAGTTTCGCT	GGCAATGGCC	CATGCTGGAG	AGGATCGCGG	CGGACCCCTT	CGGTGCTGGC	900
20	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCCCT	CCACCTGCTA	960
	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAATGGAG	GCATATGTGT	1020
	TCCAGAAGGA	CTGGACGGCT	ACCAAGTCCT	CTGCCCGCTG	GCCTTTGGAG	GGGAGGCTAA	1080
	CTGTGCGCTC	AAGCTGAGCC	TGGAATGCAG	GGTCGACCTC	CTCTTCTGCT	TGGACAGCTC	1140
	TGCGGGCACC	ACTCTGGACG	GCTTCTGCG	GGCCAAAGTC	TTCTGTGAAG	GGTTTGTGCG	1200
25	GGCCGTGCTG	AGCCAGGACT	CTCGGGCCCG	AGTGGGTGTG	GCCACATACA	GCAGGGAGCT	1260
	GCTGGTGGCG	GTGCCGTGTT	GGGAGTACCA	GGATGTGCCT	GACCTGGTCT	GGAGCCTCGA	1320
	TGGCATTTCCC	TTCCGTGGTG	GCCCCACCTT	GACGGGCAGT	GCCTTGCGGC	AGGCGGCAGA	1380
	CGCTGGCTTC	GGGAGCGCCA	CCAGGACAGG	CCAGGACCGG	CCACGTAGAG	TGGTGGTTTT	1440
	GCTCACTGAG	TCACACTCCG	AGGATGAGGT	TGCGGGCCCA	GCGGCTCACG	CAAGGGCGCG	1500
30	AGAGCTGCTC	CTGCTGGGTG	TAGGCAGTGA	GGCCGTGCGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGCAGCCCA	AAGCATGTGA	TGGTCTACTC	GGATCCTCAG	GATCTGTTCA	ACCAAATCCC	1620
	TGAGCTGCAG	GGGAAGCTGT	GCAGCCGCGA	GCGGCCAGGG	TGCCGGACAC	AAGCCCTGGA	1680
	CCTCGTCTTC	ATGTTTGACA	CCTCTGCCTC	AGTAGGGCCC	GAGAAATTTG	CTCAGATGCA	1740
	GAGCTTTGTG	AGAAGCTGTG	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTCCG	1800
35	CCTGGTGGTG	TATGGCAGCC	AGGTGCAGAC	TGCCTTCGGG	CTGGACACCA	AACCCACCCG	1860
	GGCTGCGATG	CTGCGGGCCA	TTAGCCAGGC	CCCCTACCTA	GGTGGGGTGG	GCTCAGCCGG	1920
	CACCGCCCTG	CTGCACATCT	ATGACAAAGT	GATGACCGTC	CAGAGGGGTG	CCCGCCCTGG	1980
	TGTCCCCAAA	GCTGTGGTGG	TGCTCACAGG	CGGGAGAGGC	GCAGAGGATG	CAGCCGTTCC	2040
	TGCCCAGAAG	CTGAGGAACA	ATGGCATCTC	TGCTTGGTTC	GTGGGCGTGG	GGCCTGTCTC	2100
40	AAGTGAGGGT	CTGCGAGGGC	TTGCAGGTCC	CCGGGATTC	GTGATCCACG	TGGCAGCTTA	2160
	CGCCGACCTG	CGGTACCAAC	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAGCA	2220
	GCCAGTCAAC	CTCTGCAAA	CCAGCCCGTG	CATGAATGAG	GGCAGCTGCG	TCTGTCAGAA	2280
	TGGAGGCTAC	CGCTGCAAGT	GTCCGGATGG	CTGGGAGGGC	CCCCACTGCG	AGAACCAGAT	2340
	CTTGAGACGC	CCCTGAGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCCG	TACCCCTCCC	2400
45	AGCAACTACA	GAGAAGGCCT	GGGCACTGAA	ATGGTGCCCTA	CCTTCTGGAA	TGCTGTGCC	2460
	CCAGGTCTCT	AGAATGTCTG	CTTCCCGCCG	TGGCCAGGAC	CACATATCTC	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTCAACCCAC	2580
	AAACGATGTT	GTTGAAAAGT	TTTGATGTGT	AAGTAAATAC	CCACTTTCTG	TACCTGCTGT	2640
	GCCTTGTGTA	GGCTATGTCA	TCTGCCACCT	TTCCCTTGAG	GATAACAACG	GGGTCTGAA	2700
50	GACTTAAATT	TAGCGGCCTG	ACGTTCCCTT	GCACACAATC	AATGCTCGCC	AGAATGTTGT	2760
	TGACACAGTA	ATGCCACAGA	GAGGCCTTTA	CTAGAGCATC	CTTTGGACGG		

Seq ID NO: 124 Protein sequence
Protein Accession #: Eos sequence

55	1	11	21	31	41	51	
	MPPFLLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPLDSFST	QOEVKARIKR	120
60	MVFKGGRRET	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
	FAVGVRFFPRW	EELHALASEP	RQGHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCFPGPCD	300
	SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLDLS	SAGTTLDGFL	360
	RAKVVFVRKFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPDLVWSL	DGIPFRGGPT	420
65	LTGSALRQAA	ERGFSGSATRT	GQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLLVGS	480
	EAVRAELEBI	TGSPKHVMVY	SDPQDLFNQI	PELQGLKCSR	QRPFCRTQAL	DLVFMLDTSA	540
	SVGPENFAQM	QSFVRSALQ	FEVNPDTVQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
	APYLLGGVGA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVL	GGRGAEAAV	PAQKLNRNGI	660
	SVLVVGVGPFV	LSEGLRRLAG	PRDSLHVAA	YADLRYHQDV	LIEWLCGEAK	QPVNLCKPSP	720
70	CMNEGSCVLQ	NGSYRCKCRD	GWEGPHCENR	FLRRP			

Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

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	CCCGAGCCCC	GCCCCCTCCG	GCCCCGGTCC	GCGCGCCCAG	CCTGCCAGCC	GCGCTGCTGC	60
	TGCTCTCTCT	GCTGTGGGAG	CGCTGACCGC	GCGGCTGCTC	CGCTCTCCCC	GCTCCAAGCG	120
80	CCGATCTGGG	CACCCGCCAC	CAGCATGGAC	GCTCGCCGCG	TGCCCGAGAA	AGATCTCAGA	180
	GTAAGAAGA	ACTTAAAGAA	ATTCAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCTCTGATG	CAGTGTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAACAC	GAGGCTGCAG	300
	TCAGTTCCGG	AAGGCTGTAG	GACCCGACAG	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360
	GCGATGAAGT	TTCCAGCGCG	GAGTACCAGG	GGAGCAACCA	ACAAAAAAGC	AGAGTCCCCG	420
	CAGCCCTCAG	AGAATTCTGT	GACTGATTCC	AATCCGATT	CAGAAGATGA	AAGTGAATG	480

5	AATTTTTTGG	AGAAAAAGGC	TTTAAATATA	AAGCAAAACA	AAGCAATGCT	TGCAAACTC	540
	ATGTCGAAT	TAGAAAGCTT	CCCTGGCTCG	TTCCGTGGAA	GACATCCCTT	CCCAGGCTCC	600
	GACTCACAA	CAAGGAGACC	GCGAAGGCGT	ACATTCCCGG	GTGTTGCTTC	CAGGAGAAAC	660
	CCTGAACGGA	GAGCTCGTCC	TCTTACCAGG	TCAAGGTCCC	GGATCCCTCGG	GTCCTTTGAC	720
	GCTCTACCCA	TGGAGGAGGA	GGAGGAAGAG	GATAAGTACA	TGTTGGTGAG	AAAGAGGAAG	780
	ACCGTGGATG	GCTACATGAA	TGAAGATGAC	CTGCCCAGAA	GCCGTGCTC	CAGATCATCC	840
	GTGACCCTTC	CGCATATAAT	TCGCCCAGTG	GAAGAAATTA	CAGAGGAGGA	GTTGGAGAAC	900
	GTCTGCAGCA	ATTCTCGAGA	GAAGATATAT	AACCGTTCAC	TGGGCTCTAC	TTGTCACTAA	960
10	TGCCGTGAGA	AGACTATTGA	TACCAAAACA	AACCTGCAGAA	ACCCAGACTG	CTGGGGCGTT	1020
	CGAGGCCAGT	TCTGTGGCCC	CTGCCTTCGA	AACCGTTATG	GTGAAGAGGT	CAGGGATGCT	1080
	CTGCTGGATC	CSAACTGGCA	TTGCCCGCCT	TGTCGAGGAA	TCTGCAACTG	CAGTTTCTGC	1140
	CGGCAGCGAG	ATGGACGGTG	TGCGACTGGG	GTCTTGTGT	ATTTAGCCAA	ATATCATGGC	1200
	TTTGGGAATG	TGCATGCCTA	CTTGAAAAGC	CTGAAACAGG	AATTTGAAAT	GCAAGCATAA	1260
15	TATCTGGAAA	ATTTGCTGCC	TGCCTTCTAC	TTCTCAAATC	TTTCTTGTA	AAGTTTCCAA	1320
	TTTTTTCACT	GAAACCTGAG	TTAAAAATCT	TGATGATCAG	CCTGTTTCAT	AAGAACTCC	1380
	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGGTA	TATTGCTAGT	1440
	TACACTTTGC	CCCTCTGCAG	TTTCTTCTCT	GCTCCCAACC	CCCATCTCAT	AGCATCCCC	1500
	TCTATTTCCT	ATGCTCCTCT	CCAACCGCTT	AGTTTCTGAA	TTTCTTTTAA	ATTACAGTTT	1560
20	TATGAAAGCA	TATTTTATTT	ACTTGGTGTT	GAAATAGCCC	TCATAAAACC	TAAGCACTTG	1620
	GAAACACAAT	AATAGTATTA	ACTAACTAGA	TCTATTGAAT	TTCAGAGAAG	AGCCTTCTAA	1680
	CTTGTTTACA	CAAAAACGAG	TATGATTAG	CACTCATACT	AGTTGAAATT	TTTAATAGAA	1740
	TCAAGGCACA	AAAGTCTTAA	AACCATGTGG	AAAAATTAGG	TAATTATTGC	AGATTGATGT	1800
	CTCTCAATCC	CATGTATTGC	GCTTATGTTA	CAAGTTGTTG	TCACAGTTGA	GACTTAATTT	1860
25	CTCCTAATTT	CTTCTGCCCC	AAGGGTAAGT	GGTGGCTCCA	GCTTACACGA	TCATAATTCA	1920
	AAGGTTGCTG	GGCAATGTAA	TACTTAATTA	AAATAATGAT	GGAAGAGCTA	TCTGGAGATT	1980
	ATGAGTAAGC	TGATTTGAAT	TTTCAGTATA	AACTTTAGT	ATAATTGTAG	TTTGCAAGT	2040
	TTATTTCACT	TCACATGTAA	GGTATTGCAA	ATAAATCTT	GGACAATTTT	GTATGGAAAC	2100
	TTGATATTAA	AACTAGTCT	TGTTTCTTTT	GCAGTTTCTT	GTAATTTTAT	AAACCAAGCA	2160
30	CAAGGTTCAA	GTTTAGATTT	TAAGCACTTT	TATAACAATG	ATAAGTGCTT	TTTTGGAGAT	2220
	GTAACCTTTA	GCACTTTGTT	AACCTGACAT	CTCTGCCAGT	CTAGTTTCTG	GGCAGGTTTC	2280
	CTGTGTGAGT	ATTCGCCCTC	CTCTTTGCAT	TAATCAAGGT	ATTGTTGAGA	GGTGGAACTC	2340
	AAGTGTGTTG	ATGTCCAATT	TACTTGCATA	TGTAAACCAT	TGCTGTGCCA	TTCAATGTTT	2400
35	GATGCATAAT	TGGACCTTGA	ATCGATAAGT	GTAATAACAG	CTTTTGATCT	GTAATGCTTT	2460
	TATACAAAAG	TTTATTTTAA	TAATAAAATG	TTTGTCTCAA	AAAAAATAAA		

Seq ID NO: 126 Protein sequence
Protein Accession #: NP_114148.1

40	1	11	21	31	41	51	
	MDARRVPQKD	LRVKKNLKFF	RYVKLISMET	SSSSDDSCDS	FASDNFANTR	LQSVREGCRT	60
	RSQCRHSGPL	RVAMKFPARS	TRGATNKKA	SRQPSSENSVT	DSNSDSEDES	GMNFLEKRAL	120
	NIKQNKAMLA	KLMSELESFP	GSFRGRHPLP	GSDSQSRPR	RRTFPGVASR	RNPERRARPL	180
45	TRSRSRILGS	LDALPMEEEE	EEDKYMLVRK	RKTVDGYMNE	DDLPRSRRSR	SSVTLPHIIR	240
	PVEITEEEL	ENVCSNSREK	IYNRSLGSTC	HQCRQKTIDT	KTNCRNPDCW	GVRGQFCGPC	300
	LRNRYGEEVR	DALLDPNWHC	PPCRGICNCS	FCRQRDGRCA	TGVLVYLAKY	HGFNVHAYL	360
	KSLKQEFEMQ	A					

Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: AF305616.1
Coding sequence: 1..863

55	1	11	21	31	41	51	
	ATGCACCGCT	TGATGGGGGT	CAACAGCACC	GCCGCCGCGG	CCGCCGGGCA	GCCCAATGTC	60
	TCCTGCACGT	GCAACTGCAA	ACGCTCTTTG	TTCCAGAGCA	TGGAGATCAC	GGAGCTGGAG	120
	TTTGTTCAGA	TCATCATCAT	CGTGGTGGTG	ATGATGGTGA	TGGTGGTGGT	GATCACGTGC	180
	CTGCTGAGCC	ACTACAGACT	GCTCGCACGG	TCCTTCATCA	GCCGGCACAG	CCAGGGGCGG	240
60	AGGAGAGAAG	ATGCCCTGTC	CTCAGAAGGA	TGCTGTGGC	CCTCGGAGAG	CACAGTGTCA	300
	GGCAACGGAA	TCCCAGAGCC	GCAGGTCTAC	GCCCCGCCCT	GGCCACCGA	CCGCTGGCC	360
	GTGCCGCCCT	TGCCCCAGCG	GGAGCGCTTC	CACCGCTTCC	AGCCCACTA	TCCGTACCTG	420
	CAGCACGAGA	TCGACCTGCC	ACCCACCATC	TCGCTGTGAG	ACGGGGAGGA	GCCCCACCC	480
	TACCAGGGCC	CCTGCACCTT	CCAGCTTCGG	GACCCGAGC	AGCAGCTGGA	ACTGAACCGG	540
65	GAGTCGGTGC	GCGCACCCCC	AAACAGAACC	ATCTTCGACA	GTGACCTGAT	GGATAGTGCC	600
	AGGCTGGGCG	GCCCTTGCCC	CCCCAGCAGT	AACTCGGGCA	TCAGCGCCAC	GTGCTACGGC	660
	AGCGGCGGGC	GCATGGAGGG	GCCGCCGCC	ACCTACAGCG	AGGTCATCGG	CCACTACCGG	720
	GGGTCTCTCT	TCCAGCACCA	GCAGAGCAGT	GGGCCGCCCT	CCTTGCTGGA	GGGGACCCGG	780
70	CTCCACCACA	CACACATCGC	GCCCTTAGAG	AGCGCAGCCA	TCTGGAGCAA	AGAGAAGGAT	840
	AAACAGAAAG	GACACCCTCT	CTAG				

Seq ID NO: 128 Protein sequence
Protein Accession #: AAL09357.1

75	1	11	21	31	41	51	
	MHRLMGVNST	AAAAAGQPNV	SCTCNCKRSL	FQSMETETE	FVQIIIVVV	MMVMVVVITC	60
	LLSHYKLSAR	SFISRSQGR	RREDALSSEG	CLWPSESTVS	NGIPEPQVY	APPRPTDRLA	120
	VPPFAQRERF	HRFPQTPYPL	QHEIDLPTTI	SLSDGEEPPP	YQGPTLQLR	DPEQQLNLNR	180
80	ESVRAPPNRT	IFDSLDLMSA	RLGGPCPPSS	NSGISATCYG	SGGRMBGPPP	TYSEVIGHYP	240
	GSSFQHQSS	GPPSLLEGTR	LHHTHIAPLE	SAAIWSKEKD	KQKGHPL		

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_004952.1

Coding sequence: 1..718

5
10
15

1	11	21	31	41	51	
ATGGCGGCGG	CTCCGCTGCT	GCTGCTGCTG	CTGCTCGTGC	CCGTGCCGCT	GCTGCCGCTG	60
CTGGCCCAAG	GGCCCGGAGG	GGCGCTGGGA	AACCGGCATG	CGGTGTACTG	GAACAGCTCC	120
AACCAGCACC	TGCGGCGAGA	GGGCTACACC	GTGCAGGTGA	ACGTGAACGA	CTATCTGGAT	180
ATTACTGCC	CGCACTACAA	CAGCTCGGGG	GTGGGCCCCG	GGCGGGGACC	GGGGCCCCGA	240
GGCGGGGCG	AGCAGTACGT	GCTGTACATG	GTGAGCCGCA	ACGGCTACCG	CACCTGCAAC	300
GCCAGCCAGG	GCTTCAAGCG	CTGGGAGTGC	AACCGGCCGC	ACGCCCCGCA	CAGCCCCATC	360
AAGTTCTCGG	AGAAGTTCCA	GCGCTACAGC	GCCTTCTCTC	TGGGCTACGA	GTTCACAGCC	420
GGCCACGAGT	ACTACTACAT	CTCCACGCCC	ACTCACAACC	TGCACTGGAA	GTGTCTGAGG	480
ATGAAGGTGT	TCGTCTGCTG	CGCTCCACA	TCGCATCCG	GGGAGAAGCC	GGTCCCCACT	540
CTCCCCCAGT	TCACCATGGG	CCCCAATGTG	AAGATCAACG	TGCTGGAAGA	CTTTGAGGGA	600
GAGAACCCTC	AGGTGCCCAA	GCTTGAGAAG	AGCATCAGCG	GGACCAGCCC	CAACCGGGAA	660
CACCTGCCCC	TGGCCGTGGG	CATCGCCTTC	TTCTCATGA	CGTTCTTGGC	CTCCTAG	

Seq ID NO: 130 Protein sequence
Protein Accession #: NP_004943.1

20
25

1	11	21	31	41	51	
MAAAPLLLLL	LLVPVPLPL	LAQSPGGALG	NRHAVYWNSS	NQHLRREGYT	VQVNVNDYLD	60
IYCPHYNSSG	VGPAGGPGPG	GGAEQVLYLM	VSRNGYRTCN	ASQGFKRWEC	NRPHAPHSPI	120
KFSEKFRQYS	AFSLGYEFHA	GHEYIYSTP	THNLHWKCLR	MKVFFVCCAST	SHSGEKFPVT	180
LPQFTMGPNV	KINVLDFEFG	ENPQVPKLEK	SISGTSFKRE	HLPLAVGIAF	FLMTFLAS	

Seq ID NO: 131 DNA sequence
Nucleic Acid Accession #: NM_012445.1
Coding sequence: 276..1271

30
35
40
45
50
55
60
65

1	11	21	31	41	51	
GCACGAGGGA	AGAGGGTGAT	CCGACCCGGG	GAAGGTCGCT	GGGCAGGGCG	AGTTGGGAAA	60
GCGGCAGGCC	CGCCCGCCCC	CGCAGCCCTT	TCTCCTCCTT	TCTCCACAGT	CCTATCTGCC	120
TCTCGCTGGA	GGCCAGGCCG	TGCAGCATCG	AAGACAGGAG	GAACCTGGAG	CTCATTGGCC	180
GGCCCCGGGC	GCCCGGCTCG	GGCTTAAATA	GGAGCTCCCG	GCTCTGGCTG	GGACCCGACC	240
GCTGCCGGCC	GCGCTCCCGC	TGCTCTGCTG	GGGTGATGGA	AAACCCGAGC	CCGGCCGCGC	300
CCCTGGGCAA	GGCCCTCTGC	GCTCTCTCTC	TGGCCACTCT	CGGCGCCGCC	GGCCAGCCTC	360
TTGGGGGAGA	GTCCATCTGT	TCCGCCAGAG	CCCCGGCCAA	ATACAGCATC	ACCTTCACGG	420
GCAAGTGGAG	CCAGAGCGGC	TTCCCAAGC	AGTACCCCTT	GTTCGCCCCC	CCTGCGCAGT	480
GGTCTTCGCT	GCTGGGGGCC	CGGCATAGCT	CCGACTACAG	CATGTGGAGG	AAGAACCAGT	540
ACGTCAATAA	CGGGCTGCGC	GACTTTGCGG	AGCGCGGCGA	GGCCTGGGCG	CTGATGAAGG	600
AGATCGAGGC	GGCGGGGAGG	GCGCTGCAGA	GCGTGACCGC	GGTGTTCG	GCGCCCGCCG	660
TCCCCAGCGG	CACCGGGCAG	ACGTGCGCGG	AGCTGGAGGT	GCAGCGCAGG	CACTCGCTGG	720
TCTCGTTTGT	GGTGCGCATC	GTGCCAGGCC	CCGACTGGTT	CGTGGGCGTG	GACAGCCTGG	780
ACCTGTGCGA	CGGGGACCGT	TGGCGGGAAC	AGCGCGCGCT	GGACCTGTAC	CCCTACGACG	840
CCGGGACGGA	CAGCGGCTTC	ACCTTCTCCT	CCCCCAACTT	CGCCACCATC	CCGCAGGACA	900
CGGTGACCGA	GATAAGCTCC	TCCTCTCCCA	GCCACCGCGC	CAACTCCTTC	TACTACCCGC	960
GGCTGAAGGC	CCTGCCTCCC	ATCGCCAGGG	TGACACTGGT	GCGGCTGCGA	CAGAGCCCCA	1020
GGGCCTTCAT	CCCTCCCGCC	CCAGTCTCTG	CCAGCAGGGA	CAATGAGATT	GTAGACAGCG	1080
CCTCAGTTCC	AGAAACGCCG	CTGGACTGCG	AGGTCTCCCT	GTGGTCTGTC	TGGGGACTGT	1140
GCGGAGGCCA	CTGTGGGAGG	CTCGGGACCA	AGAGCAGGAC	TCGCTACGTC	CGGGTCCAGC	1200
CCGCCAACA	CGGGAGCCCC	TGCCCGAGC	TCGAAGAAGA	GGCTGAGTGC	GTCCCTGATA	1260
ACTGCGTCTA	AGACCAAGAG	CCCGCAGCCC	CTGGGGCCCC	CGGAGCCATG	GGGTGTGCGG	1320
GGCTCTGTG	CAGGCTCATG	CTGCAGGCGG	CCGAGGCACA	GGGGGTTTCG	CGCTGTCTCT	1380
GACCGCGGTG	AGGCCGCGCC	GACCATCTCT	GCACTGAAGG	GCCCTCTGGT	GGCCGCGCAG	1440
GGCATTGGGA	AACAGCTCTC	TCCTTTCCCA	ACCTTGCTTC	TTAGGGGCCC	CCGTGTCCCG	1500
TCTGCTCTCA	CGCTCTCTCT	CCTGCAGGAT	AAAGTCATCC	CCAAGGCTCC	AGCTACTCTA	1560
AATTATGGTC	TCCTTATAAG	TTATTGCTGC	TCCAGGAGAT	TGTCTTCAT	CGTCCAGGGG	1620
CCTGGCTCCC	ACGTGGTTGC	AGATACCTCA	GACCTGGTGC	TCTAGGCTGT	GCTGAGCCCC	1680
CTCTCCGAG	GGGCATCCA	AGCGGGGGCC	ACTTGAGAAG	TGAATAAATG	GGGCGGTTTC	1740
GGAAGCGTCA	GTGTTTCCAT	GTATGATGATC	TCTCTGCGTT	TGAATAAAGA	CTATCTCTGT	1800
TGCTCAC						

Seq ID NO: 132 Protein sequence
Protein Accession #: NP_036577.1

70
75

1	11	21	31	41	51	
MENPSPAAL	GKALCALLLA	TLGAAGQPLG	GESICSARAP	AKYSITFTGK	WSQTAFFPKQY	60
PLFRPPAQWS	SLLGAHSSD	YSMWRKNQYV	SNGLRDFAE	GEAWALMKEI	EAAGEALQSV	120
HAVFSAPAVP	SGTGQTSDEL	EVQRRHSLVS	FVVRIVPSPD	WFGVDSLDDL	CDGDRWREQA	180
ALDLYPYDAG	TDSGFTFSSP	NFATIPQDTV	TEITSSSPSH	PANSFYFPR	KALPPIARVT	240
LVRRLQSPRA	FIPPAVPLPS	RNEIIVDSAS	VPETPLDCEV	SLWSSWGLOG	GHCGRGLGTS	300
RTRYVRVQPA	NNGSPCELE	EAECEVPDNC	V			

Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_019894
Coding sequence: 1..1314

80

1	11	21	31	41	51	
ATGTTACAGG	ATCCTGACAG	TGATCAACCT	CTGAACAGCC	TCGATGTCAA	ACCCCTGCGC	60

5 AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
 CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC 180
 TACTTCCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
 CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
 GCAGTGGCAG TCCGCCTCTC CAAGGACCGA TCCCACTGTC AGGTGCTGGA CTCGGCCACA 360
 GGGAAGTGGT TCTCTGCCTG TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
 GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGATGCG GAATCAAGT 540
 10 GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG 600
 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
 AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
 CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
 GGCTCAGACA AACTGGGCAG CTTCCTCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
 15 TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
 ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
 GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
 GACATACTGC TGCAGGCGTC AGTCCAGTTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
 GCGTACCAGG GGGAAAGTCAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
 20 GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
 AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

Seq ID NO: 134 Protein sequence

Protein Accession #: NP_063947.1

25 1 11 21 31 41 51
 MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPILIAL LSLASIIIV VLIKVILDKY 60
 30 YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT 120
 GNWFSACFDN FTEALAEAT RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
 GPCLSGSLVS LHCLACGKSL KTRPVVGEE ASVDSWFPQV SIQYDKQHV GGSILDPHV 240
 LTAHCFRKH TDVFNKVKRA GSKLGSFSP LAVAKIIIE FNPMPKND IALMKLQFPL 300
 TFSGTVRPIC LPFDEBELT ATPLWIIWG FTKQNGKMS DILLQASVQV IDSTRCNADD 360
 35 AYQGEVTEKM MCAGIPEGGV DTCQDSSGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT 420

Seq ID NO: 135 DNA sequence

Nucleic Acid Accession #: NM_003045

Coding sequence: 148..2037

40 1 11 21 31 41 51
 CGATCCTGCC GGAGCCCGGC CGCCGCGGCG TGGATTCTG AAACCTTCCT TGTATCCCTC 60
 45 CTGAGACATC TTTGCTGCAA GATCGAGGCT GTCCTCTGGT GAGAAGGTGG TGAGGCTTCC 120
 CGTCATATTC CAGCTCTGAA CAGCAACATG GGGTGCAAAG TCCTGCTCAA CATTGGGCAG 180
 CAGATGCTGC GCGGGAAGGT GGTGACTGT AGCCGGGAGG AGACCGGCT GTCTCGCTGC 240
 CTGAACACTT TTGATCTGGT GGCCCTCGGG GTGGGCAGCA CACTGGGTGC TGGTGTCTAC 300
 GTCTCTGGTG GAGCTGTGGC CCGTGAGAAT GCAGGCCCTG CCATTGTCTC CTCTCTCTG 360
 50 ATCGCTGCGC TGGCCTCAGT GCTGGCTGGC CTGTGCTATG GCGAGTTTGG TGCTCGGGTC 420
 CCCAAGACGG GCTCAGCTTA CCTCTACAGC TATGTACCCG TTGGAGAGCT CTGGGCCCTC 480
 ATCACCAGGT GGAAGTAAAT CCTCTCTTAC ATCATCGGTA CTTCAAGCGT AGCGAGGGCC 540
 TGGAGCGCCA CCTTCGACGA GCTGATAGGC AGACCCATCG GGGAGTTCTC ACGGACACAC 600
 ATGACTCTGA ACGCCCGCG CGTGTCTGGT GAAAACCCCG ACATATTCGC AGTGATCATA 660
 55 ATTCTCATCT TGACAGGACT TTTAACTCTT GGTGTGAAAG AGTCGGCCAT GGTCAACAAA 720
 ATATTCACTT GTATTAACGT CCTGGTCTG GGCCTCATAA TGGTGTGAGG ATTTGTGAAA 780
 GGATCGGTTA AANAAGTGGC GCTCACGGAG GAGGATTTTG GGAACACATC AGGCCGTCTC 840
 TGTTTGAACA ATGACACAAA AGAAGGGAAG CCCGGTGTG GTGGATTCTC GCCCTTCGGG 900
 TTCTCTGGTG TCCTGTGCGG GGCAGCGACT TGCTTCTATG CCTTCGTGGG CTTTGACTGC 960
 60 ATCGCCACCA CAGGTGAAGA GGTGAAGAAC CCACAGAAGG CCATCCCCGT GGGGATCGTG 1020
 GCGTCCCTCT TGAATCTGCT CATCGCCTAC TTTGGGGTGT CGGCTGCCCT CACGCTCATG 1080
 ATGCCCTACT TCTGCCTGGA CAATAACAGC CCCCTGCCCG ACGCCTTTAA GCACGTGGGC 1140
 TGGGAAGGTG CCAAGTAGC AGTGGCCGTG GGCTCCCTCT GCGCTCTTTC GCACAGTCTT 1200
 CTAGGTTCCA TGTTTCCCAT GCCTCGGGTT ATCTATGCCA TGGCTGAGGA TGGACTGCTA 1260
 65 TTTAAATCT TAGCAACGT CAATGATAGG ACCAAAACAC CAATAATCGC CACATTAGCC 1320
 TCGGGTCCCG TTGCTGCTGT GATGGCCTTC CTCTTTGACC TGAAGGACTT GGTGGACCTC 1380
 ATGTCCATTG GCACTCTCTT GGCTTACTCG TTGGTGGCTG CCTGTGTGTT GGTCTTACGG 1440
 TACCAGCCAG AGCAGCCTAA CCTGGTATAC CAGATGGCCA GTACTTCCGA CGAGTTAGAT 1500
 CCAGCAGACC AAAATGAATT GGCAAGCACC AATGATTCCC AGCTGGGGTT TTTACCAGAG 1560
 70 GCAGAGATGT TCTCTTTGAA AACCACTCTC TCACCCAAAA ACATGGAGCC TTCCAAAATC 1620
 TCTGGGCTAA TTGTGAACAT TTCAACCAGC CTTATAGCTG TTCTCATCAT CACCTTCTGC 1680
 ATTGTGACCG TGCTTGAAG GGAGGCTCTC ACCAAAGGGG CGCTGTGGGC AGTCTTTCTG 1740
 CTCGACGGGT CTGCCCTCCT CTGTGCCGTG GTCACGGGCG TCATCTGGAG GCAGCCCGAG 1800
 AGCAAGACCA AGCTCTCATT TAAGGTTCCC TTCTGTCCAG TGCTCCCATC CCGTGGACATC 1860
 75 TTCGTGAACG TCTATCTCAT GATGCAGCTG GACCAGGGCA CCTGGGTCCG GTTTGCTGTG 1920
 TGGATGCTGA TCGGCTCAT CATCTACTTT GGCTATGGCC TGTGGCACAG CGAGGAGGCG 1980
 TCCCTGGATG CAGACCAAGC AAGGACTCCT GACGGCAACT TGGACCAAGT CAAGTGACGC 2040
 ACAGCCCGCG CCCCAGGAGG TGGCAGCAGC CCCGAGGAGC GCCCCAGAG GACCGGAGG 2100
 CACCCACCC TCCCAACAGG TGCAACAGAA ACCACCTGCG TCCACACCCT CACTGCA

Seq ID NO: 136 Protein sequence

Protein Accession #: NM_003045

80 1 11 21 31 41 51

MGCKVLLNIG QQMLRRKVV D CSREETRLSR CLNTFDLVAL GVGSTLGAGV YVLGAVARE 60
 NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELWA FITGWNILS 120
 YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPGVL AENPDIFAVI IILILTGLLT 180
 LGVKESAMVN KIFTCINVLV LGFIMVSGFV KGSVKNWQLT EEDFGNTSGR LCLNNDTKEG 240
 KPGVGGFMPF GFSGLVSGAA TCFYAFVGF D CIATTGEEVK NPQKAIPVGI VASLLICFIA 300
 YFGVSAALTL MPMYFCLDNN SPLPDAFKHV GWEGAKYAVA VGSLLCALSAS LLGSMFPMMPR 360
 VIYAMAEDGL LFKFLANVND RTKTPIIATL ASGAVAAMVA FLFDLKDLDV LMSIGTLLAY 420
 SLVAACVLVL RYQPEQPNLV YQMASTDEL DPADQNELAS TNDSQLGFLP EAEMFSLKTI 480
 LSPKNMEPSK ISGLIVNIST SLIAVLIITF CIVTVLGRE A LTKGALWAVF LLAGSALLCA 540
 VVTGVIWRQP ESKTKLSFKV PFLFVLPILS IFVNVYLMQ LDQGTWVRFA VNMILIGFIY 600
 FGYGLWHSEE ASLDADQART PDGNLDQCK

Seq ID NO: 137 DNA sequence

Nucleic Acid Accession #: NM_032044.1

Coding sequence: 182..658

1 11 21 31 41 51
 AAGATATAAA AGCTCCAGAA ACGTTGACTG GGACCACTGG AGACACTGAA GAAGGCAGGG 60
 GCCCTTAGAG TCTTGGTTGC CAAACAGATT TGCAGATCAA GGAGAACCCA GGAGTTTCAA 120
 AGAAGCGCTA GTAAGGTCTC TGAGATCCTT GCACTAGCTA CATCCTCAGG GTAGGAGGAA 180
 GATGGCTTCC AGAAGCATGC GGCTGCTCCT ATTGCTGAGC TGCCTGGCCA AAACAGGAGT 240
 CCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCCTGGA TGGTTTACC ACAAGTCCAA 300
 TTGCTATGGT TACTTCAGAA AGCTGAGGAA CTGGTCTGAT GCCGAGCTCG AGTGTCTAGT 360
 TTACGGAACG GGAGCCCAAC TGGCATCTAT CCTGAGTTTA AAGGAAGCCA GCACCATAGC 420
 AGAGTACATA AGTGGCTATC AGAGAAGCCA GCCGATATGG ATTGGCCTGC ACGACCCACA 480
 GAAGAGGCAG CAGTGGCAGT GGATTGATGG GGCCATGTAT CTGTACAGAT CCTGGTCTGG 540
 CAAGTCCATG GGTGGGAACA AGCACTGTGC TGAGATGAGC TCCAATAACA ACTTTTAAAC 600
 TTGGAGCAGC AACGAATGCA ACAAGCGCCA ACACCTCCTG TGCAAGTACC GACCATAGAG 660
 CAAGAATCAA GATTCTGCTA ACTCCTGCAC AGCCCCGTCC TCTTCTCTTC TGCTAGCCTG 720
 GCTAAATCTG CTCATTATTT CAGAGGGGAA ACCTAGCAAA CTAAGAGTGA TAAGGGCCCT 780
 ACTACACTGG CTTTTTATAG CTTAGAGACA GAAACTTTAG CATTTGGCCA GTAGTGGCTT 840
 CTAGCTCTAA ATGTTTGGCC CGCCATCCCT TTCCACAGTA TCCTTCTTCC CTCTCCCTCC 900
 GTCTCTGGCT GTCTCGAGCA GTCTAGAAGA GTGCATCTCC AGCCTATGAA ACAGCTGGGT 960
 CTTTGGCCAT AAGAAGTAAA GATTGAAGA CAGAAGGAAG AAACCTCAGG GTAAGCTTCT 1020
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Seq ID NO: 138 Protein sequence

Protein Accession #: NP_114433.1

1 11 21 31 41 51
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Seq ID NO: 139 DNA sequence

Nucleic Acid Accession #: XM_051860.2

Coding sequence: 52..3042

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Seq ID NO: 140 Protein sequence
 Protein Accession #: KP_051860.2

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Seq ID NO: 141 DNA sequence
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Seq ID NO: 142 Protein sequence
 Protein Accession #: Eos sequence

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Seq ID NO: 143 NM DNA sequence
 Nucleic Acid Accession #: NM_006017
 Coding sequence: 38..2635

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 Protein Accession #: NP_006008.1

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Seq ID NO: 146 Protein sequence
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Seq ID NO: 147 DNA sequence
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Seq ID NO: 148 Protein sequence
Protein Accession #: AAH12089.1

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55	NTSSVIIIEG	KKYGRITIGY	FEHYLQWIEF	SISEKVASCK	PVATALDTAV	DVFLCSYIID	780
	PLNLFWFGIG	KATVFLLPAL	IFAVKLAKY	RMDSSEVDYD	DVETIPMKNM	ENGNNGYHKD	840
	HVYGIHNPVM	TSPSQH					

Seq ID NO: 149 DNA sequence
Nucleic Acid Accession #: NM_033049.1
Coding sequence: 28..1566

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65	CTCCTTTCTG	TAAACACAGC	CACCAACCAA	GGCAACTCAG	CTGATGCTGT	AACAACCACA	120
	GAAACTGCGA	CTAGTGGTCC	TACAGTAGCT	GCAGCTGATA	CCACTGAAAC	TAATTTCCCT	180
	GAAACTGCTA	GCACCACAGC	AAATACACCT	TCTTTCCCAA	CAGCTACTTC	ACCTGCTCCC	240
	CCATAATTA	GTACACATAG	TTCTCCACA	ATTCTACAC	CTGCTCCCCC	CATAATTAGT	300
70	ACACATAGTT	CCTCCACAAT	TCTATACCT	ACTGCTGCAG	ACAGTGAGTC	AACCACAAAT	360
	GTAAATTCAT	TAGCTACCTC	TGACATAATC	ACCGCTTCAT	CTCCAATATG	TGGATTAATC	420
	ACAATGGTTC	CTTCTGAAAC	ACAAAGTAAC	AATGAAATGT	CCCCCACCAC	AGAAGACAAT	480
	CAATCATCAG	GGCCTCCCCA	TGGCACCGCT	TTATTGGAGA	CCAGCACCCT	AAACAGCACA	540
	GGTCCAGCA	ATCCTTGCCA	AGATGATCCC	TGTGCAGATA	ATTCTGTTATG	TGTTAAGCTG	600
75	CATAATACAA	GTTTTTGCCT	GTGTTTAGAA	GGGTATTACT	ACAACTCTTC	TACATGTAAG	660
	AAAGGAAAGG	TATTCCTCTG	GGAAGATTTC	GTGACAGTAT	CAGAAACATT	TGACCCAGAA	720
	GAGAAACATT	CCATGGCCTA	TCAAGACTTG	CATAGTGAAA	TTACTAGCTT	GTTTAAAGAT	780
	GTATTTGGCA	CATCTGTTTA	TGGACAGACT	GTAATTCCTA	CTGTAGCAC	ATCTCTGTCA	840
80	CCAAGATCTG	AAATGCGTGC	TGATGACAA	TTGTTAATG	TAACAATAGT	AACAATTTTG	900
	GCAGAAACCA	CAAGTGACAA	TGAGAAGACT	GTGACTGAGA	AAATTAATAA	AGCAATTAGA	960
	AGTAGCTCAA	GCAACTTTCT	AAACTATGAT	TTGACCCCTC	GGTGTGATTA	TTATGGCTGT	1020
	AACCAAGACT	CGGATGCTGC	CCTCAATGGT	TTAGCATGCG	ATTGCAAAATC	TGACCTGCAA	1080
	AGGCCTAACC	CACAGAGCCC	TTTCTGCGTT	GCTTCCAGTC	TCAAGTGTCC	TGATGCGTGC	1140
	AACGCACAGC	ACAAGCAATG	CTTAATAAAG	AAGAGTGGTG	GGGCCCTCGA	GTGTGCGTGC	1200
	GTGCCCGGCT	ACCAGGAAGA	TGCTAATGGG	AACTGCCAAA	AGTGTGCATT	TGGCTACAGT	1260

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Seq ID NO: 150 Protein sequence
 Protein Accession #: NP_149038.1

1 11 21 31 41 51
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 PCADNSLCVK LHNTSFLCL EGYIYNSTC KKGKVFPGKI SVTVSETFDP EEKHSMAFD 240
 LHSEITSLFK DVFSTSVYQG TVILTVSTSL SPRSEMRADD KFNVTIVTI LAETTSDEK 300
 TVTEKINKAI RSSSSNLFNY DLTLRCDYVG CNQTADDCLN GLACDCKSDL QRPNPQSPFC 360
 VASSLKCPDA CNAQHKQLI KKSOGAPECV CVPGYQEDAN GNCQKCAFY SGLDCKDKFO 420
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Seq ID NO: 151 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 87..914

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5 TGGAGCAAAAC ATGAAGTTTT TGGAAACGTT TTCTCATTTG AAGCCTCCAG TATGCTGTAC 2100
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 GAATCTCCTT CC

Seq ID NO: 152 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 DRGRFKVVVS VLSAVTTCLA FVKPAINNIS LMTLGVPTCA LLIAELKRCN NMRVFKLGLF 180
 SGLWNTLALF CWISDRAFCE LLSFNFPYL HCMWHILICL AAYLGVCVFA YFDAASEIPE 240
 QGPVIFWPN EKWAFIGVPY VSLLCANKKS SVKIT

Seq ID NO: 153 DNA sequence
 Nucleic Acid Accession #: NM_001432.1
 Coding sequence: 167..676

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Seq ID NO: 154 Protein sequence
 Protein Accession #: NP_001423.1

1 11 21 31 41 51
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Seq ID NO: 155 DNA sequence
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 Coding sequence: 85..2466

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 TGCCGGTCTT GCGCTGCCA CCTGTGCGGG GGCCGGCAGG ACCCGACAA GCAGCTCATG 1080
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Seq ID NO: 156 Protein sequence
Protein Accession #: NP_037414.2

Seq ID NO: 157 DNA sequence
Nucleic Acid Accession #: NM_000756.1
Coding sequence: 186..776

1014

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Seq ID NO: 158 Protein sequence
 Protein Accession #: NP_000747.1

1 11 21 31 41 51
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Seq ID NO: 159 DNA sequence
 Nucleic Acid Accession #: NM_001200.1
 Coding sequence: 325..1514

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Seq ID NO: 160 Protein sequence
 Protein Accession #: NP_001191.1

1 11 21 31 41 51
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5	AGAACAGGCA	TGTGTTTCTC	GGGCGCTGGT	AATGGCCGCT	GTGCACAAGA	GCTCCCGGGG	1140
	AGAAATGACGA	AAATGCAGTG	CTGCTGTGAG	CCTGGCCGCT	GCTGGGGCAT	CGGAACCAATT	1200
	CCTGAAGCCT	GTCCCTGTGAG	AGGTTCCTGAG	GAATATCGCA	GACTTTGTCAT	GGATGGACTT	1260
	CCAATGGGAG	GAATCCAGG	GAGTGTCTGG	TCCAGACCTG	GAGGCACCTGG	GGGAAATGGC	1320
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10	CCTGGAGGCA	ATGGCTTTTC	TCCTGGCGTT	GGGGAGCCG	GTGTGGGGG	CGGGGACAG	1440
	GGACCTATCA	TCACCTGGAGT	AACAATTCTG	AACCAGACAA	TAGATATCTG	TAAGCATCAT	1500
	GCTAACCTTT	GTTTAAATGG	ACGCTGTATA	CCAACCTGCT	CAAGCTACCG	ATGTGAATGC	1560
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	AATCCCTGCA	CTAATGGAGA	TTGTGTTAAC	ACACCTGGTT	CCTATTATTG	TAAATGTCAT	1680
	GCTGGATTCC	AGAGGACTCC	TACCAAGCAA	GCATGCATTG	ATATTGATGA	GTGCATCCAG	1740
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	TGCAATGCCG	GCTTTGAAAT	AACACAGAT	GGAAAAAACT	GTGTTGATCA	TGATGAATGT	1860
	ACAACTACCA	ACATGTGTTT	GAATGGAATG	TGCATCAATG	AAGATGGCAG	CTTCAAGTGC	1920
	ATCTGCAAA	CAGGATTTGT	CTTGGCTCCA	AATGGGCGTT	ACTGTACTGA	TGTTGATGAA	1980
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	TGTGACTGTC	CCCCAGGCCT	GGCTGTGGGC	ATGGATGGAC	GTGTGTGTGT	TGATACTCAC	2100
	ATGCGCAGTA	CCTGCTATGG	AGGAATCAAG	AAAGGAGTGT	GTGTGCGTCC	TTTCCCGGCT	2160
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	CAGCCATGCC	CTGCAAAAAA	TTCACTGAA	TTCCACGGCC	TTTGTAGTAG	TGGAGTAGGT	2280
25	ATCACTGTGG	ATGGAAGAGA	TATCAATGAA	TGTGCTTTGG	ATCCTGATAT	ATGTGCCAAT	2340
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	GATGCTCTCG	GAAGAACTG	TATTGACATT	GATGAATGTT	TAGTAAACAG	ACTGCTTTGT	2460
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30	GTCAATGGGG	CCTGCAGAAA	CAACCTTGGA	TCTTTCAATT	GTGAATGTTT	GCCCGGCAGC	2640
	AAACTCAGCT	CCACAGGATT	GATCTGTATT	GACAGCCTGA	AGGGGACCTG	TTGGCTCAAC	2700
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	GCCACCTCTG	GAGCCCGCTG	GGGGAGCCCC	TGTGAGCGGT	GTGAACCTAGA	TACAGCTTGC	2820
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	CAGTGTACT	TGAAGTGGGA	TGAAGATGAA	TGCATCCACC	CCGTTCTCTG	AAAGTTCCCG	3060
	ATGGATGCCT	GCTGCTGTGC	TGTCGGGCGG	GCTTGGGGCA	CCGAGTGTGA	GGAGTGCCCC	3120
	AAACCTGGCA	CCAAGGAATA	CGAGACACTG	TGCCCCCGCG	GGGCTGGCTT	TGCTAACCCA	3180
40	GGGGATGTTT	TTACTTGGCG	GCCATTTTAC	AAAGACATCA	ATGAATGCAA	AGCATTTCCT	3240
	GGGATGTGCA	CTTATGGGAA	GTGCAGAAAT	ACAATCGGAA	GCTTCAATAT	CCGTTGCAAT	3300
	AGTGGCTTTG	CTCTAGACAT	GGAGGAAAGA	AACCTGCACG	ACATCGACGA	GTGCAGGATT	3360
	TCTCCTGACC	TCTGTGGCAG	TGGAATCTGC	GTCAATACAC	CGGGCAGCTT	TGAGTGCAG	3420
	TGCTTCGAAG	GCTATGAAAG	TGGCTTCATG	ATGATGAAGA	ACTGCATGGA	CATTGACGGA	3480
45	TGTGAACGTA	ACCTCTCTCT	TTGTAGGGGT	GGCAGCTGTG	TGAACACTGA	GGGCAGCTTT	3540
	CAGTGTGACT	GGCCACTGGG	ACACGAGCTG	TCACCATCCC	GTGAGGACTG	TGTGGATATT	3600
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	ACCTATCAGT	GCTCTTGCAA	TCCTGGATAT	CAGGCTACGC	CAGACCCGCA	GGGCTGTACA	3720
	GATATTGATG	AATGTATGAT	AATGAACGGA	GGCTGTGACA	CCCACTGCAC	AAATTACAGAG	3780
50	GGAAAGCTACG	AATGCAGCTG	CAGTGAAGGT	TATGCCCTGA	TGCCAGATGG	GAGATCGTGT	3840
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	ATTCTGGAG	AGTATCGCTG	CCTCTGCTAT	GATGGCTTCA	TGGCTTCCAT	GGACATGAAA	3960
	ACATGCATTG	ATGTCAATGA	ATGTGACCTA	AATTCAAATA	TCTGCATGTT	TGGGGAATGT	4020
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55	ACCACAGGAT	GTACAGATGT	GGATGAGTGT	GAATTTGGTG	CTCATAACTG	CGACATGCAT	4140
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60	AACGGACAGT	GCCTTAATGT	CCCGGGTGCA	TATCGCTGCG	AGTGTGAGAT	GGGCTTCACT	4440
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	GTCTCTGGAA	CATGTAATAA	CCTGCCTGGA	ATGTTTCATT	GCATCTGCGA	TGATGGTTAT	4560
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65	TTTCAGTTGA	ACCCAACTGG	TGTGGGTTGT	GTTGACAAAC	GTGTGGGCAA	CTGCTACCTG	4740
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	AGTGCCTCTT	CATGCTGCTG	CTCTCTGGGA	AAGGCCTGGG	GAAACCCCTG	TGAGACATGC	4860
	CCCCCTGTCA	ATAGCACTGA	ATATTACACC	CTGTGTCCCG	GAGGTGAAGG	CTTCAGACCT	4920
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70	CAGGGTGGAA	ACTGCATCAA	CACTTTGGG	AGCTTCCAGT	GTGAGTGCCC	ACAAGGCTAC	5040
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	GTGTGTGGGC	CTGGGACCTG	CTATAACACC	CTGGGAAATT	ACACCTGCAT	TTGCCACCTT	5160
	GAGTACATGC	AGGTCAATGG	AGGCCACAA	TGCATGGACA	TGAGAAAAAG	CTTTTGCTAC	5220
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Seq ID NO: 162 Protein sequence
Protein Accession #: NP_001990.1

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MGRRRRLCLQ LYFLWLGCVV LWAQGTAGQP QPPPKPPRP QPPQVVRSA TAGSEGGFLA 60
PEYREEGAAS ASRVRRRGQQ DVLRGPNVCG SRFHSYCCPG WKTLPNGNQ IVPICRNSCG 120
DGFCSRPNMC TCSSGQISST CGSKSIQCCS VRCMNGGTCA DDHCQCQKGY IGTYCGQPV 180
ENGCQNGGR C IAPACVVG FTGPQCERDY RTGPGCFQVN NQMCQQLTG IVCTKTLCCA 240
TTGRAWGHP C EMCPAQPPQC RRGFIPIRNT GACQDVDECO AIPGICQGGN CINTVGSFEC 300
RCPAGHKQSE TTKQEDIDE CSIIPIGICET GECSNTVGSY FCVCPRGVYT STDGSRCIDQ 360
RTGMCPSGLV NGRCAQELPG RMTKMQCCCE PGRCWIGITI PEACPVRGSE BYRRCLMDGL 420

5 PMGGIPGSAG SRPGGTGGNG FAPSGNGNGY GPGGTGFPII PGGNGFSPGV GGAGVGAGGQ 480
 GPIITGLTIL NQTIDICKHH ANLCLNGRCI PTVSSYRCEC NMGYKQDANG DCIDVDECTS 540
 NPCTNGDCVN TPGSYCKCH AGFQRTPTKQ ACIDIDEIQ NGVLCKNGRC VNSDGSFQCI 600
 CNAGFELTID GKNVCVDHDEC TTTNMCLNGM CINEDGSPKC ICKPGFVLAP NGRYCTDVDE 660
 CQTPGICMNG HCINSEGSFR CDCPPGLAVG MDGRVCVDTH MRSTCYGGIK KGVCVRPFPG 720
 AVTKSECCA NPDYGFGEPC QPCPAKNSAE FHGLCSSGVG ITVDGRDINE CALDPDICAN 780
 GICENLRGSY RCNCNSGYEP DASGRNCIDI DECLVNRLLC DNGLCRNTPG SYSTCPCPGY 840
 VERTETETCE DINECESNPC VNGACRNNLG SFNCECSPGS KLSSTGLICI DSLKGTCLWN 900
 IQDSRCEVNI NGATLKSECC ATLGAAWSP CERCELDTAC PRGLARIKGV TCEDVNECEV 960
 10 FPGVCPNGRC VNSKGSFHCE CPEGLTLDGT GRVCLDIRME QCYLKWEDEDE CIHPVPGKFR 1020
 MDACCAVGA AWGTBCEBPC KPGTKEYETL CPRGAGFANR GDVLTGPRFY KDINECKAFP 1080
 GMCTYGKCRN TIGSFKRCRN SGFALDMEER NCTDIDECRI SPDLCSGIC VNTPGSFECE 1140
 CFEGYESGFM MMKNMCDIDG CERNPLLCRG GTCVNTEGSF QCDCPLGHEL SPSREDCVDI 1200
 15 NECSLSDNLC RNGKCVNMIG TYQCSNPGY QATPDRQGT DIDECEMIMG GCDTQCTNSE 1260
 GSYECSCSEG YALMPDGRSC ADIDECENNP DICDGGQCTN IPGEYRCLCY DGFMAISMDMK 1320
 TCIDVNECDL NSNICMFGEBC ENTKGFSFICH CQLGYSVKKG TTGCTDVDEC BIGAHNCMDH 1380
 ASCLNIPGSF KCSREGEWIG NGIKCIDLDE CSNGTHQCSI NAQCVNTPGS YRACSEGEFT 1440
 GDGFTCSVD ECAENILCE NGQCLNVPGA YRCECEMGFT PASDSRSCQD IDECSFNIC 1500
 20 VSGTCNNLFG MFHCICDDGY ELDRITGGNCT DIDECADPIN CVNGLCVNTP GRYECNCPFD 1560
 FQLNPTGVGC VDNRVGNCYL KFGPRGDGSL SCNTEIGVGV SRSSCCCSLG KAWGNPCETC 1620
 PPNVSTEYIT LCPGGEGFRP NPITILEDI DECQELPGLC QGGNCINTFG SFQCECPQGY 1680
 YLSEDRICE DIDECAHFG VCGPGTCYNT LGNYTCICPP EYMQVNGGHN CMDMRKSPCY 1740
 RSYNGTTCEN ELPPFNVTIRM CCCTYNVGA GNKPCEPCPT PGTADEFKIC GNIPGFTFDI 1800
 25 HTGKAVIDE CKEIPGICAN GVCINQIGSF RCECPTGFSY NDLLLVCEDI DECSNGDNL 1860
 QRNADCINSP GSYRCEAAG FKLSPNGACV DRNECLEIPN VCSHGLCVDL QGSYQICHN 1920
 GFKASQDQTM CMDVDECERH PCNGTCKNT VGSYNLCYYP GFELTHNDC LDIDECSFF 1980
 GQVCRNGRCF NEISGFKLCL NEGVELTPDG KNCIDTNECV ALPGSCSPGT CQNLEGSFRC 2040
 ICPPGYEVKS ENCIDINECD EDPNICLFSG CTNTPGGFQC LCPPEGVFLSD NGRRCFDTQ 2100
 30 SFCTNFENG KCSVPKAFNT TKAKCCSKM PEGEGWDPCE LCPKDEVAF QDLCPYGHGT 2160
 VPSLHDTRED VNECLESPGI CSNGQCINTD GSFRCECPMG YNLDTYGVRC VDTDECSIGN 2220
 FCGNGTCTNV IGSFECNNE GFEPGPMNC EDINECAQNP LLCALRCMNT FGSYECTCPI 2280
 GYALREDQKM CKDLDECARG LHDCESTRGM CKNLIGTFMC ICPPGMARRP DGEVCVDENE 2340
 CRTKPGICEN GRCVNIIGSY RCECNEGFS SSSGTECLDN RQGLCEFAVL QTICQMASS 2400
 35 RNLVTKSECC CDGGRGWGHQ CELCPLPETA QYKKICPHGP GYTTDGRDID ECKVMPNLCT 2460
 NQQCINTMGS FRFCCKVGYT TDISGTSCID LDECSQSPKP CNYICNTTEG SYQCSCPRGY 2520
 VLQEDGKTK CKDLDECQTKH NCQFLCVNLT GGFTCKCPPG FTQHTTACID NNECSQPL 2580
 CGGKICQNT PGSFSCBQOR GFSLDATGLN CEDVDECDGN HRCQHGQNI LGGYRCGCPQ 2640
 GYIQHYQWQ CVDENECNPN NACGSASCYN TLGSYKCAP SGFSFDQFSS ACHDVNECSS 2700
 40 SKNPNYNGCS NTEGYLCCG PPGYRVGQG HCVSGMGFNK GQYLSLDTVE DEENALSPEA 2760
 CYECKINGYP KDSRQKRIS HEPDPTAVEQ ISLESVDMS PVMKFNLSH LGSKEHILEL 2820
 RPAIQPLNH IRYVISQND DSVFRIHQRN GLSYLHTAKK KLMPGTYTLE ITSIPLYKKK 2880
 ELKKLEESNE DDYLLGELGE ALRMLQIQI Y

Seq ID NO: 163 DNA sequence
 Nucleic Acid Accession #: NM_013372.1
 Coding sequence: 63..617

50 1 11 21 31 41 51
 GCGGCCGCAC TCAGCGCCAC GCGTCGAAAG CGCAGGCCCC GAGGACCCGC CGCACTGACA 60
 GTATGAGCCG CACAGCCTAC ACGGTGGGAG CCCTGCTTCT CCTCTTGGGG ACCCTGCTGC 120
 CGGCTGCTGA AGGGAAGAAC AAGGGTCCC AAGGTCCCAT CCCCAGGCA GACAAGGCC 180
 AGCACAATGA CTGAGAGCAG ACTCAGTCGC CCCAGCAGCC TGGCTCCAGG AACCGGGGGC 240
 GGGGCCAAGG CGGGGCACT GCCATGCCCG GGGAGGAGGT GCTGGAGTCC AGCCAAGAGG 300
 55 CCCTGCTATG GACGGAGCGC AAATACCTGA AGCAGAGACT GTGCAAAACC CAGCCGCTTA 360
 AGCAGACCAT CCACGAGGAA GGCTGCAACA GTCCGACCAT CATCAACCCG TCTCTTTACG 420
 GCGAGTGCAA CTCTTTCTAC ATCCCAAGGC ACATCCGGA GAGGAGAGGT TCCTTTTCAGT 480
 CCTGCTCCTT CTGCAAGCCC AAGAAATTCA CTACCATGAT GGTCACTC AACTGCCCTG 540
 60 AACTACAGCC ACCTACCAAG AAGAAGAGAG TCACACGTGT GAAGCAGTGT CGTTGCATAT 600
 CCATCGATTG GGATTAGGCC AAATCCAGGT GCACCCAGCA TGTCTTAGGA ATGCAGCCCC 660
 AGGAAGTCCC AGACCTAAAA CAACCAAGATT CTTACTTGGC TTAACCTAG AGGCCAGAAG 720
 AACCCTCAGC TGCCTCCTGG CAGGAGCCTG CTTGTGCGTA GTTCGTGTGC ATGAGTGTGG 780
 ATGGGTGCTT GTGGGTGTTT TTAGACACCA GAGAAACAC AGTCTCTGCT AGAGAGCACT 840
 65 CCCTATTTTG TAAACATATC TGCTTTAATG GGGATGTACC AGAAACCCAC CTCACCCCGG 900
 CTCACATCTA AAAGGGCGGG GCCGTGGTCT GGTCTGACT TTGTGTTTTT GTGCCCTCCT 960
 GGGGACAGCA ATCTCCTTTC GGAATGAATG TTCATGGAAG AGGCTCCTCT GAGGGCAAGA 1020
 GACCTGTTTT AGTGCTGCAT TCGACATGGA AAGTCTCTTT TAACCTGTGC TTGCATCCTC 1080
 CTTTCTCCT CTCTCTCACA ATCCATCTCT TCTTAAGTTG ATAGTGACTA TGTCACTCTA 1140
 70 ATCTCTTGTT TGCCAAGGTT CCTAAATTA TCACTTAAC CATGATGCAA ATGTTTTTCA 1200
 TTTTGTGAAG ACCCTCCAGA CTCTGGGAGA GGCTGGTGTG GGCAAGGACA AGCAGGATAG 1260
 TGGAGTGAGA AAGGGAGGGT GGAGGGTGAG GCCAAATCAG GTCCAGCAAA AGTCAGTAGG 1320
 GACATTGCAG AAGCTTGAAA GGCCAATACC AGAACACAGG CTGATGCTTC TGAGAAAGTC 1380
 TTTTCTTAGT ATTTAACAGA ACCCAAGTGA ACAGAGGAGA AATGAGATTG CCAGAAAGTG 1440
 75 ATTAACCTTG GCCGTGCAA TCTGCTCAA CCTAACCCA AACTGAAAC ATAAATACTG 1500
 ACCACTCCTA TGTTCCGACC CAAGCAAGTT AGCTAAACCA AACCACTCC TCTGCTTTGT 1560
 CCCTCAGGTG GAAAGAGAGA GTAGTTTAGA ACTCTCTGCA TAGGGGTGGG AATTAATCAA 1620
 AAACCKCAGA GGCTGAAATT CCTAATACCT TTCCTTTATC GTGGTTATAG TCAGCTCATT 1680
 TCCATTCCAC TATTTCCCAT AATGCTTCTG AGAGCCACTA ACTTGATTGA TAAAGATCCT 1740
 80 GCCTCTGCTG AGTGTACTCT ACAGTAAGTC TAAAGATGAR AGAGTTTAGG GACTACTCTG 1800
 TTTTAGCAAG ARATATTKTG GGGGTCTTTT TGTTTTAACT ATTGTGAGGA GATTGGGCTA 1860
 RAGAGAAGAC GACGAGAGTA AGGAAATAAA GGGGATTGCC TCTGGCTAGA GAGTAAGTTA 1920
 GGTGTTAATA CCTGGTAGAA ATGTAAGGGA TATGACCTCC CTTTCTTTAT GTGCTCACTG 1980
 AGGATCTGAG GGGACCTGTG TAGGAGACA TAGCATCATG ATGTATTAGT TGTTCTACTG 2040
 CTACTGGTTG GATGGACATA ACTATTGTAA CTATTCAGTA TTTACTGGTA GGCAGTGTCC 2100

TCTGATTAAA CTTGGCCTAC TGGCAATGGC TACTTAGGAT TGATCTAAGG GCCAAAGTGC 2160
 AGGGTGGGTG AACTTTATTG TACTTTGGAT TTGGTTAACC TGTTTTCTTC AAGCTGAGG 2220
 TTTTATATAC AAACCTCCCTG AATACTCTTT TTGCCTTGTA TCTTCTCAGC CTCCTAGCCA 2280
 AGTCCATGTG AATATGGAAG ACAAACACTG CAGACTTGAG ATTCAGTTGC CGATCAAGGC 2340
 TCTGGCATTC AGAGAACCCT TGCAACTCGA GAAGCTGTTT TTATTTCGTT TTTGTTTTGA 2400
 TCCAGTGCTC TCCCATCTAA CAACTAAACA GGAGCCATT CAAGCGGGA GATATTTTAA 2460
 ACACCCAAAA TGTGGGTCT GATTTTCAAA CTTTAAACT CACTACTGAT GATTCTCAGC 2520
 CTAGGCGAAT TTGTCCAAAC ACATAGTGTG TGTGTTTTGT ATACACTGTA TGACCCCAAC 2580
 CCAATCTTT GTATTGTCCA CATTCTCCAA CAATAAAGCA CAGAGTGGAT TTAATTAAGC 2640
 ACACAAATGC TAAGGCAGAA TTTTGAGGGT GGGAGAGAAG AAAAGGGAAA GAAGCTGAAA 2700
 ATGTAAAAAC ACACCAGGA GAAAAATGA CATTCAAGAC CAGCAACAC TGAATTTCTC 2760
 TTGTGTTTTT AACTCTGCCA CAAGAATGCA ATTTCTGTAA TGGAGATGAC TTAAGTTGGC 2820
 AGCAGTAATC TTCTTTTAGG AGCTTGTACC ACAGTCTTGC ACATAAGTGC AGATTGGCT 2880
 CAAGTAAAGA GAATTCCTC AACACTAACT TCACTGGGAT AATCAGCAGC GTAACACCC 2940
 TAAAAAGCATA TCACTAGCCA AAGAGGAAA TATCTGTTCT TCTTACTGTG CCTATATTAA 3000
 GACTAGTACA AATGTGGTGT GTCTTCCAAC TTTCAATTGAA AATGCCATAT CTATACCATA 3060
 TTTTATTGCA GTCACGTATG ATGTAATGAT ATATTTTTTC ATTATTATAG TAGAATATT 3120
 TTATGGCAAG ATATTGTGG TCTTGATCAT ACCTATTAAA ATAATGCCAA ACACCAATA 3180
 TGAATTTTAT GATGTACACT TTGTGCTTGG CATTAAAAAGA AAAAACACA CATCTGGAA 3240
 GTCTGTAAGT TGTTTTTTGT TACTGTAGGT CTTCAAAGTT AAGAGTGTAA GTGAAAAATC 3300
 TGGAGGAGAG GATAATTTC ACTGTGTGGA ATGTGAATAG TTAATGAAA AGTTATGGTT 3360
 ATTTAATGTA ATTATTACT CAAATCCTTT GGTCACTGTG ATTTCAAGCA TGTTTTCTTT 3420
 TTCTCCTTTA TATGACTTTC TCTGAGTTGG GCAAAGAAGA AGCTGACACA CCGTATGTTG 3480
 TTAGAGTCTT TTATCTGGTC AGGGGAAACA AAATCTTGAC CCAGCTGAAC ATGTCTTCTC 3540
 GAGTCAGTGC CTGAATCTTT ATTTTTTAAA TTGAATGTTC CTTAAAGTT AACATTCTA 3600
 AAGCAATATT AAGAAAGACT TTAATGTTA TTTTGAAGA CTTACGATGC ATGTATACAA 3660
 ACGAATAGCA GATAATGATG ACTAGTTCAC ACATAAAGTC CTTTAAAGGA GAAAACTAA 3720
 AATGAAAAGT GGATAACAG AACATTTATA AGTGATCAGT TAATGCCATA GAGTGAAAGT 3780
 AGTTCTATTG ACATTCCTCA AGATATTTAA TATCAACTGC ATTATGTATT ATGTCTGCTT 3840
 AAATCATTTA AAAACGGCAA AGAATTATAT AGACTATGAG GTACCTTGCT GTGTAGGAGG 3900
 ATGAAAGGGG AGTTGATAGT CTCATAAAC TAATTGGCT TCAAGTTTCA TGAATCTGTA 3960
 ACTAGAATT ATTTTCACC CCAATAATGT TCTATATAGC CTTTGCTAAA GAGCAACTAA 4020
 TAAATTAAC CTATTCTTT AAAAAAAA

Seq ID NO: 164 Protein sequence
 Protein Accession #: NP_037504.1

1 11 21 31 41 51
 MSRTAYTVGA LLLLLGLTLP AAEGKKKGSQ GAIPPPDKAQ HNDSEQTQSP QPGSRNRGR 60
 GQGRGTAMPG BEVLSSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFYCG 120
 QCNSFYIPRH IRKEEGSFQS CSFCKPKKFT TMMVTLNCPE LQPPTKKKR VTRVKQRCIS 180
 IDLD

Seq ID NO: 165 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 GAATTGCATC GGACAGAGCT TCGCCATGGC CGAGTTGCGC GTGGTTGTGG CACTAACACT 60
 GCTACGTTTC CGCCTGAGCG TGGACCGAAC GCGCAAGGTG CGGCGSAAGC CGGAGCTCAT 120
 ACTGCGCAGC GAGAACGGGC TCTGGCTCAA G

Seq ID NO: 166 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1650

1 11 21 31 41 51
 ATGCCACCTC TGCCATCCAG AATGTCTCGG GGGCCCTCCT TGGTGACAGG CAGGATGCTG 60
 CCCATCACAG ACOGCCTGCT GCACCTCCTG GGGCTGGAGA AGACGGCGTT CCGCATATAC 120
 GCGGTGTCCA CCCTTCTCCT CTTCCTGCTC TTCTTCTGT TCCGCTGCT GCTGCGGTTT 180
 CTGAGGCTCT GCAGGAGCTT CTACATCACC TGCCGCGGCG TGCGCTGCTT CCCCAGCCT 240
 CCCCAGCCTC ACTGGCTGCT GGGCCACCTG GGCATGTACC TTCCAAATGA GCGGGGCTT 300
 CAAGATGAGA AGAAGGTACT GGACAACATG CACCATGTAC TCTTGGTATG GATGGGACCT 360
 GTCCTGCCGC TGTGTGTTCT GGTGACCCCT GATTACATCA AACCCTTTT GGGAGCCTCA 420
 GCTGCCATCG CCCCAGGA TGACCTCTTC TATGGCTTCC TAAAACCTTG GCTAGGGGAT 480
 GGGCTGCTGC TCAGCAAAGG TGACAAGTGG AGCCGGCACC GTCGCTGCT GACACCCGCC 540
 TTCCACTTTG ACATCTGTAA GCCTTACATG AAGATCTTCA ACCAGAGCGC TGACATTATG 600
 CATGTAAAT GCGCGCATCT GGCAGAGGGC TCAGCGGTCT CCCTTGATAT GTTTGAGCAT 660
 ATCAGCCTGA TGACCTGGA CAGTCTTCAG AAATGTGTCT TCAGCTACAA CAGCAACTGC 720
 CAAGAGAAGA TGAGTGATTA TATCTCCGCT ATCATTGAAC TGAGCGCTCT GTCTGTCCGG 780
 CGCCAGTATC GCTTGACACA CTACCTCGAC TTCATTACT ACCGCTCGGC GGATGGGCGG 840
 AGGTTCCGGC AGGCCTGTGA CATGGTGCAC CACTTACCA CTGAAGTCAT CCAGGAACGG 900
 CGGCGGGCAC TGCCTCAGCA GGGGGCCGAG GCCTGGCTTA AGGCCAAGCA GGGGAAGACC 960
 TTGGACTTTA TTGATGTGCT GCTCTGGCC AGGGATGAAG ATGGAAGGA ACTGTGAGAC 1020
 GAGGATATCC GAGCCGAAGC AGACACCTTC ATGTTTGAGG GTCACGACAC AACATCCAGT 1080
 GGGATCTCTT GGATGCTGTT CAATTGGCA AAGTATCCGG AATACCAGGA GAAATGCCGA 1140
 GAGAGATTTC AGGAAGTCAT GAAAGGCCGG GAGCTGGAGG AGCTGGAGTG GGACGATCTG 1200
 ACTCAGCTGC CCTTTACAAC TATGTGCATT AAGGAGAGCC TGCGCCAGTA CCCACCTGTC 1260
 ACTCTGTCT CTCGCCAATG CACGGAGGAC ATCAAGCTCC CAGATGGGCG CATCATCCCC 1320
 AAAGGAATCA CTGCTGTGCT CAGCATCTAT GGAACCCACC ACAACCCAC AGTGTGGCCT 1380
 GACTCCAAGG GTTACAACCC CTACCGCTTT GACCCGACCA ACCCAGACGA GCGCTCTCCA 1440

CTGGCCTATG TGCCCTTCTC TGCAGGACCC AGGAATTGCA TCGGACAGAG CTTGCGCATG 1500
 GCCGAGTTGC GCGTGGTGTG GGCCTAACA CTGCTACGTT TCCGCTGAG CGTGGACCGA 1560
 ACGCGCAAGG TCGGCGGAA GCGGAGCTC ATACTGCGCA CGGAGAACGG GCTCTGGCTC 1620
 AAGGTGGAGC CGCTGCTCC GCGGGCTGA

Seq ID NO: 167 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 | | | | |
 MPPLPSRMSR GPSLVTGRML PITDRLLHLL GLEKTAFRY AVSTLLLFLL FFLFRLLLR 60
 LRLCRSFYIT CRRLRCPFPQ PRRNWLLGHL GMYLPNEAGL QDEKKVLDNM HHVLLVWMP 120
 VLPPLVLVHP DYIKPLLGS AATAPKDDLF YGFLKPWLG D LLLSKGDKW SRHRRLLTPA 180
 FHFIDILKPYM KIFNQSDIM HAKWRHLAEG SAVSLDMFEH ISLMTLDSLQ KCVFSYNSNC 240
 QEKMSDYISA IIELSALSVR RQYRLHHYLD FIYRSADGR RFRQACDMVH HFTTEVIQER 300
 RRALRQQGAE AWLKAKQKGT LDFIDVLLLA RDEGKELSD EDIRAEADTF MFEHDTTSS 360
 GISWMLFNLA KYPYQEKCR EETQEVKGR ELELEWDDL TQLEFFTMC I KESLRQYPPV 420
 TLVSRQCTED IKLEPDGRIIP KGIICLVSIY GTHHNPTVWP DSKVYNPYRF DPNPNQQRSP 480
 LAVVPFSAGP RNCIGQSFAM AELRVVVALT LLRFRLSVDR TRKVRKPEL ILRTENGLWL 540
 KVEPLPPRA

Seq ID NO: 168 DNA sequence
 Nucleic Acid Accession #: AK058088.1
 Coding sequence: 252..1772

1 11 21 31 41 51
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 AGGAAACCAA GGCAAGCTCC CCCTGTCAAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA 60
 GCCCCAGATG TGATGAGCGC TTCCAGGCTT CAGGCTCAGA AGCGCGCCCC AGCTCTCCTG 120
 TAACCTCAGG GCCAGTGTGA TGGGAGTTCC TCCACTCAGC ACACCTCCCC TGTAAACACG 180
 CCTGTGGTGG GCAAAAGGGC TTTGGAACGG TTGCTGTCT TTTCTCTCCT GCGTAATTTT 240
 CACTTTCATT CATGATAATG TCGAACACGC ACAAAGCTCG GCTGGAACGC CGGGTCACTG 300
 GCTCAACCAA CCGGTGCGGT TTGCCCAAAC AGCCTTTCTC TGGGGACCTG CTCTCACTTT 360
 CCCAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT 420
 TATGCATTTT ACAAAATCCAG AAGTTTTTCT TTGAGAATTT CAAGAACAAG GACATCCAAA 480
 GTGGGGAAGC AGATGTGATT CTGAGTGCC TGGGCTTCAA ATGGGAGCTC CATCAGCCCC 540
 GGCCTTTTCA GTCTGAGACC TTGGCCAAGC TCTACCTGAA AGCCCTGGCG CAGGGCACCA 600
 CACACCCCTT GAGGGAGCTT TGGGAGCTTC TGGGAGCTCA ATCACCTAAG AAGACCAAAG 660
 AAAAATCCCC TGCAAGAGG ATCATCATTT CCTTGAAGAT CAATGACCCA CTGGTCACTA 720
 AAGTCGCCTT CGCCACGGCC CTGAAGAACC TCTACATGAG TGAGGTGGAG ATTAACCTGG 780
 AAGACCTACT GGGAGTGTG GCTTCCGCCC ACATCCTCCA GTTCAGTGGC CTGTTTCAA 840
 GGTGCGTGGG TGTGATGATA GCCAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG 900
 CCGGCTGCAA GTACAAGGAA GAGCAGCTCA CCACCGGCTG CGAGAAGTGG CTGGAATAGA 960
 ACTTGGTTCC TCTAGGGGGG ACAGAGATCC ACCTCCACAA AATCCACAG GACCTGCTCC 1020
 ACAAGTGTG GAAGTCCCCC AGGTTATTTA CCTTAGTGA ATTCCATCTT CTGAAACAA 1080
 TGCTTTTGT GGTCTTCTGT CAACCTGAAC ACAAGATTC GGAATTCG ACTTATGAAA 1140
 CCGTATGATC ATTTTAAAG AGCTTCTCTG AGAACTGTTG CTTCTGAGC CGGGACATAG 1200
 GACGAGCTT GAGGCGCTC TTCTCTGCT TGGCTCTGCA CGGCATCACC AAAGGCAAGG 1260
 ATCTGAGAGT GCTGCGGCAC CTTAACTTCT TCCAGAGTCA ATGGCTCGAC CAGGTTACAG 1320
 TCAACCATTA CCACGCTACT GAGAATGGGG GCGACATGGT CCACCTGAAA GATCTTAACA 1380
 CCGAGGCTGT GAGATTGGG CTGCTCTTTA ACCAGGAGAA TACAATTAT TCGAAAACGA 1440
 TTGCTCTATA TGATTCTTC TTTAAGATAA AGGAGCTCAA ACATGATACT ACCTCTTATA 1500
 GTTTTACAT GCAGAGAATA AAGCACACAG ACCTGGAATC TCCCTCTGCG GTCTACGAGC 1560
 ACAACCAAGT CAGCCTGCGA GCGGCACGCC TGGTGAAGTA TGAGATCAGA GCAGAGGCC 1620
 TGTTGACGG CAAGTGGCAG GAGTTCAGGA CAAACCAAGT CAAGCAGAAG TTTGGGTGA 1680
 CCACGTCATC CTGCAAAAGC CATACCTTGA AAATCCAAC TGTGGGCATC CCAATCTATG 1740
 TAAGTTTTCG ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGAATCT ATGGGATTTT 1800
 CCCCCACTG GTCTGCATAA AAGAAAATAA AATGACATAA AAGGGAGC

Seq ID NO: 169 Protein sequence
 Protein Accession #: BAB71658.1

1 11 21 31 41 51
 | | | | |
 MIMSNTHKAR LERRVTGSTN RWRLPKQFFS GDLLSLSQMC KALSIDFEEA LRNPDRLCIS 60
 QIQKFFENF KNKDIQSGEA DVILECLGFK WELHQPRLFQ SETLAKLYLK ALAQGTTHPL 120
 RELEELLRAQ SPKKTKEKSP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDLL 180
 GVLASAHILQ FSGLFQRCVD VMIA RLKPST IKKFYEAGCK YKEEQLTGCE EKWLENNLVP 240
 LGGTQIHLHK IPQDLLHKVL KSPRLTFPSE FHLLKTMLLW VFLQLNYKIQ AIPTYETVMT 300
 FFKSFPENCC FLDRDIGRSL RPLFLCLRLH GITKGKDLV LRHLNFPES WLDQVTNHY 360
 HALENGGDMV HLKDLNTQAV RFGLLFNQEN TTYSKTIALY GFFFKIKGLK HDTSYSFYM 420
 QRIKHTDLES PSAVYEHNVH SLRAARLVKY EIRAEALVDG KWQEFRTNQI KQKFLGTTSS 480
 CKSHTLKIQT VGPIYVSFA FIFPAS

Seq ID NO: 170 DNA sequence
 Nucleic Acid Accession #: NM_007000.1
 Coding sequence: 1...777

1 11 21 31 41 51
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 GTTGTGGGCA ATATCATATT TCTGCTGTCA GGCCTGTCCC TGTCTGCTGA GACCATATGG 120
 GTGACAGCCG ACCAGTACCG TGTATACCCA CTGATGGGAG TCTCAGGCAA GGATGACGTC 180
 TTCGCTGGTG CCTGGATTGC CATCTTCTGC GGTCTCTCCT TCTTCATGGT AGCCAGTTTT 240

5 GGTGTGGGTG CCGCACTCTG CCGCCGCCGG TCCATGGTCC TCACGTACCT GGTGCTCATG 300
 CTCATCGTCT ACATCTTCTGA GTGCGCCTCC TGCATCACGT CCTACACCCA CCGTGACTAC 360
 ATGGTGTCCA ACCATCCCTT GATCACCAGG CAGATGCTGA CCTTCTACAG CGCGGACACC 420
 GACCAGGGCC AGGAGCTGAC CCGCTCTGG GACCGCGTCA TGATTGAGCA AGAATGCTGT 480
 GGCACATCTG GTCCCATGGA CTGGGTGAAC TTCACGTGAG CCTTCCGGGC GGCCACTCCG 540
 GAGGTGGTGT TCCCTTGCC CCACTGTGC TGTGCGCGGA CGGAAACTT CATCCCCTC 600
 AACGAGGAGG GCTGCCGCTT GGGGCACATG GACTACCTGT TCACCAAGGG CTGCTTCGAA 660
 CACATCGGCC ACGCCATCGA CAGCTACACG TGGGGTATCT CGTGGTTTGG GTTTGCCATC 720
 10 CTGATGTGGA CGCTCCCGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGA

Seq ID NO: 171 Protein sequence
 Protein Accession #: NP_008931.1

15 1 11 21 31 41 51
 MASAAAAEAE KGSPVVVGLL VVGNIIILLS GLSLFAETIW VTADQYRVYP LMGVSGKDDV 60
 FAGAWIAIFC GFSEFMVASF GVGAALCRRR SMVLTYLVLV LIVIIFECAS CITSYTHRDY 120
 MVSNPFLITK QMLFFYSADT DQGQELTRLW DRVMIQECC GTSGPMDVWN FTSAFRAATP 180
 20 EVVFPWPPLC CRRTGNFPL NEEGCRLGHM DYLFKGCFFE HIGHAIDSYT WGISWFGFAI 240
 LMWTLFVMLI AMYFYTML

Seq ID NO: 172 DNA sequence
 Nucleic Acid Accession #: NM_006760.1
 Coding sequence: 39..593

25 1 11 21 31 41 51
 GAAAGCCTGC CAGCACCTAT TCCACCTCCC AGCCCAGCAT GGCACCCCTG CTGCCCATCC 60
 30 GGACCTTGCC CTGTGATCTG ATTCTGCTGG CTCTGCTGTC CCCAGGGGCT GCAGACTTCA 120
 ACATCTCAAG CCTCTCTGGT CTGCTGTCCC CGGCGCTAAC GGAGAGCCTG CTGGTTGCCT 180
 TGCCCCCTG TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGAGAG GCCAATGACA 240
 GCAAAGTGGT GACGTCCAGC TTTGTGGTGC CTCGCTGCCG TGGGCGCAGG GAACTGGTGA 300
 GTGTGGTGGG CAGTGGTGCT GGCTTCACAG TCACTCGGCT CAGTGCATAC CAGGTGACAA 360
 35 ACCTCGTGCC AGGAACCAAA TTCTACATTT CCTACCTAGT GAAGAAGGGG ACAGCCACTG 420
 AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGGAA TCCATTGGGC 480
 TGGGTATGGC CCGCACAGGG GGCATGGTGG TCATCACGGT GCTGCTCTCT GTGCCATGT 540
 TCCTGCTGGT GCTGGGCTTC ATCATTGCCC TGGCACTGGG CTCCCGCAAG TAAGGAGGTC 600
 TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGGCACCA TCCAGCTCCC CAGCCACCT 660
 40 GCTCCAGGC CCCAGGCTG TGGCTCCCTT GGTGCCCTCG CCTCTCTC CTGCCCTCCT 720
 CTCCCTAGA GCCCTCTCCT CCTCTGTCC CTCCTCTGTC CCCAGTGCC TCACCTTCCA 780
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45 Seq ID NO: 173 Protein sequence
 Protein Accession #: NP_006751.1

50 1 11 21 31 41 51
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 VKKGTATESS REIPMSTLPR RNMBISGLGM ARTGGMVVIT VLLSVAMFLV VLGFIIALAL 180
 GSRK

55 Seq ID NO: 174 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..2733

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 65 GAGAAAAGAG ATTTGAGAAA TTTTCTGAAG CTCTGAAGC CTCCATTATT ATGGTCACAT 240
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 80 GCCAGCCATT TCAGGGTGTG CAATTCAACA ATGGAGGATG TCATCAGTAT AGCTGACAAT 1140
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Seq ID NO: 175 Protein sequence
 Protein Accession #: Eos sequence

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 ASHFRVSNST MEDVISTADN ILNSASVTNW TVLLREEKYA SSRLLLETLEN ISTLVPPAL 420
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Seq ID NO: 176 DNA sequence
 Nucleic Acid Accession #: AB035089.1
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	GCTCTTCTCA	GTGTCAGCCT	GTTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
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 TCCC

Seq ID NO: 177 Protein sequence
 Protein Accession #: BAB21525.1

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 QVTENTTEKA ATYHVDRSGN VHHQFQKLLT EFNKSTDAYE LKIANKLFE KTYQLQEYL 120

DAIKKFYQTS VESTDFANAP EESRKKINSW VESQTNEKIK NLFPPDGTIGN DTTLLVLVNAI 180
 YFKGQWENKF KKENTKEEFK WPNKNYKSV QMMRQVNSFN FALLEDVQAK VLEIPYKGD 240
 LSMIVLLPNE IDGLQKLEEK LTAEKLEMEWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300
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Seq ID NO: 178 DNA sequence
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 Coding sequence: 50..1240

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Seq ID NO: 179 Protein sequence
 Protein Accession #: NP_001901.1

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 QPSQSSTYSY PGQSFSIQYG TGSLSGIIGA DQVSVEGLTV VQQQFGESVT EPGQTFVDAB 180
 FDGILGLGYP SLAVGGVTPV PDNMQAQLNV DLPMSVYMS SNPEGAGSE LIFGGYDHS 240
 FSGSLNWVPV TKQAYWQIAL DNIQVGGTVM FCSEGCQAIV DTGTSITIGP SDKIKQLQNA 300
 IGAAPVDGEY AVECANLNV PDVTFTINGV PYTLSPXTAYT LLDFVDMQF CSSGFQGLDI 360
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Seq ID NO: 180 DNA sequence
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 Coding sequence: 319..1575

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 TACACCGACA AGTTGTTCAA GTTCCGCAAT AACCGGTGGG AAGACATCCT GAGCGATGAG 180
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 GGGCTTTGTC AACACGTG

Seq ID NO: 181 Protein sequence
 Protein Accession #: NP_060528.1

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 30 FRDIASPKFS MPSPVTRVIT ADFDNDQELE IFFNNIAYRS SSANRLFRVI RREHGDPLIE 180
 ELNPGDALEP EGRGTGGVVT DFDGDMLDL ILSHGESMAQ PLSVFRGNQG FNNNWLVRVP 240
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 KMSVRNVASG EMNSVLEILY PRDEDTLQDP APLETPMNAS SSHSCALET S PYVSTPMEAT 360
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Seq ID NO: 183 Protein sequence
Protein Accession #: CAC08451

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GRYSIIYIANY AYGNVGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
10 LSSASADIFC DNENGNPFLF HNRGDGTFVD AAASAGVDDP HQHGRGVALA DFNRDGKVDI 300
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RSSSANRLFR VIRREHGDPL IEELNPGDAL EPEGRGTGGV VTDFDGDGML DLILSHGESM 420
AQPLSVFRGN QGFNNNWLVR VPRTRFGAFA RGAKVVLVTK KSGAHLRIID GSGGYLCEME 480
PVAHFGLGKD EASSVEVTFW DGKMVSRNVA SGE MNVSLEI LYPRDEDTLQ DPAPLECGQG 540
15 FSQQENGHCM DTNECIQFFV VCPDKPVCV NTYGSYRCRT NKKCSRGYEP NEDGTACVGT 600
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Nucleic Acid Accession #: FGENESHH
Coding sequence: 1..4794

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TCACCTACT ACAGCGCTGG GGACCGGCAG GGAACGCCA TCGGGGTGAC AGCCTGCGAC 240
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30 CCACCTACAA CCCCCTGCGG CCTCCTGGGT CTGCCTCCAC TCAGCGGAAG GGACTTTTCC 420
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35 GCCTGTGTGG ACAGAAAGGG CTCTGGACGC TACTCTATCT ACATTGCCAA TTACGCTTAC 720
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5 GTCCAATCAC TACCACAGAA AGGGGCTACG GGCTCCAATC ACTACCAGGA AAAGGGGCTA 3720
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 20 CAGAAAGCTC CAGGTATTCC AGAAGCCCAA GTGTATGAAC AAGATCAGGA ATAA

Seq ID NO: 185 Protein sequence
 Protein Accession #: FGENESHH

25 1 11 21 31 41 51
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 PHPRAPGMDP KCKGRHAEPG LMAEALGAWP ALSTTVVPGG LRSWEESRQK QQAMSRCALR 480
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 35 GPGRVAKREI GRETGAVGRP LSHPLVPNFP SCLRPLEAGT VPGAALPGNP GNWVLDMAKA 600
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 RKGLRAPITT RKRGVGVQSL PGKGATGSNH YQEKGLRGPI TTRKRGYGLQ SLPGKGATGS 1200
 NHYQEKGLQG PITTRKRGYR VQSLPGKGAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE 1260
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 Nucleic Acid Accession #: NM_000584.1
 Coding sequence: 75..374

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 GCATAAAGAC ATACTCCAAA CCTTCCACC CCAAATTAT CAAAGAACTG AGAGTGATTG 240
 65 AGAGTGGACC AACTGCGCC AACACAGAAA TTATTGTAAA GCTTCTGAT GGAAGAGAGC 300
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 GAATGGGTTT GCTAGAATGT GATATTGAA GCATCACATA AAAATGATGG GACAATAAAT 780
 TTTGCCATAA AGTCAAATTT AGCTGGAAT CCTGGATTTT TTTCTGTAA ATCTGGCAAC 840
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 CTATTTATTA TTTATGTATT TATTTAAGCA TCAAATATTT GTGCAAGAAT TTGAAAAAAT 1080
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5 Seq ID NO: 187 Protein sequence
 Protein Accession #: NP_000575.1

10 1 11 21 31 41 51
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15 Seq ID NO: 188 DNA sequence
 Nucleic Acid Accession #: NM_003661.1
 Coding sequence: 1..1152

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 CAAGAAGTGT GA

40 Seq ID NO: 189 Protein sequence
 Protein Accession #: NP_003652.1

45 1 11 21 31 41 51
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 YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGLSIS SGILTLVGMG 180
 LAPFTEGSSL VLLEPGMELG ITAALTGITS STMDYGKKWW TQAQAHDLVI KSLDKLKEVR 240
 50 EFLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPISAESG 300
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55 Seq ID NO: 190 DNA sequence
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 Coding sequence: 1..1968

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Seq ID NO: 191 Protein sequence
 Protein Accession #: NP_055267.1

1 11 21 31 41 51
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 SSVMKCKAYT DCLSNLNVVI KPGTKETDNV CGTLPSFSSS TSPSPGTAIF PRPEHMETHE 240
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Seq ID NO: 192 DNA sequence
 Nucleic Acid Accession #: XM_044533
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 10 TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG 3720
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Seq ID NO: 193 Protein sequence
 Protein Accession #: XP_044533.3

15 1 11 21 31 41 51
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 20 SFKGGDPQRD CQNYIKILLP LSGSHLFTCG TAAFSPMCTY INMENFTLAR DEKGNVLLD 180
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 VASAYIPESL GSLQGGDDKI YFFFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
 TSFLKAQLLC SRPDDGFPPN VLQDVFTLSP SPQDWRDRLF YGVFTSQWHR GTTEGSAVCV 360
 FTMKDVQRVF SGLYKEVNRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
 25 NFLKDHFLMD GQVRSRMLLL QPQARYQORVA VHRVPLHHT YDVLFLGTGD GRLHKAIVSVG 480
 PRVHIIIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
 PYCAWSGSSC KHVSLYQPQL ATRPWQDIE GASAKDLCSA SSVVSPSFVP TGEKPCBQVQ 600
 FQNTVNTLA CLLLSNLATR LWLRNGAPVN ASASCHVLPT GDLLLVTGTTQ LGFEQCSWSLE 660
 EGGQQLVASV CEPVEDGDVA DQTDGGGSPV VIIISTSRVSA PAGGKASWGA DRSYWKFLV 720
 30 MCTLFVLAVL LPVLFLLYRH RNSMKVPLKO GECASVHPKT CPVVLPPETR PLNGLGPPST 780
 PLDHRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSV

Seq ID NO: 194 DNA sequence
 Nucleic Acid Accession #: NM_022819.1
 Coding sequence: 1..635

35 1 11 21 31 41 51
 ATGGCAGATG GGGCAAAGGC CAACCCCAAA GGGTTCAAAA AGAAGGTGCT GGATAGATGC 60
 TTCTCTGGGT GGAGGGGCCC ACGCTTCGGG GCCTCCTGTC CTTCAAGAAC CTCCAGGTCT 120
 40 AGCCTGGGTA TGAAGAAGTT CTTACCGTG GCCATCCTTG CTGGCAGCGT TCTGTCCACA 180
 GCTCACGGCA GCTCTCTCAA CCTGAAGGCC ATGGTGGAGG CCGTCACAGG GAGGAGCGCC 240
 ATCCTGTCTCT TCGTGGGCTA CGGTTGCTAC TGTGGGCTGG GGGGCCGTGG CCAGCCCAAG 300
 GATGAGGTGG ACTGGTCTG CCACGCCAC GACTGCTGCT ACCAGGAAC CTTTGACCAA 360
 45 GGCTGTCAAC CCTATGTGGA CCACATGAT CACACCATCG AGAACACAC TGAGATAGTC 420
 TGCAGTGACC TCAACAAGAC AGAGTGTGAC AAGCAGACAT GCATGTGTGA CAAGAACATG 480
 GTTCTGTGCC TCATGAACCA GACGTACCGA GAGGAGTACC GTGGCTTCCT CAATGTCTAC 540
 TGCCAGGGCC CCACGCCCAA CTGCAGCATC TATGAACCGC CCCCTGAGGA GGTCACTGCG 600
 AGTCACCAAT CCCAGCGCC CCCCGCCCT CCCTAG

Seq ID NO: 195 Protein sequence
 Protein Accession #: NP_073730

55 1 11 21 31 41 51
 MADGAKANPK GFKKKVLDRC FSGWRGPRFG ASCPSRTSRS SLGMKKFFTV AILAGSVLST 60
 AHGSLNLKA MVEAVTGRSA ILSFVGYGCV CGLGGRGQPK DEVDWCCAH DCCYQELFDQ 120
 GCHPYVDHYD HTIENNTIIV CSDLNKTECD KQTCMCDKNM VLCLMNQTYR EBYRGFLNVY 180
 CQGPTPNCSI YEPPEEVEVC SHQSPAPPAP P

Seq ID NO: 196 DNA sequence
 Nucleic Acid Accession #: XM_028196.1
 Coding sequence: 1315..1791

65 1 11 21 31 41 51
 GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60
 GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCCTTTCTGT CTGTCTCCTT GCTCTGCCCC 120
 AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180
 70 ATGGCCTGGG CTGGGCCCTT GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAGG 240
 CTCTTGTGGG CAAAGCAGGG GAGGCCCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG 300
 CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CTTGGGCTG 360
 GGGTCACCGT AGGCCCATG TAGCACCTG GTTCCCTGCT CTGTAGGTGA CAGGAGCCAG 420
 CCCAGCCAGG TGTGCTCCTT CCCAGGCCCT TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480
 75 CGCCCGCCCC ACCTTCCTTC CCACCCACAT GCCGAAGGGT GGCCAGGCAG GCAGGTGGAC 540
 GAGTCCAGGC AGCGGCTGAG TCAGTGTGTG TGGAAATGTT TGGCCGCTCC CAGCTGCACC 600
 CTGCCCTTAC CTGCCACCAC CTCACCTTCA TCCTCAGGCG CTGCGGCCCT GAGCCCTGCT 660
 CAGGAATGCA CCTTAGCCAC AGGCCTGCTC AGTGAGCTCC GCCGACAGCC AGCCCTGCTC 720
 CTCCCGCAT GACCTGACG ACCCTCTGG GCTTCCAAGT TCCTGGGGGC TGCAGTGAAC 780
 80 ATGCTCCACC TGCATGGCTG GCAAACCATG GTGGGCCCCA GCTGTGGTGC GTGCTGGGGT 840
 AGAGGCAAGG AAGTGATGGG ACCGCAGAGA TGAGACCCCC AGGGATGAGA TGGGACCCCC 900
 AGGACGGGCC CAGGTCCAG GGCCTCAGAG AGAGAAGCAG GGAGGGAGAG AGCTTCTG 960
 TGGAGGACGC ATCTACAGT GGGGGCAAGG GTGCTCTGAG GTCCGGTGAA GGCAGGGACT 1020
 AGGCTGCCCA GGCCCTGCCT GCTTGGCTGG GGCTGGGGGC TGCTGGGAGG TGGCTGGGAG 1080
 GCTGGGCGCT GGCAGCTTCT CTGGAGCTTT GGCCAGGGTC CAGAGCCTCC CTCCTTCAG 1140

5 CTTCCTGCTG CACAGAACCC TGGCCCTGG CCACCCCGTG CTGCTCTCTT GCCCTGGCAG 1200
 ACCCAGCACT GGCTGCTGCT AGTCAGATGG GGTAGCGGGC AGGGGCCGGA GGGGCCACCC 1260
 TCCCAGCTGA CCCAGCCTCC TGGGCCGCTT CTTCCAAACC AGCAGGGTAG AAAGATGGGG 1320
 CACCCACCAAG TCTCTCCAG TGGCCCGGCC CCAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380
 ATTCCAGACC TTGTCGCCGG GACCCCTGT GAGTTGTGGG ATTCCCAAGA GGGGTGTGGG 1440
 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC 1500
 CCAGGGGCCCC GCTGGGCTCT CATTGCCGGC GCCCTTGCCG CGGGCGTCTT CCTCGTCTCC 1560
 TGCTCTCTCT GTGCTGCTGT CTGCTGCTGC CGCCGCCACA GGAAGAAGCC CAGGGACAAG 1620
 10 GAGTCCGTGG GTCTGGGCAG TGCCCGCGGC ACCACCACCA CCCACCTGGT GAGGAGCGGC 1680
 TCCTTGCTCA CTCAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740
 GGCAGATTCA GCCCCAGGGA TGGTTTAACC CCCACAGAGG CAGGGCGTTG AGGACCTTCC 1800
 TGGCAGGGA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCAT 1860
 GGGCCCGAGG GAGCCACAGC GGGTTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT 1920
 TTTGGGTGGG TTTGGCCGGT CTCACAGAGC GAAGCCGACG ATTTGTGCTT GTTGGGTGGC 1980
 15 CTGGCCTGGA GGCAGGGGGT CTTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCACAGG 2040
 CTCGTGATGAG GCATGATGTC AGCACCACCT GCCCTTGCTC CCAACTCACT CCAGGTGCAA 2100
 CCTGATGTGG ATGGCCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCTGTCAG 2160
 CTCCTCCCTG AGTTTCGACT TGAAGCCAG GAGGTGAAGG GCCCCGCTGC GCGAGACAG 2220
 CGGTTCGCG AGTTTCCGGA AAGGGTGACG GGGGAAGGGC AGACCCCATG CCCTGGGTGG 2280
 20 TGGGAGCTG ACAGGGCAGG GGCCCTTGGC TGAGCCCAAC CCGCTGGCTC CCAGATCAGG 2340
 GTGGGCCTGA GGCAGGCAGC CGACTGAGG CCTGGGGCA CCGTGGACCC CTATGCCCGG 2400
 GTCAGCGTCT CCACCCAGGC CGGACACAGA CATGAGACAA AAGTGCACCG AGGCACGCTC 2460
 TGCCCGCTGT TTGACGAGAC CTGCTGCTTC CACGTGAGTC AGGATGGTC GGTGGGTGG 2520
 25 GCCTGGACGG CTGATGGGG CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGCCTGGGCA 2580
 GCTGGGTGGG CCTGAGCTAG GGCAGAGGG CCTGGCTCAC GCCGTGCTT CAGATCCGCG 2640
 AGGCGGAGCT GCCAGGGGCC ACCCTGCAGG TGCAGCTTTT CAACTTCAAG CGCTTCTCGG 2700
 GGCATGAGCC CCTGGGTGAG CTCGCTGCTC CACTGGGCAC CGTGGATCTG CAGCATGTT 2760
 TGGAGCACTG GTACCTGCTG GGCCTGGCGG CTGCCACTCA GGTGAGGTGC TGGTCACAG 2820
 30 GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CCTGCCCTAT GGGCCATCGG AAAGACAGGC 2880
 CTGATGGGCA GCATTTTCGG GGGTCTGAGC CCCAACTCGG CCAGAATCAC CCTCCCGGG 2940
 TGAAGCCCTT TTTGCTGCCC ACAGCCCGAG CAGGTGCGGG AGCTGTGCTT CTCTCTCCG 3000
 TACGTGCCCA GCTCAGGCGG GCTGACCGTG GTGGTGTCTG AGGCTCGAGG CCTGCGTCCA 3060
 35 GGACTTGCAG AGCCCTACGT GAAGTCCAG CTCATGCTGA ACCAGAGGAA GTGGAAGAAG 3120
 AGAAGACAG CCACCAAAAA GGCACGCGG GCCCCTACT TCAATGAGGC CTTACCTTC 3180
 CTGGTGCCCT TCAGCCAGGT CCAGAATGTG GACCTGGTGC TGGCTGTCTG GGCAGCGAGC 3240
 CTGCCGCTCC GAACCTGAGC CGTAGGCAAG GTGCACCTGG GTGCCCGGGC CTCGGGGCAG 3300
 CCCCTGCAGC ACTGGGCAGA CATGCTGGCC CACGCCCGGC GGCCTATGTC CCAGCGGCAG 3360
 40 CCCCTGCGGC CAGCCAGGGA GGTGGACGCG ATGCTGGCCC TGCAGCCCCG CCTTCGCTG 3420
 CGCCTGCCCT TGCCCCACTC CTGAATGCAC CACATGCCCT TGTCTCCCG CTGAGCCAG 3480
 GCATTGCCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC

Seq ID NO: 197 Protein sequence

Protein Accession #: XP_028196.1

45 1 11 21 31 41 51
 | | | | | |
 MGHPVPVSPA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAGWGL QLSTDALSIA 60
 STPGPRWALI AGALAAGVLL VSCLLCAACC CRRHRKKPR DKESVGLGSA RGTTHLVR 120
 50 SGLLTQGRE GLKSLRLQSPG QRGFEFSPRDG LTPTEAGR

Seq ID NO: 198 DNA sequence

Nucleic Acid Accession #: NM_000612.2

Coding sequence: 553..1095

55 1 11 21 31 41 51
 | | | | | |
 TTCTCCCGCA ACCTTCCCTT CGCTCCCTCC CGTCCCCCCC AGCTCCTAGC CTCGCACTCC 60
 CTCCCCCCT CACGCCCGCC CTCTCGCTT CGCCGAACCA AAGTGGATTA ATTACACGCT 120
 60 TTCTGTTTCT CTCCTGCTG TTCTCTCCCG CTGTGCGCCT GCCCGCTCTT CGCTGTCTCT 180
 TCTCCCCCTC GCCCTCTCTT CGGCCCCCCC CTTTCACTGT CACTCTGTCT CTCCCACTAT 240
 CTCTGCCCCC CTCTATCCTT GATACAAACAG CTGACCTCAT TTCCCGATAC CTTTTCCTCC 300
 CCGAAAAAGTA CAACATCTGG CCCGCCCCAG CCCGAAGACA GCCCGTCTCT CTTGGACAAT 360
 CAGACGAATT CTCCCCCCCC CCCCAAAAA AAAAGCCATC CCCCCTCTCT GCGCCGTGCG 420
 65 ACATTGCGCC CCCGCGACTC GGCCAGAGCG GCGCTGGCAG AGGAGTGTCC GGCAGGAGGG 480
 CCAACGCCCG CTGTTCCGTT TCCGACACGC AGCAGGGAGG TGGGCGGCAG CGTCGCCCGC 540
 TTCCAGACAC CAATGGGAAT CCCAATGGGG AAGTCGATGC TGGTGTCTCT CACTTCTTGT 600
 GCCTTCGCCT CGTGTGCTAT TGCTGCTTAC CGCCCAAGTG AGACCTGTG GCGCGGGGAG 660
 CTGGTGGACA CCTCCAGTT CGTCTGTGGG GACCGCGGCT TCTACTTTCAG CAGGCCCGCA 720
 70 AGCCGTGTGA GCCGTGCGAG CCGTGGCATC GTTGAAGAGT GCTGTTTCCG CAGCTGTGAC 780
 CTGGCCCTCC TGGAGACGTA CTGTGCTACC CCGCCCAAGT CCGAGAGGGA CGTGTCCGAC 840
 CCTCCGACCG TGCTTCCGGA CAACCTCCCC AGATACCCCG TGGGCAAGTT CTTCAATAT 900
 GACACCTGGA AGCAGTCCAC CCAGCGCCTG CGCAGGGGCC TGCCCTGCCCT CCTGCGTGCC 960
 CGCCGGGGTC ACGTGTCTCG CAAGGAGCTC GAGGCGTTCA GGGAGGCCAA ACGTCAACGT 1020
 75 CCCCTGATG CTCTACCCAC CCAAGACCCC GCCACGGGG GCGCCCCCCC AGAGATGGCC 1080
 AGCAATCGGA AGTGAGCAA ACTGCCGCAA GTCTGCAGC CGGCGCCACC ATCTGTCAGC 1140
 CTCTCTCTGA CCACGGAGCT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCACAGT 1200
 CCCCCGCGG CTCTCTCTGA CCCAGTCCCC GTGCCCGGCC TCCCGGAAC AGGCTACTCT 1260
 80 CCTCGGCCCC CTCCATCGGG CTGAGGAAGC ACAGCAGCAT CTTCAACAT GTACAAAATC 1320
 GATTGGCTTT AAACACCTTT CACATACCTT CCCCCC

Seq ID NO: 199 Protein sequence

Protein Accession #: NP_000603.1

1 11 21 31 41 51

MGIPMGKSM | VLLTFLAFAS | CCIAAYRPSE | TLCGGELVDT | LQFVCGDRGF | YFSRPASRVS 60
 RRSRGIVEEC | CFRSCDLALL | ETYCATPAKS | ERDVSTPPTV | LPDNFPRYPV | GKFFQYDTWK 120
 QSTQRLRRGL | PALLRRARRGH | VLAKELEAFR | EAKRHRPLIA | LPTQDPAHGG | APPEMASNRK

Seq ID NO: 200 DNA sequence
 Nucleic Acid Accession #: AK057131.1
 Coding sequence: 61..1146

1 11 21 31 41 51
 AGTCTGGGCG | TTTAGGTCAG | AACTACCCCG | GTAGCCTGAC | AGCAGGAGCT | CGAGAGAAGC 60
 ATGGCTCAGC | GGTGCGTTTG | CGTGCTGGCC | CTGGTGGCTA | TGCTGCTCCT | AGTTTTCCCT 120
 ACCGTCTCCA | GATCGATGGG | CCCGAGGAGC | GGGGAGCATC | AAAGGGCGTC | GCGAATCCCT 180
 TCTCAGTTCA | GCAAAGAGGA | ACGCGTCGCG | ATGAAAGAGG | CGCTGAAAGG | TGCCATCCAG 240
 ATTCCAACAG | TGACTTTTAG | CTCTGAGAAG | TCCAATACTA | CAGCCCTGGC | TGAGTTCGGA 300
 AAATACATTC | ATAAAGTCTT | TCCTACAGTG | GTCAGCACCA | GCTTTATCCA | GCATGAAGTC 360
 GTGGAAGAGT | ATAGCCACCT | GTTCACTATC | CAAGGCTCGG | ACCCCAGCTT | CGAGCCCTAC 420
 CTGCTGATGG | CTCACTTTGA | TGTGGTGCC | GCCCTGAAG | AAGGCTGGGA | GGTGCCCCCA 480
 TTCTCTGGGT | TGGAGCGTGA | TGGCGTCATC | TATGGTTGGG | GCACACTGGA | CGACAAGAAC 540
 TCTGTGATGG | CATTATGCGA | GGCCTTGGAG | CTCCTGCTGA | TCAGGAAGTA | CATCCCCCGA 600
 AGATCTTTCT | TCATTCTCT | GGGCCATGAT | GAGGAGTCAT | CAGGGACAGG | GGCTCAGAGG 660
 ATCTCAGCCC | TGCTACAGTC | AAGGGGCGTC | CAGCTAGCCT | TCATTGTGGA | CGAGGGGGGC 720
 TTCTCTTGG | ATGATTTTCT | TCCTAACTTC | AAGAAGCCCA | TCGCCTTGAT | TGCAGTCTCA 780
 GAGAAAGGTT | CCATGAACCT | CATGCTGCAA | GTAAACATGA | CTTCAGGCCA | CTCTTCAGCT 840
 CCTCCAAAGG | AGACAAGCAT | TGGCATCCTT | GCAGCTGCTG | TCAGCCGATT | GGAGCAGACA 900
 CCAATGCCTA | TCATATTTGG | AAGCGGGACA | GTGGTGACTG | TATTGCAGCA | ACTGGCAAAAT 960
 GAGGTTTATG | GAGAGAAATC | CCTTAACCAA | TGCAATAATC | AGGACCACCA | CGGCCTCAC 1020
 CATATTTCAA | GCAGGGGTCA | AGTTCAATGT | CATCCCCCA | GTGGCCAGG | CCACAGTCAA 1080
 CTTCGGGATT | CACCCCTGGC | AGACAGTCCA | AGAGGTCTTA | GAACTCACGA | AGAATCTTGT 1140
 GGTGATAAAG | AGAGTCCAGT | TCCATGTGTT | GAGTGCCTTT | GACCCCTCC | CCGTCAGCCC 1200
 TTTCTGATGAC | AAGGCTTGG | GCTACCAAGT | GCTCCGCCAG | ACCGTACAGT | CCGTCTTCCC 1260
 GGAAGTCAAT | ATTACTGCCC | CAGTTACTTC | TATTGGCAAC | ACAGACAGCC | GATTCTTTAC 1320
 AAACCTCACC | ACTGGCATCT | ACAGGTTCTA | CCCCATCTAC | ATACAGCCTG | AAGACTTCAA 1380
 ACGCATCCAT | GGAGTCAACG | AGAAAATCTC | AGTCCAAGCC | TATGAGACCC | AAGTGAATTT 1440
 CATCTTTGAG | TTGATTCAGA | ATGCTGACAC | AGACCAGGAG | CCAGTTTCTC | ACCTGCACAA 1500
 ACTGTGAGGT | CAAGGGGCTT | GCTGGGTTAG | GCATGCCCGA | CCCCGGGACA | GGACTAAGCC 1560
 AAGGGGGAAA | GCTAGTGTGG | ATGAAACTTT | TGATCAAAAC | CACATTGTAA | AACATTGCCC 1620
 ATCTGTCTTG | CTCACTCTTA | AACTCTCCCA | AGAACAAGGC | CGGGGTAAGG | TAAAGTCAGC 1680
 AGAAATCTGG | CTCTCCCTT | CCTCCGACA | TCTGCATCCC | TTGATCCACT | GGCATTGCT 1740
 GCCCTCTTGT | CCCTTATCTG | TCTTATGCTG | GTTATTTTAC | TGCTTCACCT | TCCAGGCTTG 1800
 ACTTAAACAA | TCTAGATTGG | AGAAATCTCA | ACCAGTTGTT | ACCTGATAGG | AGTCTTTAAT 1860
 TTAGGGCACT | TTTGCTGGGA | TGCTTTCTCC | AGAGCTTATA | TATTCTTCT | TACTAGAACT 1920
 TTCTTCCCTT | CTTTATTTCC | CTCTCTTCTT | GGACTCATGA | GCTGTCTCTT | CATCTCTCCT 1980
 CTCTCTCTCT | CATCTCTCCC | CTTACTCTTC | AATTTATTCT | ACTTCTGGAC | CTGGACTTAC 2040
 CCAACTGTG | ATACTACCAT | AATTGTCAAC | ATAATCAGTC | AAATAAAGTG | ATCTGTGCAT 2100

Seq ID NO: 201 Protein sequence
 Protein Accession #: BAB71368.1

1 11 21 31 41 51
 MAQRVCVCLA | LVAMLLLVFP | TVSRSMGPRS | GEHQRASRIP | SQFSKEERVA | MKEALKGAIQ 60
 IPTVTFSEK | SNTTSLAEFG | KYIHKVFPTV | VSTSFQHEV | VEEYSHLFTI | QGSDPSLQPY 120
 LLMAHFDVVP | APEBGWVFP | FSGLERDGI | YGWGLDDKN | SVMALLQALE | LLLIRKYIPR 180
 RSFFISLGH | EESSGTGAQR | ISALLQSRGV | QLAFIVDEGG | FILDDFIPNF | KKPIALIAVS 240
 EKGSMNMLQ | VNMSTGSHSA | PPKETSIGIL | AAASVRLQET | PMP1IFGSGT | VVTVLQQLAN 300
 EVYGEKSLN | Q | CNNDHGHGTH | HIQSRGQVQC | HPPSGPGHSQ | LPDSPWTDSP | RGPRTHEHC 360

Seq ID NO: 202 DNA sequence
 Nucleic Acid Accession #: NM_004217.1
 Coding sequence: 58..1092

1 11 21 31 41 51
 GGCCGGGAGA | GTAGCAGTGC | CTTGGACCCC | AGCTCTCCTC | CCCCTTTCTC | TCTAAGGATG 60
 GCCCAGAAGG | AGAACTCCTA | CCCCTGGCCC | TACGGCCGAC | AGACGGCTCC | ATCTGGCCTG 120
 AGCACCTTGC | CCCAGCGAGT | CCTCGGAAA | GAGCCTGTCA | CCCCATCTGC | ACTTGTCTCT 180
 ATGAGCCGCT | CCAATGTCCA | GCCCACAGCT | GCCCTGGGCC | AGAAGGTGAT | GGAGAATAGC 240
 AGTGGGACAC | CCGACATCTT | AACCGGGCAC | TTCACAAATG | ATGACTTTGA | GATTGGGCGT 300
 CCTCTGGGCA | AAGGCAAGTT | TGGAAACGTG | TACTTGGCTC | GGGAGAAGAA | AAGCCATTTC 360
 ATCGTGGCGC | TCAAGGTCCT | CTTCAAGTCC | CAGATAGAGA | AGGAGGGCGT | GGAGCATCAG 420
 CTGGCAGAG | AGATCGAAAT | CCAGGCCAC | CTGCACCATC | CCAACATCCT | CGCTCTCTAC 480
 AACTATTTT | ATGACCGGAG | GAGGATCTAC | TTGATTCTAG | AGTATGCCCC | CCGCGGGGAG 540
 CTCTACAAGG | AGCTGCAGAA | GAGCTGCACA | TTTGACGAGC | AGCGAACAGC | CACGATCATG 600
 GAGGAGTTGG | CAGATGCTCT | AATGTACTGC | CATGGGAAGA | AGGTGATTCA | CAGAGACATA 660
 AAGCCAGAAA | ATCTGCTCTT | AGGGCTCAAG | GGAGAGCTGA | AGATTGTGCA | CTTCGGCTGG 720
 TCTGTGATG | CGCCCTCCCT | GAGGAGGAAG | ACAATGTGTG | GCACCCCTGA | CTACCTGCCC 780
 CCAGAGATG | TTGAGGGGCG | CATGCACAA | GAGAAGGTGG | ATCTGTGGTG | CATGGAGTGG 840
 CTTTGTCTATG | AGCTGCTGGT | GGGGAACCCA | CCCTTTGAGA | GTGCATCACA | CAACGAGACC 900
 TATCGCCGCA | TCGTCAAGGT | GGACCTAAG | TTCCCGCTT | CTGTGCCAC | GGGGAGCCAG 960
 GACCTCATCT | CCAACTGCT | CAGGCATAAC | CCCTCGGAAC | GGCTGCCCTT | GGCCAGGTC 1020

TCAGCCCACC CTTGGGTCCG GGCCAACTCT CGGAGGGTGC TGCCTCCCTC TGCCCTTCAA 1080
 TCTGTGCGCT GATGGTCCCT GTCAATCACT CGGGTGCCTG TGTTTGTATG TCTGTGTATG 1140
 TATAGGGGAA AGAAGGGATC CCTAATGTGT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200
 TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 203 Protein sequence
 Protein Accession #: NP_004208

1 11 21 31 41 51
 | | | | |
 MAQKENSYPW PYGRQTAPSG LSTLPQVRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN 60
 SSGTDPDILTR HFTIDDFEIG RPLGKGFN VYLAREKKSH FIVALKVLFK SQIEKEGVEH 120
 QLRREIEIQH HLHHPNLRRL YNYFYDRRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI 180
 MEELADALMY CHGKKVIHRD IKPENLLGL KGELKIADFG WSVHAPSLRR KTMCGTLDYL 240
 PPEMIEGRMH NEKVDLWCIG VLCYELLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA 300
 QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPPSAL QSWA

Seq ID NO: 204 DNA sequence
 Nucleic Acid Accession #: AK055663
 Coding sequence: 38..1423

1 11 21 31 41 51
 | | | | |
 AGAACGGCTT CCGGCGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTCG 60
 AAAACACCAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA 120
 CCGAAGGTCC TGAAGAATAC TGCTCTTTGG TGTAAATAAAC TTGATATGTA CTGGCTTCCT 180
 GCTTATGTGG TGCAGTTCTA CTAATAGTAT AGCTTTAACT GCCTATACTT ACCTGACCAT 240
 TTTTGTATCT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAACAT TGAGGAAACC 300
 TAGCCCTGTC TATTCATTTG GGTTTGAAAG ATTAGAAGTC CTGGCTGTAT TTGCCCTCCAC 360
 AGTCTTGGCA CAGTTGGGAG CTCTCTTTAT ATTAAGAGAA AGTGCAGAAC GCTTTTGGGA 420
 ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA 480
 CCTGTTTACG ATGCTTTCTA TTCGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG 540
 TACGAGCTGG CTTCAGAGAG ATGTTGCAGA TCTTAGTCGA AGCTTGTGTG GAATTATTCC 600
 GGGACTTAGC AGTATCTTCC TTCCCGAAT GAATCCATTT GTTTTGATTG ATCTTGCTGG 660
 AGCATTTGCT CTTTGTATTA CATATATGCT CATTGAAATT AATAATTATT TTGCCGTAGA 720
 CACTGCCTCT GCTATAGCTA TTGCCTTGAT GACATTTGGC ACTATGTATC CCATGAGTGT 780
 GTACAGTGGG AAAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATTGGTC AGTTGGACAA 840
 ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTTAGAA GTCCGAAATG AACATTTTGG 900
 GACCTTAGGT TTTGGCTCAT TGGCTGGATC AGTGCATGA AGAATTCGAC GAGATGCCAA 960
 TGAACAAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTACTCTAAC 1020
 TGTTCAAAT TTCAAGGATG ACTGGATTAG GCCTGCCTTA TTGCTGCGC CTGTTGCAGC 1080
 CAATGTCTTA AACTTTTCAG ATCATCACGT AATCCCAATG CCTCTTTTAA AGGGTACTGA 1140
 TGATTTGAAC CCAAGTTACAT CAATCCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC 1200
 ATTTAACACT CCTGGGAAAA ATGTGAACCC AGTTATTCTT CTAACACAC AAACAAGGCC 1260
 TTATGGTTTT GGTCTCAATC ATGGACACAC ACCTTACAGC AGCATGCTTA ATCAAGGACT 1320
 TGGAGTTCCA GGAATTGGAG CAATCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG 1380
 TAGATATGGA ACTAATAATA GAATTGGACA ACCAAGACCA TGATAGACTC TAACCTATT 1440
 TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTTAG TAATCCAAC TTGCATTGAC 1500
 TGTTTAATCA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACATT TCATGAAACC 1560
 TATGAACTA TATTTTGTGA AAATGTATTT GTGACAGTGA AATCCTCGTA AATGTTAAAG 1620
 GCTTTAAATA GGCTCTCTTT AGAAAATGTG TTTCTTTAAA TTTGGATTTT GGTATCTTTG 1680
 GTTTTGTAGT TGACTGTCAGT GTGATGTGAC CTTACCTTTA TAAGAGCCAC TTGATGGAGT 1740
 AGATCTGTCA CATTACTAAG ATACGATATT TCTTTT TTTT TCCGAGACGG AGTCTTGCTC 1800
 TGCCACTGTG CCCGGCCAAT ACATTATTAT TAACCTAAGG CTGTACTTTA TTAAGGCTTC 1860
 CTTAGTTTTT GTTTTGTATT GTTTTGTGAG ATGGAGTCTC ACTCTGTCGC CCAGGCTGGA 1920
 ATGCAGTGGC ATGATCTCAG CTCACTGCAA CCTCTGCCCT CTGAGTTCAA ATGATTCTCC 1980
 TGCCCTCAGC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCACGCC AGCTAATTTT 2040
 TGTATTTTGA GTAAAGACGG GGGATTTCAC CATGTTGGCC AGGCTGGTCT TGAACCTCTG 2100
 ACCTCATGAT CCACCCACCT TAGCCTCCCA AAGTGCTGGG ATTAGGTGTG AGCCACCGCA 2160
 CCTGGCCGAT ATTTTCTTTA ATGAAATTTA TAAATATGCT TCTTGAATAA TACACATTTT 2220
 GGGAAAGGGA AAAATGTCTG TTCAAAAAGT AAAGTCTCT TTTATAGCTT TTCCAAACTT 2280
 AATTGCTAAA TTTTCTTTT AGGTCTCTCT GAATTATGTC TTACAACTA AAAGCAAAA 2340
 TTTTGTAGCAG AAATTTTGA ATACATTCTA TCTAGCACAA TTTGAATTTT TAATTATCAA 2400
 GATTTTTGTT AAAGTTTCTC TCCTTAAAA ATTTTAGTAC ATTTGTAAT

Seq ID NO: 205 Protein sequence
 Protein Accession #: BAB70980.1

1 11 21 31 41 51
 | | | | |
 MGTIHLFRKP QRSFPGKLLR EFRLVAADRR SWKILLFGVI NLICTGFLM WCSSTNSIAL 60
 TAYTYLTIFD LFSMLTCLIS YWVTLRKPSF VYSFGFERLE VLAVFASTVL AQLGALFILK 120
 ESAERFLEQP BIHTGRLLVG TFVALCFNLF TMLSIRNKPF AYVSEAASTS WLQEHVADLS 180
 RSLCGIIPGL SSIFLPRMNP FVLIDLAGAF ALCITYMLIE INNYFAVDTA SAIAIALMTF 240
 GTMYPMSVYS GKVLQTFPP HVIGQLDKLI REVSTLDGVL EVRNEHFNTL GFGLSLAGSVH 300
 VRIRRDANQ MVLAVHTNRL YTLVSTLTQV IFKDDWIRPA LLSGPPVAANV LNFSDDHHVIP 360
 MPELLKGTDDL NPVTSTPAKP SSPPEFSFN TPGKNVNPVI LNTQTRPYG FGLNHGHTPY 420
 SSMLNQGLGV PGIGATQGLR TGFTNIPSRV GTNNRIGQPR P

Seq ID NO: 206 DNA sequence
 Nucleic Acid Accession #: NM_016361.1
 Coding sequence: 397..1662

1 11 21 31 41 51

5
10
15
20
25
30

GGAACTCAGG	GCCGGCTCCT	GTTCCTTCAA	GAGTGTGGA	GGCCAAACTT	GAAATACAAG	60
TTTAATGTTC	CTCGTCGGGC	AAAAGATAAG	GATCCGATCT	CCCCCGGCC	GGTGTGCAGC	120
AGGAGCGACC	AACCCCGACC	CGGGTTAAAA	CTCCAGGGA	CTCTTCGCTG	CTGCCACCTC	180
TTGTTCTCTC	CCCCGTTCCT	ACTCGGGGTC	TCCCTCAGGG	CCGGGAGGCA	CAGCGGTCCC	240
TGCTTGCTGA	AGGGCTGGAT	GTACGCATCC	GCAGGTTCCC	GCGGACTTGG	GGGCGCCCGC	300
TGAGCCCCGG	CGCCCCGAGA	AGACTTGTGT	TTGCCTCCTG	CAGCCTCAAC	CCGGAGGCAG	360
CGAGGGCCTA	CCACCATGAT	CACTGGTGTG	TTCAGCATGC	GCTTGTGGAC	CCCAGTGGGC	420
GTCTGACCT	CGCTGGCGTA	CTGCCTGCAC	CAGCGGCGGG	TGGCCCTGGC	CGAGCTGCAG	480
GAGGCCGATG	GCCAGTGTCC	GGTCGACCGC	AGCCTGCTGA	AGTTGAAAAT	GGTGCAGGTC	540
GTGTTTCGAC	ACGGGGCTCG	GAGTCTCTC	AAGCCGCTCC	CGCTGGAGGA	GCAGGTAGAG	600
TGAACCCCC	AGCTATTAGA	GGTCCCACCC	CAAACTCAGT	TTGATTACAC	AGTCACCAAT	660
CTAGCTGGTG	GTCCGAAACC	ATATTCTCCT	TACGACTCTC	AATACCATGA	GACCACCTTG	720
AAGGGGGGCA	TGTTTGTGCG	GCAGCTGACC	AAGGTGGGCA	TGCAGCAAAAT	GTTTGCCTTG	780
GGAGAGAGAC	TGAGGAAGAA	CTATGTGGAA	GACATTCCCT	TTCTTTCAAC	AACCTTCAAC	840
CCACAGGAGG	TCTTTATTCG	TTCCACTAAC	ATTTTTCGGA	ATCTGGAGTC	CACCCGTTGT	900
TTGCTGGCTG	GGCTTTTCCA	GTGTCAAGAA	GAAGGACCCA	TCATCATCCA	CACTGATGAA	960
CGAGATTGAG	AAGTCTTGTA	TCCCAACTAC	CAAAGCTGCT	GGAGCCTGAG	GCAGAGAACC	1020
AGAGGCCGGA	GGCAGACTGC	CTCTTTACAG	CCAGGAATCT	CAGAGGATTT	GAAAAAGGTG	1080
AAGGACAGGA	TGGGCATTGA	CAGTAGTGAT	AAAGTGGACT	TCTTCATCCT	CCTGGACAAC	1140
GTGGCTGCCG	AGCAGGCACA	CAACCTCCCA	AGCTGCCCCA	TGCTGAAGAG	ATTGTCACGG	1200
ATGATCGAAC	AGAGAGCTGT	GGACACATCC	TTGTACATAC	TGCCCAAGGA	AGACAGGGAA	1260
AGTCTTCAGA	TGGCAGTAGG	CCCATTCCTC	CACATCCTAG	AGAGCAACCT	GCTGAAAGCC	1320
ATGGACTCTG	CCACTGCCCC	CGACAAGATC	AGAAAGCTGT	ATCTCTATGC	GGCTCATGAT	1380
GTGACCTTCA	TACGCTCTT	AATGACCTTG	GGGATTTTTG	ACCAACAATG	GCCACCGTTT	1440
GCTGTGACC	TGACCATGGA	ACTTTACCAG	CACCTGGAAT	CTAAGGAGTG	GTTTGTGCAG	1500
CTCTATTACC	ACGGGAAGGA	GCAGGTGCCG	AGAGGTTGCC	CTGATGGGCT	CTGCCCCTG	1560
GACATGTTCT	TGAATGCCAT	GTCAGTTTAT	ACCTTAAGCC	CAGAAAAATA	CCATGCACTC	1620
TGCTCTCAAA	CTCAGGTGAT	GGAAGTTGGA	AATGAAGAGT	AACTGATTTA	TAAAAGCAGG	1680
ATGTGTTGAT	TTTAAATATA	AGTGCTTTTA	TACAAAAAAA	AAAAAAAAAA	A	

Seq ID NO: 207 Protein sequence
Protein Accession #: NP_057445.1

35
40
45

1	11	21	31	41	51	
MRLWTPVGV	LSLAYLHQR	RVALAELQEA	DGQCPVDRSL	LKLMVQVVF	RHGARSPLKP	60
LPLEEQVEWN	PQLLEVPPQT	QFDYTVTNLA	GGPKPYSPYD	SQYHETTLKG	GMFAGQLTKV	120
GMQQMFALGE	RLRKNYVEDI	PFLSPTFNPO	EVFIRSTNIF	RNLESTRCLL	AGLFQCQKEG	180
PIIIHTDEAD	SEVLYPNYQS	CWSLRQRTRG	RQQTASLQPG	ISEDLKKVKD	RMGIDSSDKV	240
DFFILLDNVA	AEQAHLNLPSC	PMLKRPFARM	EQRAVDTSLY	ILPKEDRESL	QMAVGPFLHI	300
LESNLLKAMD	SATAPDKIRK	LYLYAAHDVT	FIPLLMTLGI	FDHKWPPFAV	DLTMELYQHL	360
ESKEWFWQLY	YHGKEQVPRG	CPDGLCPLDM	FLNAMSVMYTL	SPEKYHALCS	QTQVMEVGNE	420
E						

Seq ID NO: 208 DNA sequence
Nucleic Acid Accession #: CAT cluster

50
55
60

1	11	21	31	41	51	
TTTGAGGGGG	TGGTGGGGCG	AGTTTAATTC	ATAAAGAAGC	CTCCTGATCA	GAAAGGGGCC	60
TAAACGCCCTG	CCCTTGAGGA	GAAGTCCTTC	CTTGAGGATA	AGGCCTCCCA	GGGGAGGAGG	120
TGCTGGGGGG	CAGTGTTAGG	CTTCAGGCCA	TCCCTGGAGG	CCAGTCCTGT	GCTCAGCAAG	180
TAGTGGCAGA	GCCTGGAGTG	ATGAGTGGGA	TGGCCTTCTC	AGGTACAGGA	CTGTGCTGCT	240
TCGTGGCTGCT	CTTGCAATTTG	CATTTGCCAC	TCAGAACTGC	CGCGATCCCA	GCAATGGCCA	300
GGAGCCCTCC	GCAGATCAGT	CCGCTCAGCT	GCAGGTTTTT	CCAGTCATAG	TAGAAGGGAT	360
CGTCTTTTAT	GGCAAAATGG	TCATTGGCTT	CCAAGGCAGT	CAGGCCAACT	GTGTGACTCT	420
GCAGGTTCTC	CACTGCTCCT	TCACCAAGTG	CCTGCGAGGT	CACCTTGGCG	AGGGCTCACC	480
TGAGCTGGCA	GCGCAG					

Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..564

65
70
75
80

1	11	21	31	41	51	
ATGGAGCCCT	GGGCGTGGCT	GCAGGGTTTA	AAGAGCCGAC	CCACGTGCCC	AGCAGCCTCC	60
TCAGATCCGT	TCTCTGCGCT	GCCAGCTCAG	GACACTGGTG	AAGGAGCAGT	GAGGAACTCG	120
CAGAGTCACA	CAGTTGGCCT	GACTGCCTTG	GAAGCCAATG	ACCCATTTCG	CAATAAAGAC	180
GATCCCTTCT	ACTATGACTG	GAAAAACCTG	CAGCTGAGCG	GACTGATCTG	CGGAGGGCTC	240
CTGGCCATTG	CTGGGATCGC	GGCAGTTCTG	AGTGGCAAAT	GCAAATGCAA	GAGCAGCCAG	300
AAGCAGCACA	GTCCTGTACC	TGAGAAGGCC	ATCCCACTCA	TCACTCCAGG	CAGATTCTCT	360
ACCTTGGCCA	AATCAAATAA	ACCTTTATCT	CCAAGCACCT	TTGTCTTGGT	GTTTGGCATC	420
AGCTACACAT	CAGTCTTCCG	AGTGCTCTT	TCTGCGTCCC	TGTACCTGTC	CATTCTGGT	480
GATGCTGCTG	CCCTCACATC	AGGCCATCCA	AGCATGCAGA	ACATAAGCAT	GCAGAACACT	540
GGAACGAAGG	GCTGTACCTA	ATGA				

Seq ID NO: 210 Protein sequence
Protein Accession #: FGENESH predicted

1	11	21	31	41	51	
MEPWAWLQGL	KSRPTCPAAS	SDPFSALPAQ	DTGEGAVRNL	QSHTVGLTAL	EANDPFANKD	60
DPFYDWNKLN	QLSLGICGGL	LAIAGIAAVL	SGKCKCKSSQ	KQHSFVPEKA	IPLITPGRFL	120

TLAKSNKPLS PSTFVLVFGI SYTSVFRVPL SASLYPAIPG DAAALTSGHP SMQNISMQNT 180
GTKGCT

Seq ID NO: 211 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..318

1	11	21	31	41	51	
10	ATGCCCGGCC	ACCCCGTCTG	TGAAGTGAGG	AGCACCTCTG	CCCGGCTGCC	CCGTCTGGGA 60
	AGTGAGGAGC	GCCTCTGCCC	GGCTGCCACC	CCGTCTGTGA	GTGCCCTGCTG	CGCTGGGCCC 120
	AGGCCGCCCG	TGCCCTGCCA	GGCCCTCCCG	CCCCCACCT	TCCACCCAG	GGCCTGCTCC 180
	TCACCCAGG	GTTCATCTC	CCTAGTTTCC	ACCAGAGACT	GGGTCTTCAT	TCTCACCTCG 240
15	CTACACAGCC	CCTACCAGAA	CGTTCTGAAA	TGCAAACTA	ACAACGTCT	CACCCAGCA 300
	GGAAACTCCC	CAGGGTCCCG	GGCCCCCTGC	GGGGTTGCAG	GCCTCACTCT	TGCGCCCAT 360
	CCCTCCGCC	TGACCGCCCT	GAGCTCGCCC	CCAGTGCTGG	CCCTTCACGT	CCAGTTATCC 420
	CTCCAGCCT	CCAAGTCCC	CGTTACCGAA	GACCGCCACC	ATCAGACAT	AGCGCAGCAC 480
	ATATGGGACA	CTGGTGAAGG	AGCAGTGAGG	AACCTGCAGA	GTCACACAGT	TGGCCTGACT 540
	GCCTTGAAG	CCAATGACCC	ATTTGCCAAT	AAAGACGATC	CCTTCTACTA	TGACTGGAAA 600
20	AACCTGCAGC	TGAGCGGACT	GATCTGCGGA	GGGCTCTGG	CCATTGCTGG	GATCGCGGCA 660
	GTTCTGAGTG	GCAAAATGCAA	ATGCAAGAGC	AGCCAGAAGC	AGCAGAGTCC	TGTACTGTAG 720
	AAGGCCATCC	CACTCATCAC	TCCAGGCAGA	TTTCTCACCT	TGGCCAAATC	AAATAAACCT 780
	TTATCTCCAA	GCACCTTTGT	CTTGGTGTGT	GGCATCAGCT	ACACATCAGT	CTTCCGAGTG 840
25	CCTCTTTCTG	CGTCCCTGTA	CCCTGCCATT	CCTGGTGATG	CTGCTGCCCT	CACATCAGGC 900
	CATCCAAGCA	TGCAGAACAT	AAGCATGCAG	AACACTGGAA	CGAAGGGCTG	TACCTAA

Seq ID NO: 212 Protein sequence
Protein Accession #: FGENESH predicted

30	1	11	21	31	41	51	
	MPGHPVCEVR	STSRALPRLG	SEERLCPAAT	PSVSACCAGP	RPPVPCQALR	PPTFHPRACS	60
	SPQGSISLVS	TRDWVFILTL	LHSPYQNVLK	CKPNNCLTPA	GNSPGSRAPC	GVAGLTILRAH	120
35	PSALTALSSP	PVLALHVQLS	LPASKVPVTE	DRHHHDIAQH	IWDTEGAVR	NLQSHTVGLT	180
	ALEANDPFAN	KDDPFYDWNK	NLQLSGLICG	GLLAIAIGIAA	VLSGKCKCKS	SQKQHSVPPE	240
	KAIPILITPGR	FLTAKSNKP	LSPSTFVLVF	GISYTSVFRV	PLSASLYPAI	PGDAAALTSG	300
	HPSMQNISMQ	NTGTGKCT					

Seq ID NO: 213 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1758

45	1	11	21	31	41	51	
	ATGATGGGGT	CTCATGTTGC	CCAGGCTGGT	CTTGAACCTC	TGGGCTCGAG	TGACCTCCT	60
	GCCTTGGCCT	CCGAAAGTGC	TGGGATTACA	GGACTGTTAT	TACAGGAATC	CATAACACTG	120
	GAGGATGTGG	CTGTGGACTT	CACTTGGGAG	GAGTGGCAAC	TCCTGGGCGC	TGCTCAGAAG	180
	GACCTGTACC	GGGATGTGAT	GTTGGAGAAC	TACAGCAACC	TGGTGGCAGT	GGGGTATCAA	240
50	GCCAGCAAAC	CGGATGCAC	CTTCAAGTTG	GAACAAGGAG	AACAACCTGTG	GACAAATTGAA	300
	GATGGAATCC	ACAGTGGAGC	CTGTTCAAGT	TCTCCAAAGG	TCCCGTTCTC	CATTTTCTCA	360
	TCTGTGCCCT	TCACTCTTCA	AAATTGCCTT	CATTCTAACA	TATGGAAAGT	TGATCATGTG	420
	CTGGAGCGCT	TGCAGAGTGA	AAGCCTGGTG	AACAGAAGGA	AACCATGTCA	TGAACATGAT	480
	GCATTTGAAA	ATATTGTTC	TTGCAGCAAA	AGTCAGTTTC	TGTTAGGGCA	AAATCATGAT	540
55	ATATTGACT	TACGTGGAAA	AAGTTTGAAA	TCCAATTTAA	CTTTAGTTAA	CCAGAGCAAA	600
	GGCTATGAAA	TAAAGAACTC	TGTTGAGTTT	ACTGGAATG	GGGACTCCTT	TCTTCATGCT	660
	AACCATGAAC	GACTTCATAC	TGCAATTA	TTCCCTGCAA	GTCAAAACT	CATCAGCACT	720
	AAGTCCCAAT	TCATCAGTCC	CAAGCATCAG	AAAACACGAA	AATTAGAGAA	GCATCATGTG	780
	TGCAGTGAAT	GTGGGAAAGC	CTTCATCAAG	AAGTCTTGCC	TAACATGATC	CCAGGTAATG	840
60	CATACAGGAG	AGAAACCCCA	CAGATGTAGT	CTATGTGAGA	AAGCCTTCTC	CAGAAAGTTC	900
	ATGCTTACTG	AACATCAGCG	AACATCATCA	GGAGAAAAAC	CTTATGAATG	CCCTGAATGT	960
	GGCAAGCCT	TTCTCAAGAA	ATCAGCGCTC	AACATACATC	AGAAAACACA	TACCGGAGAG	1020
	AAACCCCTATA	TATGCAGTGA	ATGTGGAAAA	GGCTTCATCC	AGAAAGGAAA	TCTCATTGTA	1080
	CACCAAGCGAA	TTATACAGG	TGAGAAACCT	TATATATGCA	ATGAATGTGG	AAAAGGCTTC	1140
65	ATTCAGAAGA	CGTGTCTCAT	AGCACATCAG	AGATTTCACA	CAGGAAAGAC	GCCCTTTGTG	1200
	TGCAGTGAAT	GTGGAAAATC	CTGTTCTCAG	AAATCAGGTC	TCATTAAACA	TCAAAGAATT	1260
	CACACAGGAG	AGAAACCCTT	TGAATGTAGT	GAATGTGGGA	AAGCCTTTAG	CACAAAGCAA	1320
	AAGCTCATTG	TCCATCAAAG	GACTCATACA	GGAGAGAGAC	CCTATGGCTG	TAACGAGTGT	1380
	GGGAAAGCGT	TTGCGTATAT	GTCTGTCTCTG	GTTAAGCATA	AGAGAATACA	CACAAGGGAG	1440
70	AAACAAGAGG	CAGCCAAGGT	GGAAAAATCCT	CCTGCAGAGA	GGCAGAGCTC	ATTACACACC	1500
	AGTGATGTCA	TGCAGGAGAA	AAACTCTGCT	AACGGGGCGA	CTACACAAGT	GCCTTCTGTG	1560
	GCCCTCAGA	CATCATTA	CATCAGCGGC	CTCCTCGCAA	ACAGGAACGT	AGTCTTGTG	1620
	GGACAGCCAG	TGGTCAGATG	TGCAGCCTCA	GGAGATAACA	GAGGATTTGC	ACAGGACAGA	1680
75	AACCTTGTA	ATGCAGTGAA	TGTGGTTGTG	CCTTCCGTGA	TCAATATATG	CTTATTTTAT	1740
	GTTACAGAAA	ACCCATAG					

Seq ID NO: 214 Protein sequence
Protein Accession #: FGENESH predicted

80	1	11	21	31	41	51	
	MMGSHVAQAG	LELLGSSDPP	ALASESAGIT	GLLLQESITL	EDVAVDFTWE	EWQLLGAAQK	60
	DLYRDMLEEN	YSNLVAVGYQ	ASKPDALFKL	EQGEQLWTIE	DGIHSGACSG	SPKVFFSIFS	120
	SVPFTLQNL	HSNWKVDHV	LERLQSESLV	NRRKPCHEHD	AFENIVHCSK	SQFLLGQNH	180
	IFDLRGKSLK	SNLTLVNQSK	GYEIKNSVEF	TGNGDSFLHA	NHERLHTAIK	FPASQKLIST	240

KSQFISPKHQ KTRKLEKHHV CSECGKAFIK KSWLTDHQM HTGEKPHRCS LCEKAFSRKF 300
 MLTEHQRTHT GEKPYECPEC GKAFLLKKSRL NIHQKHTTGE KPYICSECGK GFIQKGNLIV 360
 HQRIHTGEKP YICNECGKGF IQKTCLIAHQ RFHTGKTPFV CSECGKSCSQ KSGLIKHKRI 420
 HTGEKPFECB ECGKAFSTKQ KLIVHQRTHT GERPYGCNEC GKAFAYMSCL VKHKRIHTRE 480
 QKEAAKVENP PAERHSSSLHT SDVMQEKNSA NGATTQVPSV APQTSLSNISG LLANRNVVLV 540
 GQPVVRCAS GDNRGFAQDR NLVNAVNVVV PSVINYLFLY VTENP

Seq ID NO: 215 DNA sequence
 Nucleic Acid Accession #: NM_032190.1
 Coding sequence: 502..1332

1 11 21 31 41 51
 | | | | |
 GATTCCGTGT TCTTGGCCAT GTTAGCCATA ATATCCTGTG CAGTATGTTT TTCCTGTGCA 60
 GAGGCAAAAA CATATTGGGC ATATGTTCCC AAGCCCCCAG CAGTATGACC CATACTTTGG 120
 AGTGACACTC CTCCTAAGAT TTATCATGAT TAAGGAGCAT GGGCTCCAGG ACCCTAACT 180
 CCACCTGACA TAGAACAGTT AGACTCTCAG AATAATGTCA TTAATTATAC CGCTCCATTG 240
 GAAGGACTTC CTTTGTGTGT CACCACAAAG ACATCACTCA GCCATAGCTG TCTTACAGTT 300
 CAAGCTCACA CATGGTTGAG TCACTATGGG AAAATCATGT ACTTATTAAG TCTTGGTTAT 360
 ATTAATGTAA CCGGTGTGCT AACCAACCAT TCCTGGCCCA ATCGCCTTCA TTGTGCTGAC 420
 TATACAGAAAT GGATTCCCTT CAATAGTTCC TACCCCCCTC CATAGACCCA GTGTCTTGCC 480
 CCACCTGGCTA GAAAACAATG TATGTTAACT GGAGACATTG TGGATTGGGG ACCTAAAGGC 540
 CAATTAGATG GAAAAGAAGA AAATCAGAAA TCGTGGCACA AACTTTGCTG GCATTGGTGG 600
 CAAGCTTTTA ATGCTTCTTC TTTATATAAC ACTGGGATCC AATCCCAGTC GGCCGCCCAG 660
 ATTGCTTGGC ATGGAGCAGG CTTTAGCCCG CCTCTTCCCTC AGTGGCATTG TCTAGGGAGG 720
 AAAGGACCAA TTCAAAGATG GATATGGAAG GCAGCATTC CATTATGAA TGGCAACATC 780
 TGGGTTGCCA TAATACTATC CAATAATAGC AATAGTAAGC AACACAGTCT TAATGTTACA 840
 TTTGTAAGA ATATCACCAC TCAATTTACA GTTTGTGTTT TTAATCCTTA TGTGTTTTTG 900
 GCAGCTAAGA AGGACCAGCT CCAGGTAAAC AATACCCAAT TGACCTGTAA ATCTTGCCAG 960
 TTATATCACT GCATTAATCA TAGCACATTG CAAACACATA ATATCTCTAC TTTGATGATT 1020
 TTAGGTTGCA TCCTCGGGCT ATGGATTCTT GTTAATCTGT CTGAGCCATG GGCTGCCACA 1080
 ATTGCTTTAC ATTTTGTGAA ACTTCTTCTA ACTCAGTTTA CTCATTGTGT CCGTAGAGGC 1140
 TTAGGCATGA TAATTTTGTG TATTGTTTAC TTGGTCACAC TAATAATTTT TGTGTTGATG 1200
 TCCTCTGTAG CTTTGCATAG TTCTATTCAA ACAGCTCAGT ATGTGGAGAA CTGGACACGC 1260
 ACAGTCAACC AAGGGTGGCT ACTTGAGAAAT AAAATTAACA CTGAGTTACA AACTGAAGTG 1320
 GCAGTGTAT ATCCACGAT TCTATGGTTA GGGGAACAAG TACAAAGCTT GCAATTGCAG 1380
 CAGTAATTGT GTTGTCAATT TAATCACACT CATATTGTG TAACCAACTT AGAATATAAC 1440
 CAAAGTGAGT ATCCATGGGA TCTTGTGAAA GCCCATTGCT AGGGAGCTTT CACATCCGAC 1500
 ATCACCTTTG ATATTGGTGA ATACAAAAC AAAATTCTTG ATTTAAATAA ACAAATTTCCA 1560
 GAGTTTCAGC CTCTTTTAGA AGACTGGACT GAATTCAGC AAGGCCTGGA GAGCGTCAAC 1620
 CCTTGGACCT ATCTAAAGCA CCACATTAAC ATCTTATATA TAGTCTTGG AATAATGTTG 1680
 TTTTGTCTCT GTCTCTGTGT CATAGTCTGT AAAATCGGAT GGACTGCCAA TCGGAGAATG 1740
 AAAGCTACCC AGCCTGGCCT TACATTCTTT CACTTAATAC ATAAACAAGA AGGGGGAAT 1800
 GTTGGGAGCC AAAAAGGCCA AAGGATGGT GACCAACTCA GCATTCCACT GGAGGCTACA 1860
 TGATCAAAACA GCAAACCTGT TATCATGAAT ACAGAAATGTG GGCAAACTCG CTCTGTGCCC 1920
 TGCCAGAAAG GTTGTCTGAG GGCCATCGCT CCCTGGCCCC GGCCTCTTGA GGTATCTAC 1980
 TGGGACATCT AGAGCGGAA GTTCGAGGAA TGCAGTCTTG CAAGCCTACT TGAGACCGAG 2040
 CAGCTGACCT CTCTCTCCAC ACCCCTTCTC ACTATCTCTT TTGCCTAATA AATATGGAGG 2100
 GCTGTGTAAA GCTCAGGGCC CTTGTCCACT AGAGGCAAGG TGTCCTCTGA CCCTTCTTCC 2160
 AACAT

Seq ID NO: 216 Protein sequence
 Protein Accession #: NP_115566.1

1 11 21 31 41 51
 | | | | |
 MLTGDIVDWG PKGQLDGKEE NQKSWHKLW HWWQAFNASS LYNTGSIQSQS AAQIAWHGAG 60
 FSPPLPQWHY LGRGPIQKM IWKAAPFMN GNIWVAIIS NNSNSKQHSI NVTFVKNIIT 120
 QFTVCFNFPV VFLAAKDKQL QVNNTQLTCK SCQLYHCINH STLQTHNIST LMLGCIPLG 180
 WIPVNLSEPW AATIALHFPV LLLTQFTHCV RRGLGMIIFA IVYIVTLIIS VVMSSVALHS 240
 SIQTAQYVEN WTRTVNQGWL LENKINTELO TEVAVL

Seq ID NO: 217 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1566

1 11 21 31 41 51
 | | | | |
 ATGGTGAACC CCAATCCAC TTCCTCCCTC TTCAGGTTAT GTTTTITGCT CCTGAGGAGT 60
 CAGAACCTGT GGGTTGAAGA GCAAATTCAT TGCAAAAACA TATTGGGCAT ATGTTCCCAA 120
 TCCCCAGCA GATATGGCCTA TACTTTGGAG CTCACCTCCTC CTGAGATTAT TCACGATCAG 180
 GGAGAGTGGG CTCCAGGACC CCTAACTCCC CGTGACATAG AAAAGTTAGA CTCTCAGAAC 240
 AATGTCATTA ATTATACCAC TCCACTGGAA GGACTCCCTT TGTATTATCAC CACAAAGACG 300
 TCGCTCAGCC ATAGCTGTCT TGCAATTCAA GCTCAAACAT GGTGAGTACA CTATGGAAAA 360
 ATTATGTACT TATTAGGCTC TGGTTCTATT AATGTAACCT GTGTGCTAAC CAATCATTC 420
 CAGTCCAGTC ACCCTAATGT TGCTGATTAT ACAGAAATGA TTCCATTCAA TAGTTCCTAC 480
 CCCACTCTGT GGACCCAGTG TCTTGATCCA CTGGCTAGTA AACAAATATAT GTCAACTGAA 540
 GACACTGTGG ATTGGGAACC TAAAGGTCAA TTAGATGGAA AAGGTGAAG TCAGAAATCA 600
 TGGCAAAAC TTCACCTGGCA TTGGCGGCAA GCTTTTAATG CTCTTCTTT ATACACACGC 660
 AGAATCCAAT CCCAGTCTGC TGCTCAGATT GCTTGGCATG GAGCAGGCTT TAGCCCACT 720
 CTCTCTCAGT TGCATTATCT GGGGAGGAAA GGACCAATTC AAGAACTAT ATGGAAGGCA 780
 GCACTCCCAT TTATGAATGG CAACATCTGG ATTGGAACAC TGTCTAATAA TAGCAATAGT 840
 AAGCAACACA GTCTTAATGT TGCAATTGTA AAGAATATCA CCACTCAGTT TACAGTTTGT 900
 GTTTTAATC CTTATGCTGT TTTGGCAGCT AAGAAGAACC AGCTTCAGGT GGAGAAGTGG 960

ACACGCACAG CTGACCAAGC GAGGCTACTT CAGAATAAAA TTAACACTGA GTTACAAACT 1020
 GAAGTGGCAA TGTGAAATC CATGGTCTGT TGGTTAGGAG AACAGGTACA AAGCTTGCAG 1080
 TTGCAGCAGC AATTGCGTCA TCATTTTAAT CACATTCATA TTTGCGTAAC TAACTCAGAA 1140
 TATAACCAAA GTGAGTATCC GTGGGACCTT GTGAAAGCCC ATTTGCAAGG AGCTTTTACA 1200
 TCCAACATCA CCTTTGATAT TGGTGAATTA CAAAACAAAA TTATTGATT AAATAGGCAA 1260
 ACTCAAGAAT TTCAGCCTTC TTAGAAGAC TGGACCGAAT TCCAGGAAGG CCTGGAGAGC 1320
 CTCAACCCCT GGACCTATCT AAGGCACCAC ATTAACATCT TATATGTAGT TCTTGGAAATA 1380
 ATGTTGTTTT GTCTCTGTCT TCGGTTTATA GTCTGTAAAA TCGGATGGAC CACCAATTGG 1440
 AGAATGAGAG CCTCCAGGCC CAGCCTTACA TTCTTTCAAT TAATACATAA ACAGAAAGGG 1500
 GGATATGCAG GGAGCCAAAG GCCTGTGGGA CGTGACCAAC TCAGCATTCCT GCTGGAGGCT 1560
 ATATGA

Seq ID NO: 218 Protein sequence

Protein Accession #: FGENSEH predicted

1 11 21 31 41 51
 | | | | |
 MVNPKSTSSL FRLCFLLLRS QNLWVEEQIQ CKNILGICSQ SPSSMAYTLE LTPPEIYHDQ 60
 GEWAPGPLTP RDIEKLDSQN NVINYTPLE GLPLFITTKT SLSHSCLAIQ AQTWLSHYGK 120
 IMYLLGLGSI NVGTGLTNHS QSSHPNCADY TEWIPFNSSY PTLWTQCLDP LASKQYMSTE 180
 DTVDWEFKGQ LDGKGESQKS WHKLHWHWRQ AFNASSLYNS RIQSQSAAQI AWHGAGFSPP 240
 LPQLHYLGRK GPIQETIWK AALPFMNGNIW IGTLSNNSNS KQHSNLNVAFV KNITTQFTVC 300
 VFNPYAFLLA KKNQLQVENW TRTADQARLL QNKINTELQT EVAMLKSMVL WLGEQVQSLQ 360
 LQQRLRHFFN HIHCIVTNSE YNQSEYPWDL VKAHLQGAFT SNITFDIGEL QNKIIDLNRQ 420
 TQEFQPSLED WTEFQEGLES LNPWTYLRHH INILYVVLGI MLFCLCLRFI VCKIGWTTNW 480
 RMRASQPSLT FFQLIHKQKG GYAGSQRPVVG RDQLSILLEA I

Seq ID NO: 219 DNA sequence

Nucleic Acid Accession #: FGENSEH predicted

Coding sequence: 1..900

1 11 21 31 41 51
 | | | | |
 ATGCCGCGCG GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
 CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC 120
 GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
 CGGCCCACTG CGCTGGACAC CTTCTCTGGT ACGTACGTTT AATCGCCCGT GCGGCCGCGT 240
 GGCTGCGCGG GGGCTGTGCA CCGGGGAGCT GGGGCGGCGC TCTCGGCGGG AGGGCGCAGA 300
 GGACCCCGGG GAGGAGACTG GAGCAGGCCC CGAGGTGGCG CTGGTGCGGC CCAGGACGCT 360
 CTTCTTAAGT CAGGCTCTCC CCGCCCCGCC CCTGCAGTGC AAGTCCTGGT GGATGGAGCT 420
 CCGGTGCGCA TTGAGCTCTG GGACACAGCG GGACAGGAGG ATTTTGACCG ACTTCGTTC 480
 CTTTGCTACC CGGATACCGA TGTCTTCTGT GCGTGCTTCA GCGTGCTGCA GCGCAGCTCC 540
 TTTCAAAACA TCACAGAGAA ATGGTGCCG GAGATCCGCA CGCACAAACC CCAGGCGCCT 600
 GTGCTGCTGG TGGGCACCCA GGGCAGCTG AGGGACGATG TCAACGTACT AATTAGCTG 660
 GACCAGGGGG GCCGGGAGGG CCCCCTGCCC CAACCCAGG CTCAGGGTCT GCGCGAGAAG 720
 ATCCGAGCTG GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAACTT GAAGGAAGTA 780
 TTTGACTCGG CTATCTCTAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840
 GCCAAAGGTG TGCGCACCTT CTCCCGCTGC CGCTGGAAGA AGTTCTTCTG CTTCTGTTGA

Seq ID NO: 220 Protein sequence

Protein Accession #: FGENSEH predicted

1 11 21 31 41 51
 | | | | |
 MPPRELSEAB PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTFSG TYVQSPVRPR GCGGAVHRGA GAGVSAGRRR GPRGGDWSRP RGGAGAAQDA 120
 LPNSGSPRPA PAVQVLVDGA PVRIELWDTA GQEDFDRLRS LCYPDTDFVL ACFSVVQPSS 180
 FQNITEKWL P ERTTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGVPV QPQAQGLAEK 240
 IRACCYLECS ALTQKNLKEV FDSAILSIE HKARLEKKLN AKGVRTLSRC RWKKFFCFV

Seq ID NO: 221 DNA sequence

Nucleic Acid Accession #: XM_063832.2

Coding sequence: 1..711

1 11 21 31 41 51
 | | | | |
 ATGCCGCGCG GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
 CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC 120
 GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
 CGGCCCACTG CGCTGGACAC CTTCTCTGTG CAAGTCCTGG TGGATGGAGC TCCGGTGGCG 240
 ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTCGTTT CTTTGTCTAC 300
 CCGGATACCG ATGTCTTCTT GCGGTGCTTC AGCGTGGTGC AGCCAGCTC CTTTCAAAAC 360
 ATCACAGAGA AATGGCTGCC CGAGATCCGC ACGCACAAAC CCCAGGCGCC TGTGCTGCTG 420
 GTGGGACACC AGGCCGACCT GAGGGACGAT GTCAACGTAC TAATTAGCTT GGACAGGGGG 480
 GCGCCGGGAG GCCCCGTGCC CCAACCCAGG GCTCAGGGTC TGGCCGAGAA GATCCGAGCC 540
 TGCTGCTACC TTGAGTGCTC AGCCTTGACG CAGAAGAAGT TGAAGGAAGT ATTTGACTCG 600
 GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAAACTGAA TGCCAAAGGT 660
 GTGCGCACCC TCTCCGCTG CCGCTGGAAG AAGTTCTTCT GCTTCGTTTG A

Seq ID NO: 222 Protein sequence

Protein Accession #: XP_063832.1

1 11 21 31 41 51
 | | | | |

MPPRELSEAE PPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRLRLSLCY PDTDVFLACF SVVQPSFQON 120
 ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGFVPQPQ AQGLAEKIRA 180
 CCYLECSALT QKNLKEVFDS AILSAIEHKA RLEKKLNAKG VRTLSCRWK KFFCFV

Seq ID NO: 223 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1161

1 11 21 31 41 51
 | | | | | |
 ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAATAG ACAAGAAGAA CTGCTGTGTG 60
 TTCCGAGATG ACTTCATTGC CAAGGTGTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTT 120
 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTTGAAA 180
 TCCAGCCGGA TTTTCTGTG CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 240
 CCGTTCGTGA TGGACTACTA TGTGCGGCGT TCAGACTGGA AGTTTGGGGA CATCCCTTGC 300
 CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 360
 GTGGCGGTAG ACAGGTATTT CCGGTGGTGC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420
 AATTGGACAG CAGCCATCAT CTCTTGCTT CTGTGGGGCA TCACTGTGTG CCTAACAGTC 480
 CACCTCTGTA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 540
 AGCATCTGCC ATACCTTCCG GTGGCAGGAA GCTATGTTCC TCCTGGAGTT CCTCTGCCC 600
 CTGGGCATCA TCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660
 GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720
 GTCATCTGCT TCTTCCCAG CGTGGTTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT 780
 TCGGGCAGCG AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTCTT TATCACTCTC 840
 AGCTTCACCT ACATGAACAG CATGCTGGAC CCGGTGGTGT ACTACTTCTC CAGCCCATCC 900
 TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 960
 CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC 1020
 GCTCCAGAGG CGTTAATGGC CAACCTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080
 ACCTCAATA ACCATTCCAA GAAGGACAT TGTACCAAG AACAGCATC TCTGGAGAAA 1140
 CAGTTGGGAT GTTCATCGA G

Seq ID NO: 224 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | | |
 MNRHHLQDHF LEIDKKNCCV FRDDFIKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK 60
 SSRIFLFLNA VADFLLIICL PFVMDYYVRR SDWKFGDIPC RLVLFMFAMN RQGSIIFLT 120
 VAVDRYFRVV HPHHALNKIS NWTAAIISCL LWGITVGLTV HLLKKKLLIQ NGPANVCISF 180
 SICHTRWHE AMFLLEFFLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFIMVVAIVF 240
 VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SFTYMNMLD PVVYFSSPS 300
 FPNFFSTLIN RCLQRKMTGE PDNNRSTSV L TGDPNKTRG APEALMANSG EPWSPSYLGP 360
 TSNHSHKXGH CHQEPASLEK QLGCCIE

Seq ID NO: 225 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1092

1 11 21 31 41 51
 | | | | | |
 ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAATAG ACAAGAAGAA CTGCTGTGTG 60
 TTCCGAGATG ACTTCATTGT CAAGGTGTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTC 120
 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTTGAAA 180
 TCCAGCCGGA TTTTCTGTG CAACCTGGCA GTGGCTGACT TTCTACTGAT CATCTGCCTG 240
 CCCTTCTCTG TGGACAACTA TGTGAGGCGT TGGGACTGGA AGTTTGGGGA CATCCCTTGC 300
 CGGCTGATGC TCTTCATGTT GGTATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 360
 GTGGCGGTAG ACAGGTATTT CCGGTGGTGC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420
 AATCGGACAG CAGCCATCAT CTCTTGCTT CTGTGGGGCA TCACTATTGG CCTGACAGTC 480
 CACCTCTGTA AGAAGAAGAT GCCGATCCAG AATGGCGGTG CAAATTTGTG CAGCAGCTTC 540
 AGCATCTGCC ATACCTTCCA GTGGCAGGAA GCCATGTTCC TCCTGGAGTT CTTCCTGCCC 600
 CTGGGCATCA TCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660
 GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720
 GTCATCTGCT TCTTCCCAG CGTGGTTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT 780
 TCGGGCAGCG AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTCTT TATCACTCTC 840
 AGCTTCACCT ACATGAACAG CATGCTGGAC CCGGTGGTGT ACTACTTCTC CAGCCCATCC 900
 TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 960
 CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC 1020
 GCTCCAGAGG CGTTAATGGC CAACCTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080

Seq ID NO: 226 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | | |
 MNRHHLQDHF LEIDKKNCCV FRDDFIVKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK 60
 SSRIFLFLNA VADFLLIICL PFLMDNYVRR WDWKFGDIPC RLMLFMLAMN RQGSIIFLT 120
 VAVDRYFRVV HPHHALNKIS NRTAAIISCL LWGITIGLTV HLLKKKMPIQ NGGANLCSF 180
 SICHTRWHE AMFLLEFFLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFIMVVAIVF 240
 VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SFTYMNMLD PVVYFSSPS 300
 FPNFFSTLIN RCLQRKMTGE PDNNRSTSV L TGDPNKTRG APEALMANSG EPWSPSYLGP 360
 TSP

Seq ID NO: 227 DNA sequence
Nucleic Acid Accession #: NM_006018
Coding sequence: 61..1224

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5      1      11      21      31      41      51
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CGCCACTTTG CTGGAGCATT CACTAGGCGA GCGCTCCAT CGGACTCACT AGCCGCACTC 60
ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG 120
TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTT 180
GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTGGAAAA 240
TCCAGCCGGA TTTTCTGTGT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 300
CGTTCGTGTA TGGACTACTA TGTGCGGCGT TCAGACTGGA ACTTTGGGGA CATCCCTTGC 360
CGGCTGGTGC TCTTCACTGT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 420
GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 480
15    AATTGGACAG CAGCCATCAT CTCTTGCCCT CTGTGGGGCA TCACTGTTGG CCTAACAGTC 540
CACCTCCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 600
AGCATCTGCC ATACCTTCCG GTGGCAGCAA GCTATGTTCC TCCTGGAGTT CCTCCTGCCC 660
TCGGGCATCA TCTGTCTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 720
20    GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 780
GTCATCTGCT TCCTTCCCAG CGTGGTGTGT CGGATCCGCA TCTTCTGGCT CTGTCACACT 840
TCGGGCACGC AGAATTGTGA AGTGATCCGC TCGGTGGACC TGGCGTCTTT TATCACTCTC 900
AGCTTCACTT ACATGAACAG CATGCTGGAC CCGTGGTGTG ACTACTTCTC CAGCCCATCC 960
TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 1020
25    CCAGATAATA AGAAGAAAGT GAGCGTCGAG CTCACAGGGG ACCCAACAAA AACCAGAGGC 1080
GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTCTA TCTGGGCCCCA 1140
ACCTCAAATA ACATTCCCAA GAAGGACAT TGTACCAAG AACCAAGCAT CTGGAGAAAA 1200
CAGTTGGGCT GTTGATCGA GTAATGTCT TGGACTCGGC CTAAGTGTTC CTGGAACCTC 1260
CAGATTGAGA GAATCTGATT TAGGGAAACT GTGGCAGATG AGTGGGAGAC TGGTTGCAAG 1320
30    GTGTGACCA AGGAATCCTG GAGGAACAGA GAGTAAAGCT TCTAGGCATC TGAAACTTGC 1380
TTTATCTCTG AGCTCGCAG GACTGAAGAT GGGCAAATTG TAGGCGTTTC TGCTGAGCAG 1440
AGTTGGAGCC AGAGATCTAC TTGTGACTTG TTGGCCTTCT TCCACATCT GCCTCAGACT 1500
GGGGGGGGCT CAGCTCCTCG GGTGATATCT AGCCTGCTTG TGAGCTCTAG CAGGGATAAG 1560
GAGAGCTGAG ATTGGAGGGA ATTGTGTTGC TCCTGGAGGA AGCCAGGCA TCATTAAACA 1620
35    AGCCAGTAGG TCACCTGGCT TCCGTGGACC AATTCACTCT TCAGACAAGC TTTAGAGAAA 1680
TGGACTCAGG GAAGAGACTC ACATGCTTTG GTTAGTATCT GTGTTTCCGG TGGGTGTAAT 1740
AGGGGATTAG CCCCAGAAGG GACTGAGCTA AACAGTGTTA TTATGGGAAA GGAAATGGCA 1800
TTGTGCTTTT CAACAGCAG CTAATGCAAT CCATTCTCTC CTTGTTTATA GTAATCTAAG 1860
GGTTGAGCAG TTAACACGGC TTCAAGATAG AAAGCTGTTT CCCACCTGTT TCGTTTACC 1920
40    ATTAAGAGG AAACGTGCCT CTGCCCCACG GGTAGAGGGG GTGCACGTTT CTCTGTTTC 1980
CTTCGCTTGT GTTCTGTGAC TTACCAAAAA TCTACCACTT CAATAAATTT TGATAGGAGA 2040
CAAAAAAAA A

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Seq ID NO: 228 Protein sequence
Protein Accession #: NP_006009.1

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45      1      11      21      31      41      51
      |      |      |      |      |      |
MNRHHLQDHF LEIDKKNCCV FRDDFIKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK 60
SSRIFLFNLA VADFLLIICL PFVMDYVRR SDWNFGDIPC RLVLFMFAMN RQGSIIIFLT 120
VAVDRYFRVV HPHHALNKIS NWTAAIISCL LWGITVGLTV HLLKKLLIQ NGPANVCISF 180
SICHTFRWHE AMPLLEFLLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFMVVAIVF 240
VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFITL SFTYMNMLD PVVYFSSPS 300
FPNFSTLIN RCLQRKMTG PDNNRSTSV LTGDPNKTG APEALMANS EPWSPSYLGP 360
55    TSNHSHKKGH CHQEPASLEK QLGCCIE

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Seq ID NO: 229 DNA sequence
Nucleic Acid Accession #: NM_014398.1
Coding sequence: 64..1314

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60      1      11      21      31      41      51
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GGCACCATTG CCGGGCCTGC CCGGACTTCG CCGCACGCTG CAGAACCTCG CCCAGCGCCC 60
ACCATGCCCC GGCAGCTCAG CGCGGCGGCC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG 120
CACGATGGCA GTCAAAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
65    ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACACAGC TAAGCAAGCA 240
CCTCACCAAA CTTTAGCAGC AAGATTCAAT GATGTCATA TCACCTTTCA AACAGCGGCC 300
ACAGTAAAAA TTCCAACAAC TACCCAGCA ACTACAAAAA AACTGCAAC CACCAGCCCA 360
ATTACTPACA CCCTGGTCAC AACCCAGGCC ACACCAACA ACTCACACAG AGCTCCTCCA 420
GTTACTGAAG TTACAGTCGG CCCTAGCTTA GCCCTTATT CACTGCCACC CACCATCACC 480
70    CCACCAGCTC ATACAGCTGG AACAGTTCA TCAACCGTCA GCCACAAC TGGGAACACC 540
ACTCAACCCA GTAACAGAC CACCCTTCCA GCAACTTTAT CGATAGCACT GCACAAAAGC 600
ACAACCGGTC AGAAGCCTGA TCAACCCACC CATGCCCCAG GAACAACGGC AGCTGCCACC 660
AATACCAACC GCACAGCTGC ACCTGCCTCC ACGGTTCTCG GGCCACCCCT TGCACCTCAG 720
CCATCGTCAG TCAAGACTGG AATTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA 780
75    GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAAATCC 900
AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTTACCAA GGATGAAGAA 960
TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
CAAGGAATCA AACATGCGGT GGTGATGTTT CAGACAGCAG TCGGGCATTC CTTCAAGTGC 1080
80    GTGAGTGAAC AGAGCCTCCA GTTGTGAGCC CACCTGCAGG TGAAACAAAC CGATGTCCAA 1140
CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAAATG TGGATGAGTG CTCGTCTGAC 1200
TACACAATTG TGTCTCTGTG GATTGGGGCC ATCGTGGTTG GTCTCTGCCT TATGGGTATG 1260
GGTGTCTATA AAATCCGCCT AAGGTGTCAA TCATCTGGAT ACCAGAGAAAT CTAATGTTG 1320
CCCGGGGGGA ATGAAAATAA TGAATTTAG AGAACTCTTT CATCCTTACC AGGATGGATG 1380

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5 TTGGGAAATT CCCTCAGAGT GTGGGTCCTT CAAACAATGT AAACCACCAT CTTCTATTCA 1440
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACTTTT 1500
 GTTTATTTTA TGAAGATAT AGTGAGCTGT TTATTTTCTA GTTTCCTTTA GAATATTTTA 1560
 GCCACTCAAA GTCACATTT GAGATATGTT GAAATTAACAT AATATATGTA AAGTAGAATA 1620
 AGCCTTCAAA TTATAAACCA AGGTCATTT GTAACATAA CTAAGTGTG TGCATGAAG 1680
 ATTTTATTTT ACCCTTGATC TTAACAAAGC CTTTGCTTTG TTATCAAATG GACTTTCAGT 1740
 GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCTCTGT GTAGCACTTA 1800
 10 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGGAGAC GGAGTTTCAC TCTTGTCCAC 1860
 CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCCGCCTCC CGGGTTCAG 1920
 TGATTCTCCT GCTTCAGCTT CCCGAGTAGC TGGGATTACA GGCACACACT ACCACGCCTG 1980
 GCTAATTTTT GTATTTTTAT TATAGACGGG TTTCACCATG TTGGCCAGAC TGGTCTTGAA 2040
 CTCTTGACCT CAGGTGATCC ACCCACCTCA GCCTCCCAAA GTGCTGGGAT TACAGGCATG 2100
 AGCCATTGCG CCCGGCCTTA AATGTTTTT TTAATCATCA AAAAGAACA CATATCTCAG 2160
 15 GTTGTCTAAG TGTTTTTATG TAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTTAT 2220
 CTGTGATGACT CCTGCTCCAG AATTGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280
 CTAACAATA AGCAAGAGAC AATAATAATG GCCCTTAATT ATTAACAAAG TGCCAGAGTC 2340
 TAGGCTAAGC ACTTTATCTA TATCTCATTT CATTCTCACA ACTTATAAGT GAATGAGTAA 2400
 ACTGAGACTT AAGGGAAGT AATCACTTAA ATGTCACCTG GCTAACTGAT GGCAGAGCCA 2460
 20 GAGCTTGAAT TCATGTGTGT CTGACATCAA GGTCTTTGGT CTTCTCCCTA CACCAAGTTA 2520
 CCTACAAGAA CAATGACACC ACACTCTGCC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580
 TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640
 AGCTTTGCAG ATAACAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700
 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTTA TGGGATTGCT TAGCTGGGCT 2760
 25 GTAAAGATGA AGGCATCAA TAAACTCAAA GTATTTTTTA ATTTTTTTGA TAATAGAGAA 2820
 ACTTCGCTAA CCAACTGTTT TTTCTTGAGT GTATAGCCCC ATCTTGTGGT AACTTGCTGC 2880
 TTCTGCACTT CATATCCATA TTCTCTATTG TTCACCTTAT TCTGTAGAGC AGCCTGCCAA 2940
 GAATTTTTAT TCTGCTGTTT TTTTGTCTGC TAAAGAAAGG AACTAAGTCA GGATGTTAAC 3000
 AGAAAAGTCC ACATAACCCT AGAATCTCTA GTCAAGGAAT AATTCAAGTC AGCCTAGAGA 3060
 30 CCATGTTGAC TTTCTTCATG TGTTCCTTTA TGACTCAGTA AGTTGGCAAG GTCTGCACTT 3120
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG

Seq ID NO: 230 Protein sequence

Protein Accession #: NP_055213.1

35 1 11 21 31 41 51
 | | | | | |
 MPROLSAAAA LFLASLAVILH DGSQMRKAF PETRDYSQPT AAATVQDIKK PVQPPAKQAP 60
 HQTLAARFMD GHITFQTAAT VKIPTTTTAT TKNTATTSPY TYTLVTTQAT PNNSHATPPV 120
 40 TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHTTGNTT QPSNQTTLPA TLSIALHKST 180
 TGQKPDQPTH APGTATAAHN TTRTAAPAST VPGPTLAPQP SSVKTGIYQV LNSRLCIKA 240
 EMGIQLIVQD KESVFSRRY FNIDPNATQA SGNCGRKSN LLLNFQGGFV NLFTTKDEES 300
 YYISEVGAYL TVSDPEVYQ GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTDDVQL 360
 QAFDFEDDFH GNVDECSDDY TIVLPVIGAI VVGLCLMGGM VYKIRLRQCS SGYQRI

Seq ID NO: 231 DNA sequence

Nucleic Acid Accession #: NM_005409.3

Coding sequence: 94..378

50 1 11 21 31 41 51
 | | | | | |
 TTCCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 55 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT 300
 AAAGGACAA GATGCCTAAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360
 GAAAGAAAAG ATTTTAAAA ATATCAAAAC ATATGAAATC CTGAAAAAGG GCATCTGAAA 420
 AACCTGAAC AAGTTTAAT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 60 AGACTTTTCT ATGGTTTTGT GACTTTCAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCTGAAT GAATGACAAT CAGAATTCCT 600
 CTGCCCAAAG GAGTCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTGTGAT ATACATTCAT 720
 GCATTCTTAG CTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 65 GAGAACATT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAAATACAC ACTTCTTTCC 960
 CCAATATCA TGTAGACAT CAATATGTAG GGAAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAAATTCAT AAAATGTACT ATGAAAAAA TTATACGCTA 1080
 70 TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAAAT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTCT AACTTTTAT CATTGAGATG TTTTGAAACA ATTAGGATAT GTGTGTTTAC 1200
 TGTACTTTTT GTTTTGTATC GTTTGTATAA ATGATAGCAA TATCTTGAC ACATTGAAA 1260
 TACAAAATGT TTTTGTCTAC CAAAGAAAA TGTGAAAAA TAAGCAAATG TATACCTAGC 1320
 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAA ACATAATCTA ATCAATTTCT 1380
 75 TGTTCATGCT CTATATACGT TAAAAATTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440
 GTCATTTTTT TCTCTAATAA ACTACCACAA CTTTCTTTT TTAAAAAAA AAA

Seq ID NO: 232 Protein sequence

Protein Accession #: NP_005400.1

80 1 11 21 31 41 51
 | | | | | |
 MSVKGMAIAL AVILCATVVQ GFPMFKRGRG LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

Seq ID NO: 233 DNA sequence
Nucleic Acid Accession #: NM_000577.1
Coding sequence: 41..520

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5      1      11      21      31      41      51
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      GGCACGAGGG GAAGACCTCC TGTCTATCA GGCCTCCCC ATGGCTTTAG AGACGATCTG 60
      CCGACCCTCT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACCA 120
10     GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAATGT 180
      CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
      CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
      GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT 360
      CATCCGCTCA GACAGTGGCC CCACCACAG TTTTGAGTCT GCCGCCTGCC CCGGTTGGTT 420
      CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
15     CGTCATGGTC ACCAAATTCT ACTTCCAGGA GGACGAGTAG TACTGCCAG GCCTGCCTGT 540
      TCCCATTCTT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCCCTGCCCC AGGGCTCCCG 600
      GCTATGGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA 660
      CTTGGTCACT GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCGAATG 720
      GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCCTGCA CAAAGCCCTT CCATGTCGCC 780
20     TCTGCATTCA GGATCAAAACC CCGACCACCT GCCCAACCTG CTCTCCTCTT GCCACTGCCT 840
      TTCTCTCCCT CATTCCACCT TCCCATGCCC TGGATCCATC AGGCCACTTG ATGACCCCA 900
      ACCAAGTGGC TCCACACCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
      TTTAAGGGTT TGTGGAAAAT GAAAATTAGG ATTCATGAT TTTTTTTTTT CAGTCCCCGT 1020
25     GAAGGAGAGC CCTTCATTG GAGATTATGT TCTTTCGGGG AGAGGCTGAG GACTTAAAT 1080
      ATTCCTGCAT TTGTGAAATG ATGGTGAAAG TAAGTGGTAG CTTTTCCTT CTTTTCCTT 1140
      TTTTTCCTG ATGTCCCAAC TTGTAAAAAT TAAAGTTAT GGTACTATGT TAGCCCCATA 1200
      ATTTTTTTTT TCCTTTTAAA ACACTTCCAT AATCTGGACT CCTCTGTCCA GGCACCTGTG 1260
      CCCAGCCTCC AAGCTCCATC TCCACTCCAG ATTTTTTACA GCTGCCTGCA GTACTTTACC 1320
      TCCTATCAGA AGTTTCTCAG CTCCCAAGGC TCTGAGCAAA TGTGGCTCCT GGGGGTTCTT 1380
30     TCTTCTCTG CTGAAGGAAT AAATGTCTCC TTGACATTGT AGAGCTTCTG GCACCTGGAG 1440
      ACTGTATGA AAGATGGCTG TGCTCTGCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
      GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CCTAGCCTCG 1560
      CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAAAG TCCTACTTTC 1620
      CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAATAA GCCTAAAAAA AAAAAA 1680
35     AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

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Seq ID NO: 234 Protein sequence
Protein Accession #: NP_000568.1

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40     1      11      21      31      41      51
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      MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGPVNLE EKIDVVPFEP 60
      HALEFLGIHGG KMCLSCVKSG DETRLQLEAV NITDLSENRK QDKRFAFIRS DSGPTTSFES 120
45     AACPGWFLCT AMEADQPVS L TNMPDEGVMV TKFYFQEDE

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Seq ID NO: 235 DNA sequence
Nucleic Acid Accession #: NM_001840.1
Coding sequence: 149..1567

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50     1      11      21      31      41      51
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      GGGGACTACG GAGAGCTCTG CAGGGAGCCG AGGCCCCCGC CGGGCCCAAG GGAGCTTCTG 60
      TCCCGAGGAC CAGGGGATGC GAAGGGATTG CCCCTGTGG GTCACTTTCT CAGTCATTTT 120
55     GAGCTCAGCC TAATCAAAGA CTGAGGTTAT GAAGTCGATC CTAGATGSCC TTGCAGATAC 180
      CACCTTCGCG ACCATCACCA CTGACCTCCT GTACGTGGGC TCAATGACA TTCAGTACGA 240
      AGACATCAAA GGTGACATGG CATCCAAATT AGGTACTTC CCACAGAAAT TCCCTTTAAC 300
      TTCCTTTAGG GGAAGTCCCT TCCAAGAGAA GATGACTGCG GGAGACAACC CCCAGCTAGT 360
      CCCAGCAGAC CAGGTGAACA TTACAGAATT TTACAACAAG TCTCTCTCGT CCTTCAAGGA 420
      GAATGAGGAG AACATCCAGT GTGGGGAGAA CTTTATGGAC ATAGAGTGT TCAATGGTCT 480
60     GAACCCAGC CAGCAGCTGG CCAATTGCACT CCTGTCCCTC ACGCTGGGCA CCTTCAAGGT 540
      CCTGGAGAAC CTCCTGGTGC TGTGCGTCAT CCTCCACTCC CGCAGCCTCC GCTGCAGGCC 600
      TTCCTACCAC TTCATCGGCA GCCTGGCGGT GGCAGACCTC CTGGGGAGTG TCATTTTTGT 660
      CTACAGCTTC ATTGACTTCC ACGTGTTCCT CCGCAAGAT AGCCGCAACG TGTTCCTGTT 720
      CAAACTGGGT GGGGTACAGG CCTCCTTCAC TGCCTCCGTG GGCAGCCTGT TCCTCACAGC 780
65     CATCGACAGG TACATATCCA TTCACAGGCC CCTGGCTTAT AAGAGGATTG TCACCAGGCC 840
      CAAGGCCGTG GTGGCGTTTT GCCTGATGTG GACCATAGCC ATTGTGATCG CCGTGTCTGC 900
      TCTCTGGGCG TGGAACTGCG AGAAACTGCA ATCTGTTTGC TCAGACATTT TCCACACAT 960
      TGATGAAACC TACCTGATGT TCTGGATCGG GGTCAACAGC GTACTGTCTC TGTTCATCGT 1020
      GTATGCGTAC ATGTATATTC TCTGGAAGGC TCACAGCCAC GCCGTCCGCA TGATTACGCG 1080
70     TGGCACCAG AAGAGCATCA TCATCCACAC GTCTGAGGAT GGGAGGTGAC AGGTGACCG 1140
      GCCAGACCAA GCCCGCATGG ACATTAGGTT AGCCAAAGAC CTGGTCCTGA TCCTGGTGGT 1200
      GTTGATCATC TGCTGGGGCC CTCTGCTTGC AATCATGGTG TATGATGTCT TTGGGAAGAT 1260
      GAACAAGCTC ATTAAGACGG TGTTTGCATT CTGCAGTATG CTCTGCCTGC TGAATCCAC 1320
      CGTGAACCCC ATCATCTATG CTCTGAGGAG TAAGGACCTG CGACACGCTT TCCGGAGCAT 1380
75     GTTTCCTCT TGTGAAGGCA CTGCGCAGCC TCTGGATAAC AGCATGGGGG ACTCGGACTG 1440
      CCTGCACAAA CACGCAACA ATGCAGCCAG TGTTCACAGG GCCGCAGAAA GCTGCATCAA 1500
      GAGCAGGTC AAGATTGCCA AGGTAACCAT GTCTGTGTCC ACAGACACGT CTGCCAGGCC 1560
      TCTGTGAGCC TGATGCCTCC CTGGCAGCAC AGGAAAAGAA TTTTTTTTTT TAAGCTCAA 1620
      ATCTAGAGA GTCTATTGTC TCCTTGGTTA TATTTTTTTA ACTTTACCAT GCTCAATGAA 1680
80     AAGGTGATTG CCACATGTCA CTTATTGTCT TAGTTTCCGT TTGGGCTAAT CTTCCGGGGT 1740
      TCGTAGGAAA CCTTT

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Seq ID NO: 236 Protein sequence
Protein Accession #: NP_001831.1

	1	11	21	31	41	51	
5	MKSILDGLAD	TFRTITITDL	LYVGSNDIQY	EDIKGDMSK	LGYFPQKFFL	TSFRGSPFQE	60
	KMTAGDNPQL	VFPADQVNITE	FYNKSLSSFK	ENEENIQCGE	NFMDIECFMV	LNPSQQLAIA	120
	VLSLTLTGFT	VLENLLVLCV	ILHSRSLRCR	PSYHFIGSLA	VADLLGSVIF	VYSFIDFHFV	180
	HRKDSRNVFL	FKLGGVTASF	TASVGSFLFT	AIDRYISIHR	PLAYKRIVTR	PKAVVAFCLM	240
	WTIAIVIAVL	PLLGWNCEKL	QSVCSDFPH	IDETYLMEFI	GVTSVLLLF	VYAYMYILWK	300
10	AHSHAVRMQ	RGTKSIIH	TSDEGKVQVT	RPDQARMDIR	LAKTLVLILV	VLIICWGPLL	360
	AIMVYDVFGK	MNKLKTVFA	FCSMLCLLNS	TVNPIIYALR	SKDLRHAERS	MFPSCGTAQ	420
	PLDNSMGDS	CLHKHANNAA	SVHRAAESCI	KSTVKIAKVT	MSVSTDTSAE	AL	

Seq ID NO: 237 DNA sequence
 Nucleic Acid Accession #: NM_016083.2
 Coding sequence: 64..1482

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20	GATTGCCCCC	TGTGGGTAC	TTTCTCAGTC	ATTTTGAGCT	CAGCCTAATC	AAAGACTGAG	60
	GTTATGAAGT	CGATCCTAGA	TGGCCTTGCA	GATACCACT	TCCGCACCAT	CACCACTGAC	120
	CTCCTGTAGC	TGGGCTCAAA	TGACATTGAG	TACGAAGACA	TCAAAGGTGA	CATGGCATCC	180
	AAATTAGGGT	ACTTCCCA	GAAATTCCT	TTAACTTCCT	TTAGGGGAAG	TCCCTTCCAA	240
	GAGAAGATGA	CTGGGGGAGA	CAACCCCAAG	CTAGTCCAG	CAGACCAAGT	GAACATTACA	300
25	GAATTTTACA	ACAAGTCTCT	CTCGTCTTC	AAGGAGAATG	AGGAGAACAT	CCAGTGTGGG	360
	GAGAACTTGA	TGGACATAGA	GTGTTTCATG	GTCCTGAACC	CCAGCCAGCA	GCTGGCCATT	420
	GCAGTCTGT	CCCTCACGCT	GGGCACCTTC	ACGGTCTGG	AGAACCTCCT	GGTGTGTGC	480
	GTCATCTCC	ACTCCCGAG	CCTCCGCTGC	AGGCCTTCT	ACCACTTCAT	CGGCAGCTG	540
	GCGGTGGCAG	ACCTCCTGG	GAGTGTCAAT	TTTGTCTACA	GCTTCATTGA	CTTCCAGTGC	600
	TTCCACCGCA	AAGATAGCCG	CAACGTGTTT	CTGTTCAAAC	TGGGTGGGGT	CACGGCCTCC	660
30	CTCACTGCTT	CCGTGGGAG	CCTGTTCTTC	ACAGCCATCG	ACAGGTACGT	ATCCATTAC	720
	AGGCCCTGG	CCTATAAGAG	GATTGTCAAC	AGGCCCAAGG	CCGTGGTGGC	GTTTGTGCTG	780
	ATGTGGACCA	TAGCCATTGC	GATCGCCGTG	CTGCCTCTCC	TGGGCTGGAA	CTGCGAGAAA	840
	CTGCAATCTG	TTTGCTCAGA	CATTTTCCCA	CACATTGATG	AAACCTACCT	GATGTTCTGG	900
	ATCGGGGTCA	CCAGCGTACT	GCTTCTGTTC	ATCGTGTATG	CGTACATGTA	TATTTCTGCG	960
35	AAGGCTCAG	GCCAGCGCGT	CCGCATGATT	CAGCGTGGCA	CCCAGAAGAG	CATCATCATC	1020
	CACACGCTG	AGGATGGGAA	GGTACAGGTG	ACCCGCGCAG	ACCAAGCCCG	CATGGACATT	1080
	AGGTTAGCCA	AGACCCTGGT	CCTGATCCTG	GTGGTGTGTA	TCATCTGTCTG	GGGCCCTTTG	1140
	CTTGCAATCA	TGGGTATGTA	TGTCTTTGGG	AAGATGAACA	AGCTCATTA	GACGGTGTTC	1200
	GCATTTCTGA	GTATGCTCTG	CCTGCTGAAC	TCCACCGTGA	ACCCCATCAT	CTATGCTCTG	1260
40	AGGAGTAAGG	ACCTGCGACA	CGCTTCCGG	AGCATGTTTC	CCTCTTGTGA	AGGCACTGCG	1320
	CAGCCTCTGG	ATAACAGCAT	GGGGGACTCG	GACTGCCTGC	ACAAACACGC	AAACAATGCA	1380
	GCCAGTGTTC	ACAGGGCGCG	AGAAAGCTGC	ATCAAGAGCA	CGGTCAAGAT	TGCCAAGGTA	1440
	ACCATGCTG	TGTCCACAGA	CACGTCTGCC	GAGGCTCTGT	GAGCCTGATG	CCTCCCTGGC	1500
45	AGCACAGGAA	AAGAATTTT	TTTTTAAGC	TCAAAATCTA	GAAGAGTCTA	TTGTCTCCTT	1560
	GGTTATATTT	TTTTAACTTT	ACCATGCTCA	ATGAAAAGGT	GATTGTCAAC	ATGATCACTT	1620
	ATCAGTTTGC	TAATGTTTCC	ATAGTTTAGG	TACTCAAAC	CCATTCTCCA	GGGGTTTACA	1680
	GTGAAGAAAG	CCGTGTGTTT	AAGTGACTGA	ACGATCCTTC	AAAGTCTCAA	TGAATATAGGA	1740
	GGGAAACCTT	TGGCTACACA	ATTGGAAGTC	TAAGAACCCA	TGGAAAAATG	CCATCAAATG	1800
	AATAATGCTT	TTGTAACCA	AACTTTCACT	ATAATGTGAA	ATGTAACGTG	CCGTAGTATC	1860
50	AGAGATGCTC	ATTTTTCACA	GTTATAGTAC	TAGAGATATT	TTGTAAATG	TATTATGTCC	1920
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	AGGTAGACTT	TTATGAGAAC	AATGGACRA	CAGTGGATAC	GTGTCAATGT	GTGCACTTTT	2040
	TTTCTATATT	ATTGCCCATG	ATATAACTTT	AGAAATAAAC	CTTAATATTT	CTTCAATAT	2100
	CTCTATTATA	TTTTGACACT	GAAATAACCG	TAAAGGTTTA	TTTTTCTGTT	ACCTCAACAA	2160
55	GAAGAATTTC	AAGACTCTCA	AATATTGAGC	AGAATTCATT	CATACTTAAA	AATTTATTAG	2220
	CCCTGCATTT	TCATAGGAAG	ACACATTATC	TTCTGGACTA	TAGCTGTCTT	AATGGATTAT	2280
	AATCAGAAAT	GAAGAGAGAA	AGCATATTGA	CTTTTTTTGA	GCGACATCTC	TGACTTTCTT	2340
	TAGTCTTTAG	CTATTACTGG	ATCTCTTAAG	ACAGCATGTG	TTAATCTTAA	TGTATATCGT	2400
	TATCACTGTG	CAGTGTCTGT	TTACTTGAAT	AGTATTGTGT	TCCTATATTC	CAGGTTTAAG	2460
60	TAGATTTTCA	GCCTGGGTGG	CCAAACAACA	GTCTTCATTT	TTTTTAATTG	AAAAGAAAGTA	2520
	GTGTCTGGAT	CAGTAAATTT	ATACTGTGTG	TGAGTGTGAA	TATAAATGTG	TGTATGTGTG	2580
	TTTCTGTCCG	TAACGTGTTAC	AGTAATGTCA	TAAAGTGAGA	AAACTGTGAC	CAAGTATAAA	2640
	CTTTTACCAC	TGCTGTCACT	CTTGACATG	GATTCAAGTT	CTAAAATTGA	GTTCTTCTCG	2700
65	TAATCTTGTT	GATAAAAATA	CTGACTCCAA	CCATTCAAAA	ATTTCAACCC	ATCCCTCCTT	2760
	AAGAGATTGG	ATCAAGTATT	ACTAAATTGA	CCTTTAGGTA	TTACACAAGA	CCAGTGCTTA	2820
	GCAAAAAATA	ATGACAGGGA	TCCAAGGAAG	GGATGTATTT	GTAGTGTAT	TGCCAGGAAA	2880
	GGAGAGTACT	TTGGTTTCTG	AGCACCGAAT	ATTGAGCAAT	ATGTCAGTCA	CTAAAAGGAA	2940
	GACAGTTCTA	CAGAAAAACA	AATGGTAACA	TTTTTCAATA	GCGTGTGTAG	ATAGTATGCA	3000
70	CTATATACAT	CACGTTAAAG	TAGGACTATC	ACACCCAGCC	CATGTGGCTA	AAAAAGCTGA	3060
	ATCAGACAGT	GGATGAGACA	CACAACGGCA	GTGAAGAAC	GATACACTTG	GCATTGACGT	3120
	CTAGCTATGC	TGTATCTGTG	CTTTGCCAC	ATGCCCTTGG	TGACAGCTGA	GCACCCAGCT	3180
	CTGTCTTGTT	AGGTTTGGGC	TAAGGAACAA	ATCTCTCCTT	TGCTCGTGGT	TAGCAAGATA	3240
	CACTCAAGCA	TGAAGATAAA	CACAGCTGCT	TTCTTCTTAC	ACCCCGGTCT	CATGCTCCTT	3300
75	AATGGCGCCA	TGGGTGCTTG	TTGGGCTTTT	TTCCAGTAAG	GAATGATATT	GCTGAAGAA	3360
	CTACTTAAAC	CTGACAAAT	TTAATTATAA	TCTCTTCTTA	TACAGATAAA	ACATGACTCC	3420
	TACAAGGCC	CAAGGTTTAC	ATAGTCTGAA	GTGAAGTACA	GAGCTGGCAT	CTATCTGGTG	3480
	ATTTCTAGCT	CTCGAGATAC	CCAAGCAGCC	TGATGGGGCA	GTTCCCTTTC	TTACGGTTCA	3540
	CGCTCTAAG	CAGGATGTGG	CTTATGAGAT	ACTTTGCATT	GTCTGTCTGC	ACACCTTGAA	3600
80	TCTGCTGCT	GGCTCCCTTA	CTTTACCTCT	CTGTCAATG	CAGATGAAGG	CTCAGGGTGC	3660
	TAGAGGATTA	GTAAGATCTC	TTTCTAAAGA	CAGGAGAGAT	TATTTACAAG	AAGAACTCAC	3720
	CAGGTTTAG	TTTGTCATTT	AGAATTGCCA	GTCTTTTGTC	CTGCATCATC	TTGAACATTA	3780
	ATCCACATGT	TTCAGAGCTC	ACCAGGCAGT	ACCAATGCTC	TTTTTACAGC	TATGAAGAGC	3840
	TAGAGAAAT	CTTGTTATGG	TAGAAAAAT	TCACGGTTCA	TTTTTGAAAC	TGCATTGTG	3900
	CGTATGCAGT	GTAGATTTTA	TAGTGTGTTG	TGCTTTCAAG	ATCTAAATCA	TATATAATAA	3960

ATTAAGGGAC AATGGGGCTG ACAGCACTAA ACTTGGTGCT TATTGATATT CTAAGAAATA 4020
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 AGATTCACCT TGACACTTTT CATATCATTT CTTAACCCAA GTGACGAAAA CATTGTCCCC 4140
 AATGAATATA CTCATTAGAA TTACCATTTG TTAATATCAC TCATTAATTA ACCCCATAAT 4200
 TAGATCCATT AATTTAAATG ATTTAAATT AAGTAAGTTT TATAAGGTCT GACATCAGAG 4260
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 ATGAAGAACA TA

Seq ID NO: 238 Protein sequence
 Protein Accession #: NP_057167.1

1 11 21 31 41 51
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 KMTAGDNPQL VPADQNVITE FYNKSLSEFK ENEENIQCGE NFMDIECFMV LNPSQQLAIA 120
 VLSLTLGTFT VLENLLVLCV ILHSRSLRCR PSYHFIGSLA VADLLGSVIF VYSFIDFHFV 180
 HRKDSRNVFL FKLGGVTASL TASVGSFLFT AIDRYVSIHR PLAYKRIVTR PKAVVAFCLM 240
 WTIAIAIAVL PLLGWNCEKL SVCSDFPH IDETYLMFEWI GVTSVLLLFV VYAYMYILWK 300
 AHSHAVRMIQ RGTQKSIH TSEDGKVQVT RPDQARMDIR LAKTLVLILV LLIICWGPLL 360
 AIMVYDVFGK MNKLIKTVFA PCSMLCLLNS TVNPIIYALR SKDLRHAERS MPFSCEGTAQ 420
 PLDSMGDSD CLHKHANNA SVHRAESCI KSTVKIAKVT MSVSTDTSAE AL

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 Coding sequence: 17..1252

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 TGCCAAGGTA ACCATGTCTG TGTCACAGA CACGTCTGCC GAGGCTCTGT GA

Seq ID NO: 240 Protein sequence
 Protein Accession #: NP_149421.1

1 11 21 31 41 51
 | | | | |
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 LSLTLGTFTV LENLLVLCVI LHSRSLRCR PSYHFIGSLV ADLLGSVIFV YSFIDFHFVH 120
 RKDSRNVFLF KLGVTASFT ASVGSFLFTA IDRYISIHPR LAYKRIVTRP KAVVAFCLMW 180
 TTAIVIAVLV LLGWNCEKLQ SVCSDFPHI DETYLMFEWI VTSVLLLFV YAYMYILWKA 240
 HSHAVRMIQ RGTQKSIH TSEDGKVQVT RPDQARMDIR AKTLVLILV LLIICWGPLLA 300
 IMVYDVFGKM NKLIKTVFAF CSMLCLLNST VNPIIYALRS KDLRHAERSM FPSCGTAQP 360
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Seq ID NO: 241 DNA sequence
 Nucleic Acid Accession #: NM_003596.1

Coding sequence: 82..1194

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	CTGGTGATTA	GTTCTGTGAC	TGTGTTTAC	CTGGCCAGC	ATGCCATGGA	ATGCCATCAC 180
	CGGATAGAGG	AACGTAGCCA	GCCAGTCAAA	TTGGAGAGCA	CAAGGACCAC	TGTGAGAACT 240
10	GGCCTGGACC	TCAAAGCCAA	CAAAACCTTT	GCCTATCACA	AAGATATGCC	TTTAATATTT 300
	ATTGGRGGTG	TGCTCTGGAG	TGGAACCACA	CTCATGAGGG	CCATGCTGGA	CGCACATCCT 360
	GACATTGCT	GTGGAGAGGA	AACCAGGGTC	ATTCCTCGAA	TCCTGGCCCT	GAAGCAGATG 420
	TGGTCACGGT	CAAGTAAAGA	GAAGATCCGC	CTGGATGAGG	CTGGTGTAC	TGATGAAGTG 480
	CTGGATTCTG	CCATGCAAGC	CTTCTTACTA	GAAATTATCG	TTAAGCATGG	GGAGCCAGCC 540
15	CCTTATTTAT	GTAATAAAGA	TCCTTTTGCC	CTGAAATCTT	TAACTTACCT	TTCTAGGTTA 600
	TTCCCCAATG	CCAAATTCT	CCTGATGGTC	CGAGATGGCC	GGGCATCAGT	ACATTCAATG 660
	ATTCTCGAA	AAGTACTAT	AGCTGGATTT	GATCTGAACA	GCTATAGGGA	CTGTTTGACA 720
	AAGTGGAATC	GTGCTATAGA	GACCATGTAT	AACCAGTGTA	TGGAGGTG	TTATAAAAG 780
	TGCATGTTGG	TTCACTATGA	ACAACTTGTC	TTACATCCTG	AACGGTGGAT	GAGAACACTC 840
20	TTAAAGTTCC	TCCAGATTCC	ATGGAACCAC	TCAGTATTGC	ACCATGAAGA	GATGATTGGG 900
	AAAGCTGGGG	GAGTGTCTCT	GTCAAAAGTG	GAGAGATCTA	CAGACCAAGT	AATCAAGCCA 960
	GTCAATGTAG	GAGCTCTATC	AAAATGGGTT	GGGAAGATAC	CGCCAGATGT	TTTACAAAGAC 1020
	ATGGCAGTGA	TTGCTCTCTAT	GCTTGCCAAG	CTTGGATATG	ACCCATATGC	CAACCCACCT 1080
	AACATCGGAA	AACCTGATCC	CAAAATTATT	GAAAACACTC	GAAGGGTCTA	TAAGGGAGAA 1140
25	TTCCAACCTAC	CTGACTTCT	TAAAGAAAA	CCACAGACTG	AGCAAGTGGG	GTAGCAGAAC 1200
	CAGGAGCCTC	TTCCATACAT	GAGGAAAGAT	TGCTGCTCTT	TCAGCAGAA	GGAAATTCCT 1260
	AGGATTGGCT	GTCCCTGCTC	AAGCTTGGTG	GAGCGTCTGC	ACCTTGGCTG	CGCCGCTGT 1320
	GCATTTGCCA	GTTTCTCTCC	ACTGAGAGGA	TGGAGGTGTC	CGCACAGCTT	TGGGCTCGT 1380
	GAGGATCTG	CCTCTGAGC	AAAGAGCTCT	TGATCCCGAT	TTCAATGCACA	GCCCTGCAGT 1440
30	AAGGAGCCCA	GAAGGAACAT	GTGTTTCTCT	TTAAACTCTC	TCTGTCTCTC	TTTTCTTACA 1500
	TTATGACGTT	TGTTTTCAAG	GAGAGGGTTT	AAAAATGGGA	TCCTGTAAAG	AGACTTGGG 1560
	AGTCTCTCTT	TGAATAGGT	TGCTCTAATG	TTTTGTAGAA	CACGTGTGCC	1620
	TGTTTAAAGT	TATTGATGTG	AATAATATTA	AATATCTTAA	TTATTTAATT	CATTGTATTG 1680
	TTTCTGAGAA	GTTGGGAAAT	TACCATTATA	CATTTACAAC	CTAATGACTT	TTGTATTTTA 1740
35	TTTTTCAAAA	TAAAGCTTT	CAATGTGA			

Seq ID NO: 242 Protein sequence
Protein Accession #: NP_003587.1

1	11	21	31	41	51	
40	MVGKLLKQNL	LACLVISSVT	VFYLGQHAME	CHHRIEERSQ	PVKLESTRRT	VRTGLDLKAN 60
	KTFAYHKDMP	LIFIGGVPRS	GTTLMRAMLD	AHPDIRCGEE	TRVIPRILAL	KQWRSRSKE 120
	KIRLDEAGVT	DEVLDSAMQA	FLLEIIVKHG	EPAPYLNCND	PFALKSLTYL	SRLFNPNAKFL 180
45	LMVRDGRASV	HSMISRKVTI	AGFDLNSYRD	CLTKWNRAIE	TMYNQCMVEG	YKKMLVHYE 240
	QLVLHPPERWM	RTLKFLQIP	WNHSLVHHEE	MIGKAGGVSL	SKVERSTDQV	IKPVNVGALS 300
	KWVGKIPDPV	LQDMAVIAPM	LAKLGYDPYA	NPPNYGKPD	KIIENTRRVY	KGEFQLPDFL 360
	KEKPQTEQVE					

Seq ID NO: 243 DNA sequence
Nucleic Acid Accession #: NM_001492.3
Coding sequence: 1395..2513

1	11	21	31	41	51	
55	ACGCGGGGCG	CGCGGCTCCG	TCGGCTACCG	CGGGCGGGCG	CAGGCGACGG	GCACGGCGGG 60
	CGAGCGGGCG	GTATGGGGCG	GGCGGGGGCC	GCGCGGGGGC	CGAGCGGGCC	CGAGCCCATG 120
	CCGAGCTACG	CGCAGCTAGT	GCAGCGCGGC	TGGGGCAGCG	CGCTGGCGGC	GGCGCGGGGC 180
	TGCACGGAAT	GCGGCTGGGG	GCTGGCGCGT	CGCGGCTGGG	CTGAGCACGC	GCACCTGGCG 240
60	CCGCGCGAGC	TGCTGCTGCT	GGCGCTCGGC	CGCGTGGGCT	GGACCGCGCT	GCGCTCCGCG 300
	GCCACTGCGC	GCCCTCTTTC	GCCCTGGCG	AAGCGGTGCT	GCCTCCAGCC	CAGAGATGCC 360
	GCCAAGATGC	CCGAGAGCGC	TTGGAAGTTT	CTCTTCTACC	TGGGCAGCTG	GAGCTACAGT 420
	GCTACCTGTC	TGTTTGGCAC	CGACTACCCC	TTCTTCCATG	ACCCACCATC	TGTCTTCTAC 480
	GACTGGAGCG	CGGGCATGGC	AGTGCCACGG	GACATTGCAG	CCGCCTACCT	GCTCCAGGGA 540
65	AGCTTCTATG	GCCACTCCAT	CTACGCTACG	CTATACATGG	ACACCTGGCG	CAAGGACTCG 600
	GTGGTCATGC	TGCTCCACCA	CGTGGTCACT	CTCATCTCTA	TGCTCTCTCT	CTACGCTTTC 660
	CGGTACCACA	ATGTGGGCAT	CCTTGTGCTC	TTCTTGACAG	ATATCAGTGA	CGTGACGCTT 720
	GAGTTCACCA	AGCTCAACAT	TTACTTCAAG	TCCCGCGGCG	GCTCCTACCA	TCCGCTGCAT 780
	GCCTTGGCAG	CAGACTTGGG	CTGCTCAGC	TTCCGCTTCA	GCTGGTCTTG	GTTCCGCTCT 840
70	TACTGGTTCC	CGCTCAAGGT	CCTGTATGCC	ACCACTCACT	GCAGTCTGCG	CACGGTGCCT 900
	GACATCCCTT	TCTACTTCTT	CTTCAATGCG	CTCCTGCTGC	TGCTCACCTT	TATGAACCTC 960
	TACTGGTTCC	TGTACATCGT	GGCGTTTGCA	GCCAAGGTGT	TGACAGGCCA	GGTGCACGAG 1020
	CTGAAGGACC	TGCGGGAGTA	TGACACAGCC	GAGGCCAGAG	GCCTGAAGCC	CAGCAAGGCC 1080
	GAGAAGCCAC	TGAGGAACGG	CCTGGTGAAG	GACAAGCGCT	TCTGAACCCC	TCCGCCCCCG 1140
75	CCCCGTGGAC	CCGGCCCCAC	CCCGAATACC	CCGGCCACGC	TCCCCGTCCT	TGGCCGCCCC 1200
	TCCACCCCTC	CCAACCTCTG	TCCTCTAGGG	CCGCCGCCAC	CTCCCTGGG	ACCCCGCCCC 1260
	CTCATCCTGC	CTCCATTCTC	CGGCCACGCC	CCCCAGGACC	CCTGCCCTTC	CGGGGACACC 1320
	GGCCCCGCCC	TCAGCCCACT	GGTCCCGGGC	CGCCGCGGAC	CCTGCGCACT	CTCTGTCTAT 1380
	CGCTGGGAG	GAAGATGCCA	CCGCCGAGC	AAGTCCCTG	CGGCCACCAC	CTCTCTCTCC 1440
80	TCCTGGCCCT	GCTGCTGCCC	TCGCTGCCCC	TGACCCGCGC	CCCCGTGCCC	CCAGGCCACG 1500
	CCGCCGCCCT	GCTCCAGGCT	CTAGGACTGC	GCGATGAGCC	CGAGGGTGCC	CCCAGGCTCC 1560
	GGCCGGTTCC	CCCGGTCTAT	TGGCGCTGT	TTCCAGCCCG	GGACCCACAG	GAGACAGGTT 1620
	CTGGCTCGCG	GCGGACGTCC	CCAGGGGTCA	CCCTGCAACC	GTGCCACGTG	GAGGAGCTGG 1680
	GGGTCCCGCG	AAACATCGTG	CGCCACATCC	CGGACCGCGG	TGCGCCACAC	CGGGCCTCGG 1740
	AGCCTGTCTC	GGCCCGGGGG	CATTGCCCTG	AGTGGACAGT	CGTCTTCGAC	CTGTCCGGCTG 1800

TGAACCCGCG TGAGCGCCCG AGCCGGGCCC GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG 1860
 CGGCAGCCCC GGAGGGCGCG TGGGAGCTGA GCGTGGCGCA AGCGGGCCAG GGCGCGGGCG 1920
 CGGACCCCGG GCCGGTGCCTG CTCCGCCAGT TGGTGCCCGC CCTGGGGCCG CCAGTGC GCG 1980
 CGGAGCTGCT GGGCGCCGCT TGGGCTCGCA ACGCCTCATG GCCGCGCAGC CTCGCGCTGG 2040
 CGCTGGCGCT ACGCCCCCGG GCCCTGCGG CCTGCGCGCG CCTGGCCGAG GCCTGCTGTC 2100
 TGCTGGTGAC CCTCGACCCG CGCCTGTGCC ACCCCTTGGC CCGGCGCGCG CGCGACGCGG 2160
 AACCCGTGTT GGGCGGCGGC CCCGGGGGCG CTGTGTCGCG GCGGCGGCTG TACGTGAGCT 2220
 TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCCGCG CGGCTTCCTG GCCAACTACT 2280
 GCCAGGGTCA GTGCGCGCTG CCGCTCGCGC TGTGCGGGTC CCGGGGGCCG CCGGCGCTCA 2340
 ACCACGCTGT GCTGCGCGCG CTCATGCACG CGGCCGCCCG GGGAGCGCGC GACCTGCCCT 2400
 GCTGCGTGCC CGCGCGCCTG TCGCCCATCT CCGTGCTCTT CTTTGACAAC AGCGACAACG 2460
 TGGTGCTGCG GCAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCCG TAACCCGGGG 2520
 CGGGCAGGGA CGCGGGCCCA ACAATAAATG CCGCGTGGTC TGCTC

Seq ID NO: 244 Protein sequence
 Protein Accession #: NP_001483.2

1 11 21 31 41 51
 | | | | |
 MPPFPQQGPGC HLLLLLLALL LPSLPLTRAP VPPGPAAAL QALGLRDEPQ GAPRLRPVPP 60
 VMWRLFRRRD PGETRSGSRR TSPGVTLQPC HVEELGVAGN IVRHIPDRGA PTRASEPVSA 120
 AGHCPEWTVV FDLSAVEPAE RPSRARLELR FAAAAAAPE GWELSVQA GOGAGADPGP 180
 VLLRQLVPAL GPPVRAELLG AAWARNASWP RSLRLALALR PRAPAACARL AEASLLLVTL 240
 DPLRCHPLAR PRRDAEPVLG GPGGACRAR RLYVSFREVW WHRWIAPRG FLANYCQGQC 300
 ALPVALSGSG GPPALNHAVL RALMHAAAPG AADLPCCVPA RLSPISVLFF DNSDNVVLRLQ 360
 YEDMVVDECG CR

Seq ID NO: 245 DNA sequence
 Nucleic Acid Accession #: NM_021267.1
 Coding sequence: 17..1125

1 11 21 31 41 51
 | | | | |
 ACGCGGGGCG CGCGGCTCCG TCGGCTACCG CGGGCGGGCG CAGGCGACGG GCACGGCGGG 60
 CGAGCGGGCG GTATGGCGGC GCGGGGGCCC GCGCGGGGCG CGACGGGGCC CGAGCCCATG 120
 CCGAGCTACG CGCAGCTAGT GCAGCGCGGC TGGGGCAGCG CGCTGGCGGC GCGCGGGGCG 180
 TGACGGGACT GCGGCTGGGG GCTGGCGCGT CGCGGCTGG CTGAGCACGC GCACCTGGCG 240
 CCGCCCGAGC TGCTGCTGCT GCGGCTCGGC GCGCTGGGCT GGACCGCGCT GCGCTCCGCG 300
 GCCACTGCGC GCCTCTTTTCG GCCCTTGGCG AAGCGTGTCT GCCTCCAGCC CAGAGATGCC 360
 GCCAAGATGC CCGAGAGCGC TTGGAGTTT CTCTTCTACC TGGGCAGCTG GAGCTACAGT 420
 GCCTACCTGC TGTTTGGCAC CGACTACCCC TTCTTCCATG ACCCACCATC TGTCTTCTAC 480
 GACTGGAGCG CCGGCATGGC AGTGCCACGG GACATTGCAG CCGCCTACCT GCTCCAGGGA 540
 AGCTTCTATG GCCACTCCAT CTACGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG 600
 GTGGTCTATG TGCTCCACCA CGTGGTCACT CTCATCCTCA TCGTCTCCTC CTACGCTTTC 660
 CGGTACACACA ATGTGGGACT CCTTGTGCTC TTCTGTGACG ATATCAGTGA CGTGACGCTT 720
 GAGTTACACA AGCTCAACAT TTACTTCAAG TCCCGCGGCG GCTCCTACCA TCGGCTGCAT 780
 GCCTTGGCAG CAGACTTGGG CTGCTCAGC TTCGCTTCA GCTGGTTCTG GTTCCGCTC 840
 TACTGGTTCC CGCTCAAGGT CCGTGTATGCC ACCAGTCACT GCAGTCTGCG CACGGTGCCT 900
 GACATCCCTT TCTACTTCTT CTTCATGCG CTCCTGTGCG TGCTCACCTT TATGAACCTC 960
 TACTGGTTCC TGTACATCGT GCGTTTGA GCGAAGGTGT TGACAGGCCA GGTGCACGAG 1020
 CTGAAGGACC TGCGGGAGTA TGACACAGCC GAGGCCCAGA GCCTGAAGCC CAGCAAAGCC 1080
 GAGAAGCCAC TGAGGAACCG CCTGGTGAAG GACAAGCGCT TCTGAACCCC TCGGCCCGCG 1140
 CCGCGTGAAC CCGGCCCCAC CCGGAATACC CCGGCCACGC TCCCGTCTCT TGGCGCGCCC 1200
 TCCACCCCTT CCAACTCTGC TCCTCTAGGG CCGCGGCCAC CTCCTCTGGG ACCCGCGCCC 1260
 CTATCTCTG CTCCATTTCG CGGCCACGCC CCGCAGGACC CCGTCCCTCT CCGGGACACC 1320
 GGCCCGGCCC TCAGCCCACT GGTCCCGGGC CGCCGCGGAC CCTGCGCACT CTCTGGTCT 1380
 CGCCTGGGAG GAAGATGCCA CCGCGCGAGC AAGGTCCCTG CCGCCACCAC CTCCTCTCTC 1440
 TCCTGGCCCT GCTGCTGCCC TCGCTGCCCC TGACCCGCGC CCGCGTGCCC CCAGGCCGAG 1500
 CCGCGCCCTT GCTCCAGGCT CTAGGACTGC GCGATGAGCC CCAGGGTGCC CCCAGGCTCC 1560
 GGCCGGTTCC CCCGCTCATG TGGCGCCTGT TTCGACGCGG GACCCCCAG GAGACCAGT 1620
 CTGGCTCGCG GCGGACGTC CCAGGGTCA CCCTGCAACC GTGCCACGTG GAGGAGCTGG 1680
 GGGTGCGCGG AAACATCGTG CGCCACATCC CGGACCGCGG TGCGCCACC CCGGCTCGG 1740
 AGCCTGTCTC GGCCGCGGGG CATTGCCCTG AGTGGACAGT CBTCTTCGAC CTGTGCGCTG 1800
 TGAACCCGCG TGAGCGCCCG AGCCGGGCCC GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG 1860
 CGGCAGCCCC GGAGGGCGCG TGGGAGCTGA GCGTGGCGCA AGCGGGCCAG GGCGCGGGCG 1920
 CGGACCCCGG GCGGCTGCTG CTCCGCCAGT TGGTGCCCGC CCTGGGGCCG CCAGTGC GCG 1980
 CGGAGCTGCT GGGCGCCGCT TGGGCTCGCA ACGCCTCATG GCCGCGCAGC CTCGCGCTGG 2040
 CGCTGGCGCT ACGCCCCCGG GCCCTGCGG CCTGCGCGCG CCTGGCCGAG GCCTGCTGTC 2100
 TGCTGGTGAC CCTCGACCCG CGCCTGTGCC ACCCCTTGGC CCGGCGCGCG CGCGACGCGG 2160
 AACCCGTGTT GGGCGGCGGC CCCGGGGGCG CTGTGTCGCG GCGGCGGCTG TACGTGAGCT 2220
 TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCCGCG CGGCTTCCTG GCCAACTACT 2280
 GCCAGGGTCA GTGCGCGCTG CCGTTCGCGC TGTGCGGGTC CCGGGGGCCG CCGGCGCTCA 2340
 ACCAGCTGTG GCTGCGCGCG CTCATGCACG CGGCCGCCCG GGGAGCCGCG GACCTGCCCT 2400
 GCTGCGTGCC CGCGCGCCTG TCGCCCATCT CCGTGCTCTT CTTTGACAAC AGCGACAACG 2460
 TGGTGCTGCG GCAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCCG TAACCCGGGG

Seq ID NO: 246 Protein sequence
 Protein Accession #: NP_067090.1

1 11 21 31 41 51
 | | | | |
 MAAAGPAAGP TGPEPMPSYA QLVQRGWGSA LAAARGCTDC GWGLARRGLA EHAHLAPPEL 60
 LLLALGALGW TALRSAATAR LFRPLAKRCC LQPRDAAKMP ESAWKFLFYL GSWSYSAVLL 120
 FGTDYPPFFHD PPSVFIYDWTG GMAVPRDIAA AYLLQGSFYG HSIYATLYMD TWRKDSVVML 180

LHHVTLILI VSSYAFRYHN VGILVLFLHD ISDVQLEFTK LNIYFKSRGG SYHRLHALAA 240
 DLGLSFGFS WFWRLYWFP LKVLATSHC SLRTVPDIPF YFFFNALLLL LTLMLNLYWFL 300
 YIVAFAPAKVL TGVHLEKDL REYDTAEAS LKPSKAEKPL RNGLVKDKRF

5

Seq ID NO: 247 DNA sequence
 Nucleic Acid Accession #: NM_002081.1
 Coding sequence: 222..1898

10 1 11 21 31 41 51
 | | | | |
 GGCTGCCCGA GCGAGCGTTC GGACCTCGCA CCCCGCGCGC CCCCGCGCGC CGCCGCGCGC 60
 GGCTTTTGT GTCTCCGCCT CCTCGGCCGC CGCCGCTCT GGACCCGAG CGCGCGCGC 120
 CGGACCTTG GCTCTGCCCT TCGCGGGCGG GAACTGCGCA GGACCCGCC AGGATCCGAG 180
 15 AGAGGCGCGG GCGGGTGGCC GGGGGCGCGG CCGGCCCGGC CATGGAGTTC CGGGCCCGAG 240
 GCTGGTGGCT GCTATGTGCG GCGGCAGCGC TGGTGCCTG CGCCCGCGGG GACCCGGCCA 300
 GCAAGAGCCG GAGCTGCGGC GAGGTCCGCC AGATCTACGG AGCCAAGGC TTCAGCCTGA 360
 GCGACGTGCC CCAGGCGGAG ATCTCGGGTG AGCACTGCG GATCTGTCCC CAGGGCTACA 420
 CCTGCTGCAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480
 20 CCGCGCTCCG GGACAGCAGC CGGTCTCTGC AGGCCATGCT TGCCACCCAG CTGCGCAGCT 540
 TCGATGACCA CTTCCAGCAC CTGCTGAACG ACTCGGAGCG GACGCTGAC GCCACCTTCC 600
 CCGGCGCCTT CGGAGAGCTG TACACGCAGA ACGCGAGGGC CTTCCGGGAC CTGTACTCAG 660
 AGCTGCGCCT GTACTACCGC GGTGCCAACC TGCACCTGGA GGAGACGCTG GCCGAGTTCT 720
 GGGCCCGCCT GCTCGAGCGC CTCTTCAAGC AGCTGCACCC CCAGCTGCTG CTGCCTGATG 780
 25 ACTACCTGGA CTGCCTGGGC AAGCAGGCCG AGGCGCTGCG GCCCTTCGGG GAGGCCCGGA 840
 GAGAGCTGGC CCGTGGCGGC ACCCGTGCCT TCGTGGCTGC TCGCTCCTTT GTGCAGGGCC 900
 TGGGCGTGGC CAGCGACTGT GTCCGAAAG TGGCTCAGGT CCCCCTGGGC CCGGAGTGCT 960
 CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTACTGCTCT GGGAGTCCCC GGGCCAGGC 1020
 CCTGCGCTGA CTATTGCCGA AATGTGCTCA AGGGCTGCCT TGCCAAACCA GCGGACCTGG 1080
 30 ACGCCGAGTG GAGGAACCTC CTGGACTCCA TGGTGTCTAT CACCGACAAG TTCTGGGGTA 1140
 CATCGGGTGT GGAGAGTGTC ATCGGCAGCG TGCAACGCTG GCTGCGGAG GCCATCAACG 1200
 CCCTCCAGGA CAACAGGGAC ACGCTCACGG CCAAGGTCAT CCAGGGCTGC GGAACCCCA 1260
 AGGTCAACCC CAGGGCCCTT GGGCCTGAGG AGAAGCGGCG CCGGGCAAG CTGGCCCGCG 1320
 GGGAGAGGGC ACCTTCAGCG ACGCTGAGGA AGCTGGTCTC TGAAGCCAAG GCCCAGCTCC 1380
 35 GCGACGTCCA GACTTCTGAG ATCAGCTTCC CAGGGACACT GTGCAGTGAG AAGATGGCCC 1440
 TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGGATGGC CAGAGGCCGG TACCTCCCCG 1500
 AGGTCAATGG TGACGGCCTG GCCAACCAAG TCAACAACCC CGAGGTGGAG GTGGACATCA 1560
 CCAAGCCGGA CATGACCATC CGGCAGCAGA TCATGCAGCT GAAGATCATG ACCAACCCGC 1620
 TGCGCAGCGC CTACAACGGC AACGACGTGG ACTTCCAGGA CGCCAGTGAC GACGCGAGCG 1680
 40 GCTCGGGCAG CCGTGATGGC TGTCTGGATG ACCTCTGCGG CCGGAAGGTC AGCAGGAAGA 1740
 GCTCCAGCTC CCGGACGCC TTGACCCATG CCTTCCGAG CCGTGCAGAG CAGGAAGGAC 1800
 AGAAGACCTC GGTGCGCAGC TGCCCCCAGC CCCCAGCCTT CCTCTGCCCC CTCTCTCTCT 1860
 TCCTGGCCCT TACAGTAGCC AGGCCCGGT GCGGTAACT GCCCAAGGC CCCAGGACA 1920
 GAGGCCAAGG ACTGACTTTG CCAAAAATAC AACACAGACG ATATTTAATT CACCTCAGCC 1980
 45 TGAGAGGGCC TGGGGTGGGA CAGGGAGGGC CCGCGGCTCT GAGCAGGGGC AGGCGCAGAG 2040
 GTCCAGCCCC CAGGCTGGC CTGCGCTGCC TTCTGCTTCT TTAATTTTGT ATGAGTCTCT 2100
 CAGGTCACTT GGGAGCCAGT GTGCCCAAAA GCCATGTATT TCAGGGACCT CAGGGGCACC 2160
 TCGGGCTGCC TAGCCCTCCC CCCAGCTCCC TGCACCGCCG CAGAAGCAGC CCTCGAGGC 2220
 50 CTACAGAGGA GGCTTCAAG CAACCCGCTG GAGCCACAG CGAGCCTGTG CCTTCTCTCC 2280
 CGCTCTCTCC CACTGGGACT CCCAGCAGAG CCCACAGGCC AGCCCTGGCC CACCCCCAG 2340
 CCTCCAGAGA AGCCCCGCAC GGGCTGTCTG GGTGTCCGCC ATCCAGGGTC TGGCAGAGCC 2400
 TCTGAGATGA TGCATGATGC CCTCCCTCA GCGCAGGCTG CAGAGCCCGG CCCCACCTCC 2460
 CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGGTGACGCC TGAGACAGCA CCACTGCTGA 2520
 55 GGAGTCTGAG GACTGTCTTC CCACAGACCC TGCAGTGAGG GGCCCTCCAT GCGCAGATGA 2580
 GGGGCACTAT ACCACCTGCG GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCCAG 2640
 GGAGCAGCGG TGGGCTCTGC CAATGTGGGC TGCCCTTCGC ACACAGGGCT CACAGGCGAG 2700
 GCCTTGTCTG GGTCCAGGGC TGTGAGGGA CCCCAGGGGC TGAGGAGCAG CCAGGACCCG 2760
 CCTGCTCCCA TCCTCACCCA GATCAGGAAC CAGGGCCTCC CTGTTACAGG TGACACAGGT 2820
 60 CAGGGCTCAG AGTGACCTTC GGCTGTCAAC TGCTCACAGG GATGCTGGTG GCTGGTGAGA 2880
 CCCGCACTG CACACGGGAA TGCTAGGTGC CCTTCCGAC CCAGCCAGCT GCACTGCAGG 2940
 GCACGGGGAC CTGGATAGTT AAGGGCTTTT CCAACATGCT ATCCATTTAC TGACACTTCC 3000
 TGTCTTGTTC CATGGAGAGC TGTTCGCTCC TCCAGATGG CTTGCGAGGC CCGCAGGGCC 3060
 CACCTTGGAC CCTGGTGAAC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120
 65 CTGACCGGGC CCTCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG 3180
 TGTGGTGTG GGAAGGGGTC CTGAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG 3240
 TCCTGAACCG ACTGACCTTC AGGAGGCCGC TTAGTGCTGC TTTGCTTTTC ATCACCCTCC 3300
 CGCAGGTGG ACGGAGGTC CCGTTGCTG GTCAAGTCCC CATGGCTTGT TCTCTGGAAC 3360
 70 CTGACTTTAG ATGTTTGGG ATCAGGAGCC CCAACACAG GCAAGTCCAC CCCATAATAA 3420
 CCCTGCCAGT GCCAGGGTGG GCTGGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG 3480
 CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CTAACGCTCA 3540
 TCTCTGGAAG GGGCAGCCCT GAGTGGTCACT TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT 3600
 CCTTCTCCA CAAGGTCCCC CCACGCTCA GTGTCAGCGG GTGACGTGTG TTTCTTTGAG 3660
 TCCTGTATG AATAAAGGC TGAACCTA AA

75

Seq ID NO: 248 Protein sequence
 Protein Accession #: NP_002072.1

80

1 11 21 31 41 51
 | | | | |
 MELRARGWNL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSVDP QAEISGEHLR 60
 ICPQGYTCTT SEMEENLANR SHAELETALR DSSRLVQAML ATQLRSFDDH FOHLNDSESR 120
 TLQATFPFAG GELYTQNLARA FRDLYSELRL YRGANLHLE ETLAEFWARL LERLFKQLHP 180
 QLLLPDDYLD CLGKQAEALR PFGEAPREL RLRATRAFAA RSFVQGLGVA SDVVRKVAQV 240
 PLGPBCSRAV MKLVYCAHCL GVPGARPCPD YCRNVKGLCL ANQADLDAEW RNLLDSMVL I 300
 TDKFWGTSGV ESVGSVHTW LAEAINALQD NRDTLTAKVI QCGNPKVNP QGPGEFKRR 360

RGKLA PRERF PSQTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA 420
 RGRYLPEVMG DGLANQINNP EVEVDITKPD MTRQIQIMQL KIMTNRLRSA YNGNDVDFQD 480
 ASDDGSGSGS

Seq ID NO: 249 DNA sequence
 Nucleic Acid Accession #: NM_001492.3
 Coding sequence: 8..1864

1	11	21	31	41	51	
GAAGGCCATG	GTCTCCCCAC	GGATGTCCGG	GCTCCTCTCC	CAGACTGTGA	TCCTAGCGCT	60
CATTTTCCTC	CCCCAGACAC	GGCCCGCTGG	CGTCTTCGAG	CTGCAGATCC	ACTCTTTCGG	120
GCCGGGTCCA	GGCCCTGGGG	CCCCCGGGTC	CCCCTGCAGC	GCCCGGCTCC	CCTGCCGCT	180
CTTCTTCAGA	GTCTGCCTGA	AGCCTGGGCT	CTCAGAGGAG	GCCCGCGAGT	CCCCGTGCGC	240
CCTGGGCGCG	GCGCTGAGTG	CGCGCGGACC	GGTCTACACC	GAGCAGCCCG	GAGCGCCCGC	300
GCGTGATCTC	CCACTGCCCC	ACGGGCTCTT	GCAGGTGCCC	TTCCGGGACG	CCTGGCCTGG	360
CACCTTCTCT	TTTCATCCTG	AAACCTGGAG	AGAGGAGTTA	GGAGACCAGA	TTGGAGGGCC	420
CGCCTGGAGC	CTGCTGGCGC	GCGTGGCTGG	CAGGCGGCGC	TTGGCAGCCG	GAGGCCCGTG	480
GGCCCCGGAC	ATTACGCGCG	CAGGCGCCTG	GGAGCTGCGC	TTCTCGTACC	GCGCGCGCTG	540
CGAGCGCGCT	GCCGTGCGGA	CCGCGTGCAC	GCGCCTCTGC	CGTCCGCGCA	GCGCCCCCTC	600
GCGGTGCGGT	CCGGGATGCG	GCCCTGCGCG	ACCGCTCGAG	GACGAATGTG	AGGCGCCGCT	660
GGTGTGCCGA	GCAGGCTGCA	GCCCTGAGCA	TGGCTTCTGT	GAACAGCCCG	GTGAATGCCG	720
ATGCTAGAG	GGCTGGACTG	GACCCCTCTG	CACGGTCCCT	GTCTCCACCA	GCAGCTGCCT	780
CAGCCCCAGG	GGCCCTCTCT	CTGTACACAC	CGGATGCCCT	GTCCCTGGGC	CTGGGCCCTG	840
TGACGGGAAC	CGGTGTGCCA	ATGGAGGCAG	CTGTAGTGAG	ACACCCAGGT	CCTTTGAATG	900
CACCTGCCCG	CGTGGTCTCT	ACGGGCTGCG	GTGTGAGGTG	AGCGGGGTGA	CATGTGCAGA	960
TGGACCTGCG	TTCAACGGCG	GCTTGTGTGT	CGGGGTGCA	GACCCGACT	CTGCCTACAT	1020
CTGCCACTGC	CCACCTGGTT	TCCAAGGCTC	CAACTGTGAG	AAGAGGGTGG	ACCGGTGCAG	1080
CCTGCAGCCA	TGCCGCAATG	GCGGACTCTG	CCTGGACCTG	GGCCACGCCC	TGCGCTGCCG	1140
CTGCCGCGCG	GGCTTGCCTG	GTCTCGCTG	CGAGCAGCAC	CTGGACGACT	GCGCGGGCCG	1200
CGCTTGCCT	AACGGCGGCA	CGTGTGTGGA	GGGCGCGCGC	GCGCACCGCT	GCTCCTGCGC	1260
GCTGGGCTTC	GGCGGCGCGC	ACTGCCGCGA	GCGCGCGGAC	CCGTGCGCCG	GCGGCCCTTG	1320
TGCTACGGC	GGCCGCTGCT	ACGCCCACTT	CTCCGCGCTC	GTCTGCGCTT	GCGCTCCCGG	1380
CTACATGGGA	GCGCGGTGTG	AGTTCCAGT	GCACCCGAC	GGCGCAGCG	CCTTGCCCGC	1440
GGCCCCCGCG	GGCTCAGGC	CCGGGAGACC	TCAGCGCTAC	CTTTGCTCTC	CGGCTCTGGG	1500
ACTGCTCGTG	GCGCGGGCGG	TGGCCGGCGC	TGCGCTCTTG	CTGGTCCACG	TGCGCGCCCG	1560
TGGCCACTCC	CAGGATGCTG	GGTCTCGCTT	GCTGGCTGGG	ACCCCGGAGC	CGTCAGTCCA	1620
CGCACTCCCG	GATGCACTCA	ACAACCTAAG	GACGCAAGAG	GGTTCGGGG	ATGGTCCGAG	1680
CTCGTCCGTA	GATTGGAATC	GCCCTGAAGA	TGTAGACCTT	CAAGGGATT	ATGTCATATC	1740
TGCTCCTTCC	ATCTACGCTC	GGGAGGTAGC	GACGCCCTT	TTCCCCCGC	TACACACTGG	1800
GCGCGCTGGG	CAGAGGCAGC	ACCTGCTTTT	TCCTACCTT	TCCTCGATTC	TGTCGGTGAA	1860
ATGAATTGGG	TAGATCTCT	GGAAGGTTTT	AAGCCCATTT	TCAGTTCTAA	CTTACTTTCA	

Seq ID NO: 250 Protein sequence
 Protein Accession #: NP_058637.1

1	11	21	31	41	51	
MVSPRMSGLL	SQTIVILALIF	LPQTRPAGVF	ELQIHSFPGP	PGPGAPRSPC	SARLPCRLEFF	60
RVCLKPLGLSE	EAESPICALG	AALSARGPVY	TEQPGAPAPD	LPLPDGLLQV	PFRDAWPPTF	120
SFIETWREE	LGDQIGGPAW	SLLARVAGRR	RLAAGGPPAR	DIQRAGAWEL	RFSYRARCEP	180
PAVGTACTRL	CRPRSAPSRC	GPGLRPCAPL	EDECEAPLVC	RAGCSPHGF	CEQPGECL	240
EGWTGPLCTV	PVSTSSCLSP	RGPSSATTGC	LVPGPSPCDG	NPCANGGSCS	ETPRSFECTC	300
PRGFYGLRCE	VSGVTGADGP	CFNGGLCVGG	ADPDSAYICH	CPPGFQGSNC	EKRVDRCSLQ	360
PCRNGLCLD	LGHALRCRCR	AGFAGPRCEH	DLDDCAGRAC	ANGGTCVEGG	GAHRCSCALG	420
FGGRDCRERA	DFCAARPCAH	GGRCYAHFSG	LVCACAPGYM	GARCEFPVHP	DGASALPAAP	480
PGLRPGDPQR	YLLPPLGALL	VAAGVAGAAL	LLVHVRRRGH	SQDAGSRLLA	GTPEPSVHAL	540
PDALNNLRQT	EGSGDGPSSS	VDWNRPEVD	PQGIYVISAP	SIYAREVATP	LFPPLHTGRA	600
GQRQHLLFPY	PSSILSVK					

Seq ID NO: 251 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1	11	21	31	41	51	
GAAATATAAC	CATTGCAATT	AGAAAATATC	CAAAATAGCC	TGTTATCTTC	CACGTGGCCT	60
AGATTATTGA	CAATCCCAAA	TATACAAATT	TTCTTTAAAA	GTAGTACAAT	TTCTTTTGTA	120
GCTTCAATTC	CTTATATGAC	TTCAAGCTGG	AGAAGCCTGT	TAAACCACTG	TTAGTTTCAG	180
TTAGAAAGTC	TGAGAGACTT	TATACATAAA	TTCTCAATTT	GGCTGCTGTA	CACGTGCCAG	240
AGTTTACTA	CTGTAGTGAC	CGTTGAGAAG	ACCCTTGTTT	ATTTACATTT	GAAGCACTGT	300
TTGTGCAAA	AACCTTTTCT	TGTTAAGTGC	CTGTATTCCT	TTCAATTACT	TCATGTCCAG	360
GGGTGCTATT	TACCTAGAAC	CATTGTCTAC	TACAATTAAC	ATTTACATTA	CAAAGTGTGT	420
GGTTTTCTTT	TTCAAGGAGG	TTCAATTAAG	GCAATAAGAT	GTTTGCTGGA	GAAACCTATT	480
GTTTACTGAA	AGCACTCAAT	GAAAGTCAAT	TACTGAAGCT	TTTGCTTACA	TCTTGGTCTT	540
TTATGTAAAT	ATGTTAAATA	TAACATCTAA	GGAAAATAAA	CAATATTATA	ATTATGTGTT	600
TGCCATTGTC	ATATCAAACT	TGCTTTGTAT	CATACTAATG	TTACATAACT	TATCGATCAA	660
TAAAAATACA	TTTCAATGTT	AAAAAATAAA	AAAAAATAAA			

Seq ID NO: 252 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1	11	21	31	41	51	
AGGTACTGCC	AGAAAGGATC	AGGACCTGGA	GTCTGGCAAG	AGGAAGACAG	AGGCCGTGTGT	60

	GGGAAGCGAG	TTGTTATCTT	TGTTTATCTA	GCTGTATGAG	TGTATTGGTC	TTCATAAAGC	120
	TAGATAACCG	AAAGTAAAAA	CTTCTTCAAG	ATCGCCGGGG	AGCGTGTGAG	AATGAAGAC	180
	TACAGCCGAG	AGACAGTAAA	AACCAGAAAG	GTCAGGAATA	CTTATTGAAT	CTAACTTTGT	240
5	TTTTGTTTTG	TTTTTTTCCCT	TATGATTAAA	GGTGGGATGA	GAGAAAATTA	AATGACACAC	300
	ACATGCTAAA	ATATCAAGGT	TCCAGATATG	TCTTGAGAGG	GGTTGTTGCA	GCTGCAAAGG	360
	AGAAGTGAT	AGTGATAATG	AGTAAAGATG	CATGTGCAGT	TTGTTCTATT	TTAAGGCCAA	420
	AGTTATATCA	GGGATTTTTT	TCTAGAAAAG	GTGTTGCAGA	GATGTCTGGT	ACCTAGTTTA	480
	AAAATGATTC	CATAATATGT	AGACTTGGGC	AGTTCTTTTG	GGAGGCACCT	CCCTCTCAAA	540
10	ATTTGAAGAT	TGTGCTTGGG	AATTACTTTA	CATGTATTTG	GGCTGTATGT	CAATTTGTAC	600
	GAAATTAGAG	TTTCAGAAAA	GTTTATACTG	GAAGGTAAAT	AATTTGTATC	TACTGAGGAC	660
	TTAGAGCTAG	CAGGCAAAAT	GAAAAAAR	CAAGGGCTGA	TTTTTATTCT		720
	TCTATTCAAA	ATACAAGGAC	AGATGCTTCT	CTGTTCCAAG	AGGGTTTCCCT	TGAGGAAGCT	780
	ACTGAAGCAG	AAAGACATGA	TGGAGACGAG	ATCGCCTCCC	CTCTTGTCAA	AGTGTAAAAA	840
	AAATGTTCTG	TCTTACTCTG	CGCCTAGCAT	TGGAATGAA	AGTGACATTT	ACGCCACAAC	900
15	CCACGTGTGC	GCCCTCTCTC	TTTTTGTTA	AGGATGATCA	GGTCTATCCA	GGAACACGCT	960
	CTGGCATCCC	AAACTGAAAT	AATTAGGACG	TATATAGACC	TGACAAAAAT	GGAAGGGGG	1020
	TGGGGAATCT	GAGGGTCTGT	CTTGCCCTAAT	TGATTCGGCT	AAACGGAATG	CAGGAGATGT	1080
	GAACGGCAGG	ACGCTCCGAT	TCCCACGCTC	GGGGCAAGT	GATAAAGCGG	GGCCGGGCAG	1140
20	CCTATGACAG	ACAGCCCTGT	TGGGGGTGG	GGGTATGAAA	AAAACATCAA	GTGCACACAC	1200
	CATACTCATC	TCCATCGCTT	AAGAAAGTAA	AGGCATTTCC	CACCCACAGC	CATCTGCAGC	1260
	TTCCCAAATG	GCAGACCAA	CTGGTCTGTA	GCTGCTACAT	AGTCTGCTTC	TGTTAATTTT	1320
	TTAACCACTG	TTTAATCTGG	CCATAATTAA	GTTTGGCTTT	CTTCGTTGTT	TGAGATTTTC	1380
	AGAATTCAAG	CGAAGCTAGT	AGAAAGCAAT	TCCAAGAAAG	TCCCATGACT	GCCTGCCCTT	1440
25	AATGTCAAAA	TCTCAGTCCA	TGAGATTATG	GCCTTGTGAC	CACATTTTTC	CTTTTGTTTT	1500
	GGGTGGGCAA	ATGTGTATAG	AGATAAAATA	CATATCTCTA	TATAACAGTC	GTTATTATAA	1560
	TTTCTAGAGG	CTTTTACCTG	CTTAACATGA	TACATCTAGG	AACTTGGTCT	AATTTGGCTA	1620
	GTAGATATAC	ACTAGAAGTA	AACTATATAA	GTCATTAGCC	TGTAGAAAGT	TGATTATGAT	1680
	AACAATATGA	TAAAAAGTTT	GTTTTGGAAT	AGTCTCAGCT	AGATGGGCTC	AAATAGCCAT	1740
30	TTTAATGTAA	TCTAAAAATA	ACACTATGCC	TAGCAGAAAC	TTTGGCGCTT	TGGAGGTCCC	1800
	CATTGTGCGC	TTTTTCATAA	AGTCCTTAAG	TTTTCCATAT	GTCACCAAGC	AAACATTTGT	1860
	ATAGGCATT	ACACAGAAAT	ATAACCATG	CAATTAGAAA	ATATCCAAAA	TAGCTTGTTA	1920
	TCTTCCACGT	GGCCTAGATT	ATTGACAATC	CCAAATATAC	AATTTTTCTT	TAAAAGTAGT	1980
	ACAATTTCTT	TTGTAGCTTC	AATTCCTTAT	ATGACTTCAG	ACTGGAGAAG	CCTGTTAAAC	2040
35	CACGTGTAGT	TTTCAGTTAGA	AAGTCTGAGA	GACTTTATAC	ATAAATTCTC	AATTTGGCTG	2100
	CTGTACACGT	GCCAGAGTTT	TACTACTGTA	GTGACCGTTG	AGAAGACCCT	TGTTTATTTA	2160
	CATTGGAAGC	ACTGTTTGTG	CAAACAACCT	TTCATTGTTA	AGTGCCTGTA	TTCCTTTTCAT	2220
	TTACTTCATG	TCCAGGGGTG	CTATTTACCT	AGAACCATTG	TCTACTACAA	TTAACATTTA	2280
	CATTACAAAG	TGTTGTGTTT	TCTTTTTCAA	GGAGGTTCAA	TTAAGGCAAT	AAGATGTTTG	2340
40	CTGGAGAAAC	CTATTGTTTA	CTGAAAGCAC	TCAATGAAGT	CAAATTACTG	AAGCTTTTGC	2400
	CTACATCTTG	GTCCTTTTATG	TAAATATGTT	AAATATAACA	TCTAAGGAAA	ATAACAATA	2460
	TTATAATTAT	GTGTTTGCCA	TTGTCATATC	AACTTGTCTT	TGTATCATAC	TAATGTTTACA	2520
	TAACCTTATCG	ATCAATAAAA	ATACATTCCA	ATGTT			

Seq ID NO: 253 DNA sequence

Nucleic Acid Accession #: NM_001650.2

Coding sequence: 40.1011

	1	11	21	31	41	51	
50	GGGGCAGGCA	ATGAGAGCTG	CACCTCTGGT	GGGGAAGGCA	TGAGTGACAG	ACCCACAGCA	60
	AGGCGGTGGG	GTAAGTGTGG	ACCTTTGTGT	ACCAGAGAGA	ACATCATGGT	GGCTTTCAAA	120
	GGGGTCTGGA	CTCAAGCTTT	CTGGAAGCA	GTCACAGCGG	AATTTCTGGC	GATGCTTATT	180
	TTTGTTCTCC	TCAGCCTGGG	ATCCACCATC	AACCTGGGGT	GAACAGAAAA	GCCTTTACCG	240
	GTGACATAGG	TTCTCATCTC	CCTTTGCTTT	GGACTCAGCA	TTGCAACCAT	GGTGCACTGC	300
55	TTTGGCCATA	TCAGCGGTGG	CCACATCAAC	CCTGCAGTGA	CTGTGGCCAT	GGTGTGCACC	360
	AGGAAGATCA	GCATCGCCAA	GTCTGTCTTC	TACATCGCAG	CCCAGTGCCT	GGGGGCCATC	420
	ATTGGAGCAG	GAATCCTCTA	TCTGGTCACA	CCTCCAGT	TGGTGGGAGG	CCTGGGAGTC	480
	ACCATGTTTC	ATGGAATCT	TACCGCTGGT	CATGGTCTCC	TGGTTGAGTT	GATAATCACA	540
	TTTCAATTGG	TGTTTACTAT	CTTTGCCAGC	TGTGATTCCA	AACGGACTGA	TGTCACTGGC	600
60	TCAATAGCTT	TAGCAATTGG	ATTTTCTGTT	GCAATTGGAC	ATTTATTTGC	AATCAATTAT	660
	ACTGGTGCCA	GCATGAATCC	CGCCCGATCC	TTTGGACCTG	CAGTTATCAT	GGGAAATTGG	720
	GAAAACCAT	GGATATATTG	GGTTGGGCCC	ATCATAGGAG	CTGTCTCTGC	TGGTGGCCTT	780
	TATGAGTATG	TCTTCTGTCC	AGATGTTGAA	TTCAAACGTC	GTTTAAAGA	AGCCTTCAGC	840
65	AAAGCTGCCC	AGCAACAAA	AGGAAGCTAC	ATGGAGGTGG	AGGACAACAG	GAGTCAGGTA	900
	GAGACGGATG	ACCTGATTCT	AAAACCTGGA	GTGGTGCATG	TGATTGACGT	TGACCGGGGA	960
	GAGGAGAAGA	AGGGGAAAGA	CCAATCTGGA	GAGGTATTGT	CTTCAGTATG	ACTAGAAGAT	1020
	CGCACTGAAA	GCAGACAAGA	CTCCTTAGAA	CTGTCCTCAG	ATTTCTCTCC	ACCCATTAA	1080
	GAAACAGATT	TGTTATAAAT	TAGAAATGTG	CAGGTTTGT	GTTTCATGTC	ATATTACTCA	1140
70	GTCTAAACAA	TAAATATTTC	ATAATTACAA	AAGGAGGAAC	GGAAGAAACC	TATTGTGAAT	1200
	TCCAATCTA	AAAAAAGAAA	TATTTTAAAG	ATGTTCTTAA	GCAATATAT	ACCTATTTTA	1260
	TCTAGTTACC	TTTCAATTAAC	AACCAATTTT	AACCGTGTGT	CAAGATTG	TTAAGTCTTG	1320
	CCTGACAGAA	CTCAAAGACA	CGTCTATCAG	CTTATTCCTT	CTCTACTGGA	ATATTGGTAT	1380
	AGTCAATTCT	TATTTGAATA	TTTATTCTAT	TAAACTGAGT	TTAACAATGG	C	

Seq ID NO: 254 Protein sequence

Protein Accession #: NP_001641.1

	1	11	21	31	41	51	
80	MSDRPTARRV	GKCGPLCTRE	NIMVAFKGVW	TQAFWKAVTA	EFLAMLIFVL	LSLGSTINWG	60
	GTEKPLEPDM	VLLSLCFGLS	IATMVQCFGH	ISGGHINPAV	TVAMVCTRKI	SIKSVFYIA	120
	AQCLGAIIGA	GILYLVTPPS	VVGGLGVMTV	HGNLTAGHGL	LVELIITFQL	VFTIFASCDS	180
	KRTDVTGSIA	LAIGFSAVIG	HLFAINYTGA	SMNPARSFGP	AVIMGNWENH	WIYVWGPPIG	240
	AVLAGGLYIE	VFCPDVEFKR	RFKEAFSKAA	QQTKGSYMEV	EDNRSQVETD	DLILKPGVVH	300

VIDVDRGEEK KGKQDSGEVL SSV

Seq ID NO: 255 DNA sequence
 Nucleic Acid Accession #: U26742.1
 Coding sequence: 325..1449

5

1	11	21	31	41	51	
10	CAGGAAACCC	TGGTACTGGC	AGCAGCCAGC	CTCTGCTGTG	CCCACATGAC	CCACAACCTCT 60
	GGCAGCGGAC	CCGGCACTTC	CAACATTATT	AAATAATAAG	AAAGCGGCTC	CTACTCCAGG 120
	CTCAAACCTC	CCTGCAGACC	AATGGACACC	TTCTAAGAGT	TTGGCGAGTC	AGTGACTGAA 180
	GGCCCCGTCC	ATTCCAAGAT	AAATAGGATT	TACCAATCCT	TGGATGAAAT	GCTTGGGAAG 240
	TCITTAAGTG	CCATAATCAA	CTGCCATTTT	AAAGAATATA	GATGGTTTTG	AAAAGTTCAT 300
15	GCTGTCCCTT	CATTGAATTT	TAGAATGATT	GAAGATAGTG	GGAAAAGAGG	AAATACCATG 360
	GCAGAAAGAA	GACAGCTGTT	TGCAGAGATG	AGGGCTCAAG	ATCTGGATCG	CATCCGACTC 420
	TCACCTTACA	GAACAGCATG	CAAGCTTAGG	TTTGTTTCAGA	AGAAATGCAA	TTTGCACCTG 480
	TGGACATAT	GGAATGTCAT	AGAAGCATTG	CGGGAATAATG	CTCTGAACAA	CCTGGACCCA 540
	AAACTGGAAC	TCAACGTGTC	CCGCTTAGAG	GCTGTGCTCT	CCACTATTTT	TTACCAGCTC 600
20	AACAAACGGA	TGCCAACCCAC	TCACCAAATC	CATGTGGAGC	AGTCCATCAG	CCTCCTCCTT 660
	AACTTCTCTG	TTGCAGCGTT	TGATCCGGAA	GGCCATGGTA	AAATTTTCAGT	ATTGTCTGTC 720
	AAAATGGCTT	TAGCCACATT	GTGTGGAGGG	AAGATCATGG	ACAAATTAAG	ATATATTTTC 780
	TCAATGATTT	CTGACTCCAG	TGGGGTGATG	GTTTATGGAC	GATATGACCA	ATTCCTTCGG 840
	GAAGTTCTCA	AACTACCCAC	GGCAGTTTTT	GAAGGTCCTT	CATTTGGTTA	CACAGAACAC 900
25	TCAGCCAGAT	CCTGTTTCTC	CCAACAGAAA	AAAGTCACGT	TAAATGGTTT	CTTGGACACG 960
	CTTATGTGAC	ATCCTCCCCC	GCAGTGTCCTG	GTCTGGTTGC	CTCTTCTGCA	TCGACTAGCA 1020
	AATGTGGAAA	ATGCTTTCCA	TCCGGTTGAG	TGTTCTTACT	GCCACAGTGA	GAGTATGATG 1080
	GGATTTTCGCT	ACCGATGCCA	ACAGTGTAC	AATTACCAGC	TCTGTGAGGA	CTGCTTCTGG 1140
	AGGGGACATG	CCGGTGGTTC	TCATAGCAAC	CAGCACCAAA	TGAAAGAGTA	CACGTGATGG 1200
	AAATCACCTG	CTAAGAAAGT	GACTAATGCA	TTAAGCAAAGT	CCCTGAGCTG	TGCTTCCAGC 1260
30	CGTGAACCTT	TGCACCCCAT	GTTCCAGAT	CAGCCTGAGA	AGCCACTCAA	CTTGGCTCAC 1320
	ATCGTTGATA	CTTGGCCTCC	CAGACCTGTA	ACCAGCATGA	ACGACACCTT	GTTCTCCAC 1380
	TCCTGTTCCCT	CCTCAGGAAG	TCCTTTTATT	ACCAGGAGCT	CGGACGGTGC	TTTTGGTGGA 1440
	TGCGTCTAGA	TGGATAACAT	GACTTCTTCT	ACCCTAAAAAT	ATTCTCTATA	TACTTTGAGC 1500
35	TGTTCTGGTT	CCTCCAGGGT	GCAATGTTACC	CATTAACCCA	AAATATGATT	ATTTCCCTTT 1560
	TTTCCCATTT	TCAGTCATTT	TGGAATGTTT	TCTGTGAACC	ACAGTTGGGT	TGTTTAAAGC 1620
	TCACATTTCT	TTCTGTCAAC	ACAGAGATTG	GCCTACGGTT	TCTGTTTGA	GGGTGCTGTT 1680
	CAATAAAGCT	GTGTACACTA	AATGTCC			

Seq ID NO: 256 Protein sequence
 Protein Accession #: AAC50424.1

1	11	21	31	41	51	
45	MIEDSGKGRN	TMAERRQLFA	EMRAQDLDR	RLSTYRTACK	LRFVQKKCNL	HLVDIWNVIE 60
	ALRENALNNL	DPNTELVNVR	LEAVLSTIFY	QLNKRMPPTH	QIHVEQSISL	LLNFLLAAFD 120
	PEGHGKISVF	EKKMALATLC	GGKIMDKLRY	IFSMISDSSG	VMVYGRYDQF	LREVLKLFTA 180
	VFEGPSFGYT	BQSARSCFSQ	QKKVTLNGFL	DTLMSDPPFQ	CLVNLPLLHR	LANVENVFHF 240
	VECSYCHSES	MMGFYRRCQQ	CHNYQLCQDC	FWRGHAGGSH	SNQHQMKEYT	SWKSPAKKLT 300
50	NALSKSLSCA	SSREPLHPMF	PDQPEKPLNL	AHIVDTWPPR	PVTSMNNTLF	SHSVSPSGSP 360
	FITRSSDGAF	GGCV				

Seq ID NO: 257 DNA sequence
 Nucleic Acid Accession #: NM_004172.1
 Coding sequence: 179..1807

1	11	21	31	41	51	
60	GCGGATTGTT	GCTCCGTTGT	ACCTGCTGGG	GAATTCACCT	CGTTACTGCT	TGATATCTTC 60
	CACCCCTTAC	AAAATCAGAA	AAGTTGTGTT	TTCTAATACC	AAAGAGGAGG	TTTGGCTTTC 120
	TGTGGGTGAT	TCCAGACAC	TGAAGTGCAA	AGAAGAGACC	CTCCTAGAAA	AGTAAAATAT 180
	GACTAAAAGC	AATGAGAGAAG	AGCCCAAGAT	GGGGGGCAGG	ATGGAGAGAT	TCCAGCAGGG 240
	AGTCCGTAAA	CGCACACTTT	TGGCCAAGAA	GAAAGTGCA	AACATTACAA	AGGAGGATGT 300
	TAAAAGTTAC	CTGTTTCGGA	ATGCTTTTGT	GCTGCTCACA	GTCAACCGCTG	TCATTTGTGGG 360
65	TACAATCCTT	GGATTTACCC	TCCGACCATA	CAGAATGAGC	TACCGGGAAG	TCAAGTACTT 420
	CTCCTTTCTT	GGGGAACCTC	TGATGAGGAT	GTTACAGATG	CTGGTCTTAC	CACCTATCAT 480
	CTCCAGTCTT	GTCAACAGAA	TGGCGGCGCT	AGATAGTAAG	GCATCAGGGA	AGATGGGAAT 540
	GCGAGCTGTA	GTCTATTATA	TGACTACCAC	CATCATTGCT	GTGGTGATTG	GCATAATCAT 600
	TGTCTATCAT	ATCCATCCTG	GGAAGGGCAC	AAAGGAAAAC	ATGCACAGAG	AAGGCAAAAT 660
70	TGTACGAGTG	ACAGCTGCAG	ATGCCTTCCT	GGACTTGATC	AGGAACATGT	TCCCTCCAAA 720
	TCTGGTAGAA	GCCTGCTTTA	AACAGTTTAA	AACCAACTAT	GAGAAAGAGAA	GCTTTAAAGT 780
	GCCCATCCAG	GCCCAAGAAA	CGCTTGTGGG	TGCTGTGATA	AACAATGTGT	CTGAGGCCAT 840
	GGAGACTCTT	ACCCGAATCA	CAGAGGAGCT	GGTCCAGTGT	CCAGGATCTG	TGAATGGAGT 900
	CAATGCCCTG	GGTCTAGTTG	TCTTCTCCAT	GTGCTTCGGT	TTTGTGATTG	GAAACATGAA 960
75	GGAACAGGGG	CAGGCCCTGA	GAGAGTTCTT	TGATTCTCTT	AACGAAGCCA	TCATGAGACT 1020
	GGTAGCAGTA	ATAATGTGGT	ATGCCCCCGT	GGGTATTCTC	TTCTCTGATTG	CTGGGAAGAT 1080
	TGTGGAGATG	GAAGACATGG	GTGTGATTGG	GGGGCAGCTT	GCCATGTACA	CCGTGACTGT 1140
	CATTGTTGGC	TTACTCATTC	ACGCAGTCAT	CGTCTTGCCA	CTCCTCTACT	TCTTGGTAAC 1200
	ACGGAAAAAC	CCTTGGGTTT	TTATTGGAGG	GTGTGTGCAA	GCACTCATCA	CCGCTCTGGG 1260
80	GACCTCTTCA	AGTCTTGCCA	CCCTACCCAT	CACCTTCAAG	TGCCTGGAAG	AGAAACAATGG 1320
	CGTGGACAAG	CGCGTCACCA	GATTCTGTCT	CCCCGTAGGA	GCCACCATTAA	ACATGGATGG 1380
	GACTGCCCTC	TATGAGGCTT	TGGCTGCCAT	TTTCAATTGCT	CAAGTTAACA	ACTTTGAACT 1440
	GAACTTCGGA	CAAATTATTA	CAATCAGCAT	CACAGCCACA	GCTGCCAGTA	TTGGGGCAGC 1500
	TGGAATTCTT	CAGGCGGGCC	TGGTCACTAT	GGTCATTGTG	CTGACATCTG	TCGGCCTGCC 1560
	CACTGACGAC	ATCACGCTCA	TCATCGCGGT	GGACTGGTTC	CTGGATCGCC	TCCGACCACC 1620

CACCAACGTA CTGGGAGACT CCCTGGGAGC TGGGATTGTG GAGCACTTGT CACGACATGA 1680
 ACTGAAGAAC AGAGATGTTG AAATGGGTAA CTCAGTGATT GAAGAGATG AAATGAAGAA 1740
 ACCATATCAA CTGATTGCAC AGGACAATGA AACTGAGAAA CCCATCGACA GTGAAACCAA 1800
 5 GATGTAGACT AACATAAAGA AACACTTTCT TGAGCACCAG GTGTAAAAA CCATTATAAA 1860
 ATCTTTCCAT CTCTATTACG CTCTTCGCT CCAGCAAGCC CGTCATCTTC CCTTCCCTCC 1920
 CTCTGATAA GACTGGAAAA TAGTCTCTCA AAACACAAGG GAGGATTTTG GGTGGCCCAA 1980
 GTGTACAATT TTCTCCAC AAATGAAATT TTTAAATCAT TTCATGTTAG TCTTACCGAA 2040
 10 TAAGGTACCA AGATCACAAA TAGTGTGTAT CAGATCTTAC AAGTTTATGT GGCACACAAT 2100
 TCCTATAAAT GTGATTTTTT TATATAAGTT AAAGAGACAA ATAGTAGGCT AAAAACATTT 2160
 TAAAATCAAC TTTTGAAATT TAAAAATCTT TCAGAATACA ATTCAAGTTT AGTTTCAAAA 2220
 TGTTAACAACT TTGAATTACA ACCGGTTATC AGTTGGACAG TAAGATTTTA TCCCTTTCTC 2280
 TTCTGACTGG TATACCTATT TCATTAGTAG CTAGGTGCAC ATATACATCT AGCAGAGCTG 2340
 15 TGAGGACAGA CAGAAGGCAA AGTTTCCATG TGGCCTTGAG CAAGTCCCAT CTCACCTCTA 2400
 GGCCTCAGTG TCCTCATCTA TAAAATGAGG GACTTCCCTA GAAGTCTTCA TGGTCTCTTC 2460
 CAGCCCAGAC ATCTGTGTAT GTCATGAAAG CACCTGCCCT CTGTTTCCCC TCAGAACACC 2520
 CTGTACCATC CATGGAGCAC GAGGCCTTCA GAAAAGACAC TTCAATGGGA GTGAACATTT 2580
 CTAACAAAG ACAGGATGGC TGTGTGTGGT GGTCAACCAG TCCTGTGAGC AAAGTGCAGG 2640
 TTATGCAAGT CGCCAGGCAG GAGGCCATTC CAGGAGTGGG ATTATTCATC AAACCTTTTG 2700
 CCCAGTTTCA CCCAATGGGG GAAGTATTCC CTCTTTCTCT ACTCGGGAA GAATGTCTCC 2760
 20 TGCCACTCCT CAATGATGA TAGACTTCGA AAACAGATGA GAAGACTAGC AGCTAGCAAG 2820
 GGTGCTTGTA GTCACACTGT GGAACACTAA AGAGCTAGGA AAGAGTTGAG CACAGGCAAC 2880
 ATTACAAACA AAGGATTTGA AAACACCAAG AGTACAGGTC TTCTTTAAGG AAGAATAAAA 2940
 AAGAAGAGGT TCATTTTTCT GGCTTTTTTT TTCACCTGAA ACATTTTTTC TCGAGTCCAA 3000
 25 AATCATTCCT CCCGTGAAAG CTGCTTACCA AAACATAAGA CGACTTATAT ATTTGAAAGA 3060
 AGTCAAATGA ATGAGCTCTC TAATAGAAGT CCATGAGTTG AGTGGGTATT TCTTATTGTA 3120
 AAGTGTTTTT CTTTAATCAA AAGTCTTAG AATGAGGGAA ACAAATATT TATTTGTTTT 3180
 GGAATCCAC TTATCAAAAT ATTCAAACT TTCAGCTGGA GTGGGGTTTG CTTTGTTTTT 3240
 GTTTGTGTCC ATAAGAGAAA TGGTAGAAGA TGAATCAGTA TGAAGACT GTCAATGAGG 3300
 30 TTATGAGAAA AAAACAGCAG GGGCATTAGT TTCAGGCAAG GCAGCTCCCA GGTTAGAGA 3360
 TTAATTTTTA CCCCTAAGG AATATCCAGT CAAAGACGCT GAGTGGGAGC TGTCAGGCAG 3420
 TAGCAGCTGT GTTTGAGTTT CTGGCTGAAA ATGGTGAAGA ATGGACTTAA TTATGCTAAC 3480
 AAACGAAAA ATCTAGACAT AGATCCTCTG ATATACAATT AGAGATATT TTATATAGAC 3540
 CCCAAGCATT CTGTGCATAA AAGTTAACAT TAGGCTGTGG TGCAAGTACC ATTTAATGTC 3600
 35 GAGGCTCTAT TTCGGAATTA CACTACAAAT GTTAAAGTAC GTGGCTGTCC TCTTAAGACA 3660
 CTAGTAGAGC AAAGACTTAA TCATATCAAC TTAATCTGT TACACAATAT GTGTTTTTTA 3720
 ATATACTAAC CATTTCTTAT GGAAAGGTCC TGTGGGGAGC CCATCTCTC GCCAAGCCAT 3780
 CACAGGCTCT GCATACACAT GCACTCAGTG TGGACTGGGA AGCATTACTT TGTAGATGTA 3840
 TTTTCAATAA AGAAAAAAT AGTTTTACAT T

Seq ID NO: 258 Protein sequence
 Protein Accession #: NP_004163.1

1 11 21 31 41 51
 45 MTKSNGEPEK MGRMERFQQ GVRKRTLLAK KKVQNITKED VKSYLFRNAF VLLTVTAVIV 60
 GTILGFTLRP YRMSYREVKY FSFPGLLMR MLQMLVPLI ISSLVTGMAA LDSKASGKMG 120
 MRADVYMTT TIIAVVIGII IVIIHPGKG TKENMHREGK IVRVTAADAF LDLIRNMFFP 180
 NLVEACFKQ KTNYEKRSFK VPIQANETLV GAVINNVEA METLTRITEE LVPVPGSVNG 240
 50 VNALGLVVFS MCFGFVIGNM KEQGQALREF FDSLNEAIMR LVAVIMWYAP VGILFLIAGK 300
 IVEMEDMGVI GQGLAMTVT VIVGLLIHAV IVLPLLYFLV TRKNPNWVFI GLLQALITAL 360
 GTSSSSATLP ITFKCLEENN GVDKRVTRFV LPVGATINMD GTALYEALAA IFIAQVMNFE 420
 LNFQGIITIS ITATAASIGA AGIPQAGLVT MIVILTSVGL PTDDITLIIA VDWFDLRLRT 480
 35 TTNVLGDSLQ AGIVEHLRSH ELKNRDVEMG NSVIEENEMK KPYQLIAQDN ETEKPIDSET 540
 KM

Seq ID NO: 259 DNA sequence
 Nucleic Acid Accession #: NM_021948.1
 Coding sequence: 48..2783

1 11 21 31 41 51
 60 TGTGGCACTG CCTGCGTACC CAACCCAGC CCTGGGTAGC CTGCAGCATG GCCCAGCTGT 60
 TCCTGCCCTT CTGGCAGGCC CTGGTCTTGG CCCAGGCTCC TGCAGCTTTA GCAGATGTTT 120
 65 TGGAAAGGAGA CAGCTCAGAG GACCGCGCTT TTCGCGTGCG CATCGCGGGC GACGCGCCAC 180
 TGCAGGGCGT GCTCGGCGGC GCCCTCACCA TCCCTTGCCA CGTCCACTAC CTGCGGCCAC 240
 CGCCGAGCCG CCGGGCTGTG CTGGGCTCTC CGCGGGTCAA GTGGACTTTC CTGTCCCGGG 300
 GCGGGGAGGC AGAGGTGCTG GTGGCGCGGG GAGTGC CGT CAAGGTGAAC GAGGCCTACC 360
 GGTTCGCGGT GGCACGCTCT GCGTACCCAG CGTGCCTCAC CGACGTCTCC CTGGCGCTGA 420
 70 GCGAGCTGCG CCCCAACGAC TCAGTATCT ATCGCTGTGA GGTCCAGCAC GGCAATCGATG 480
 ACAGCAGCGA CGCTGTGGAG GTCAAGGTCA AAGGGGTCTT CTTTCTCTAC CGAGAGGGCT 540
 CTGCCCCGCTA TGCTTTCTTC TTTTCTGGGG CCCAGGAGGC CTGTGCCCCG ATTGGAGCCC 600
 ACATCGCCAC CCCGAGCAG CTCTATGCCG CCTACCTTGG GGGCTATGAG CAATGTGATG 660
 CTGGCTGGCT GTCCGATCAG ACCGTGAGGT ATCCCATCCA GACCCACAGA GAGGCCTGTT 720
 75 ACGGAGACAT GGATGGCTTC CCCGGGGTCC GGAACATATG TGTGGTGGAC CCGGATGACC 780
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 80 GGCTAGCTGA TGGCAGTGTG CGCTACCCCA TCGTCAACCC CAGCCAGCGC TGTGGTGGGG 1020
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5	TCTCAGAAGA	GGAAAGGTAAG	GCATTGGAGG	AAGAAGAGAA	ATATGAAGAT	GAAGAAGAGA	1440
	AAGAGGAGGA	AGAAGAAGAG	GAGGAGGTGG	AGGATGAGGC	TCTGTGGGCA	TGGCCCAGCG	1500
	AGCTCAGCAG	CCCCGGCCCT	GAGGCCTCTC	TCCCCACTGA	GCCAGCAGCC	CAGGAGGAGT	1560
	CACTCTCCCA	GGCGCCAGCA	AGGGCAGTCC	TGCAGCCTGG	TGCATCACC	CTTCCTGATG	1620
	GAGAGTCAGA	AGCTTCCAGG	CCTCCAAGGG	TCCATGGACC	ACCTACTGAG	ACTCTGCCCA	1680
	CTCCCAGGGA	GAGGAACCTA	GCATCCCCAT	CACCTTCCAC	TCTGGTTGAG	GCAAGAGAGG	1740
	TGGGGGAGGC	AACCTGGTGT	CCTGAGCTAT	CTGGGGTCCC	TCGAGGAGAG	AGCGAGGAGA	1800
	CAGGAAGCTC	CGAGGGTGCC	CCTTCCCTGC	TTCCAGCCAC	ACGGGCCCCCT	GAGGGTACCA	1860
10	GGGAGCTGGA	GGCCCCCTCT	GAAGATAATT	CTGGAAGAAC	TGCCCCAGCA	GGGACCTCAG	1920
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	CCGCATCAGG	TGACTGTGTC	CCCAGCCCCCT	GCCACAATGG	TGGGACATGC	TTGGAGGAGG	2040
	AGGAAGGGGT	CCGCTGCCTA	TGTCTGCCTG	GCTATGGGGG	GGACCTGTGC	GATGTTGGCC	2100
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	TCGGACTCAA	CGACAGGACC	ATCGAAGGCG	ACTTCTTGTG	GTCCGATGGC	GTCCCCCTGC	2340
	TCTATGAGAA	CTGGAACCTT	GGGCAGCCTG	ACAGCTACTT	CCTGTCTGGA	GAGAACTCGC	2400
	TGGTCATGGT	GTGGCATGAT	CAGGACAAT	GGAGTGACGT	GCCCTGCAAC	TACCACTGT	2460
20	CCTACACCTG	CAAGATGGGG	CTGGTGTCTT	GTGGGCCGCC	ACCGGAGCTG	CCCCTGGCTC	2520
	AAGTGTTCGG	CCGCCACGCG	CTGCCGTATG	AGGTGGACAC	TGTGCTTCGC	TACCGGTGCC	2580
	GGGAAGGACT	GGCCCAGCGC	AATCTGCCGC	TGATCCGATG	CCAAGAGAAC	GGTCGTGGGG	2640
	AGGGCCCCCA	GATCTCCTGT	GTGCCCAGAA	GACCTGCCCG	AGCTCTGCAC	CCAGAGGAGG	2700
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25	CCAGCCCCAT	GCCAGGTCCC	TAGGGGGCAA	GGCCTTGAAC	ACTGCCGGCC	ACAGCACTGC	2820
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Seq ID NO: 260 Protein sequence
Protein Accession #: NP_068767.1

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35	SLALSELRPN	DSGIYRCSEVQ	HGIDSSDAV	EVKVKGVVFL	YREGSARYAF	SFSGAQEACA	180
	RIGAHIAIPE	QLYAYLGGY	BQCDAWGLSD	QTVRYPIQTP	REACYGDMGD	FPGVNRNYGVV	240
	DPDDLVDVYC	YAEIDLNGELF	LGDPPPEKLT	EARAYCQER	GAEIATTGQL	YAAWDGGLDH	300
	CSPGWLADGS	VRYPIVTPSQ	RCGGGLPGVK	TLFLFPNQTG	FPNKHRSRNV	YCFRDSAQPS	360
	AIPEASNPA	NPASDGLAEI	VTVTETLEEL	QLPQEAETESE	SRGAIYSIPI	MEDGGGGSST	420
40	PEDPAEAPRT	LLEFETQGMV	PPTGFSEEEG	KALEEBEEKYE	DEEBEKEEBEE	EEVEDEALW	480
	AWPELSLSPG	PEASLPTBPA	AQEESLSQAP	ARAVLQPGAS	PLPDGESEAS	RPPRVHGPFT	540
	ETLPTPRERN	LASPSPTLV	BAREVGEATG	GPESLGVPRG	ESEETGSSEG	APSLLPATRA	600
	PEGTRELEAP	SEDNSGRAP	AGTSVQAQPV	LPTDSASRGG	VAVVPASGDC	VPSPCNHGTT	660
	CLEEEEGVRC	LCLPGYGGDL	CDVGLRFCNP	GWDAFQGACY	KHFSTRRSWE	EAETQCRMVY	720
45	AHLASISTPE	BYQWIGLNDR	TYEGDFLWSD	GVPLLYENWN	PGQPDSDYFLS		780
	GENCVVMVWH	DQGNLSDVPC	NYHLSYTCMK	GLVSCGPPPE	LPLAQVFGRP	RLRYEVDTVL	840
	RYRCREGLAQ	RNLPLIRQCE	NGRWEAPQIS	CVPRRPARAL	HPEEDPEGRQ	GRLLGRWKAL	900
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Seq ID NO: 261 DNA sequence
Nucleic Acid Accession #: NM_004386.1
Coding sequence: 2..3967

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	CTTTACCCTG	CAGCCACGGC	CAAGCGCAGC	CCGAGATGCC	CCTCGGATAA	AGTGGACCAA	240
60	GGTGCGGACT	CGCTCGGGCC	AGCGACAGGA	CTTGCCCATC	CTGGTGGCCA	AGGACAAATG	300
	CGTAGAGGTP	GCCAAAAGCT	GGCAGGGACG	AGTGTCACTG	CCTTCTTACC	CCCGCGCCG	360
	AGCCAACGCC	ACGCTACTTC	TGGGGCCACT	GAGGGCCAGT	GACTCTGGGC	TGTACCGCTG	420
	CCAGGTGGTG	AGGGGCATCG	AGGATGAGCA	GGACCTGGTG	CCCTTGGAGG	TGACAGGTGT	480
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65	GGCCTGCCGT	CTCAGCTCAG	CCATCATTGC	AGCCCTCGG	CATCTACAGG	CTGCCTTTGA	600
	GGATGGCTTT	GACAACTGTG	ATGCTGGCTG	GCTCTCTGAC	CGCACTGTTC	GGTATCCTAT	660
	CACCCAGTCC	CGTCTGTGTT	GCTATGGCGA	CCGTAGCAGC	CTTCCAGGGG	TTCCGAGCTA	720
	TGGGAGGCGC	AACCCACAGG	AACTCTACGA	TGTGTATTGC	TTTGCCCGGG	AGCTGGGGGG	780
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70	CCGCCGCGAG	GGTGCCGCGC	TGGCCTCGGT	GGGACAGCTG	CACCTGGCCT	GGCATGAGGG	900
	CCTGGACCA	TGCGACCGGG	GCTGGCTGGC	CGACGGCAGC	GTGCGCTACC	CGATCCAGAG	960
	GCCGCGCCGG	CGCTGCGGGG	GCCAGCCGCC	GGGCGTGCGC	ACCGTCTACC	GCTTCGCTAA	1020
	CCGAGCCGGC	TTCCCTCTAC	CCGCCGAGCG	CTTCGACGCC	TACTGCTTCC	GAGCTCATCA	1080
	CCCAACGTCA	CAACATGGAG	ACCTAGAGAC	CCCATCTCT	GGGGATGAGG	GGGAGATTCT	1140
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	GGAGCCTCCG	TTGGCCATGC	CAGTCACAGA	GATGTTGGGC	AGTGGCCAGA	GCCGGAGCCC	1620
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	CTCCCCAGAG	CCCTCTGCTG	GGCCCCCTAC	CATGGTCCCA	CCCAGCATCT	CAGGCCACAG	1740
	CAGGGCCCTC	GTCTCTGGAG	TAGAGAAAGC	CGAGGGCCCC	AGTGCCAGGC	CAGCCACCTC	1800

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Seq ID NO: 262 Protein sequence

Protein Accession #: NP_004377.1

1 11 21 31 41 51
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	ACRLSSAIIA	APRHQAFAE	DGFDNCDAGW	LSDRTVRYPI	TQSRPGCYGD	RSSLPGVRSY	240
5	GRNRPQELYD	VYCFARELGG	EVFYVGPARR	LTLAGARAQC	RRQGAALASV	GQLHLAWHEG	300
	LDQCDPGLWA	DGVSRYPIQT	PRRRCGGPAP	GVRTVYRFAN	RTGFPSPAER	FDAYCFRAHH	360
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	EKQESQQTLS	PTPGDPLMAS	WPTGEVWLST	VAPSPSDMGA	GTAASSHTEV	APTDPMPRRR	480
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Seq ID NO: 263 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 7..2085

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	GTGAGTGGAA	GGCGGCAGGT	CTGGCCTGAC	TGCGGAGCCG	GCCTTGAAGT	TTTTGAATTA	2040
65	GGTAGCCGGG	AGCTGCCCTC	ACATGGAAAGT	TGGTGCCTTC	CGTAGTCCTA	TTTCATATGA	2100
	AGATTGGCTT	GGCATGTGGA	GGGCACTCAT	TCGGCAATC	CCAGGCTTTG	GGCACTGTGT	2160
	GGAGGGGCTT	GTGTAGGGAC	CAGCAGGCCT	GGTGTAGGG	GTCCAGGCGT	CAAGGAGCTC	2220
	CTGGCTGGGC	CCTCTGGGCA	GCTGCTTCCA	CTCTTGTCTC	TGCCTTCTCA	TCTAGAGAGA	2280
	CTCCCAAGCC	CTGGAGGGGT	GTGTTGTGTT	AGGAATTAAC	TCCCTGCCTA	CCCCAAGGCC	2340
70	TCAGAAATAG	ATTATTAGAG	ATGTGAATTA	TTCTTTGAGA	CTTGGGATAA	GAAACAGCCA	2400
	AAGCTAAACA	TATTTCAAGT	TTAAAAATC	AGTGTTTTAT	AAAACACAGT	TTGGGGCTTT	2460
	TAAAGGTACA	TAACTAAGGA	AAAAAATATA	TATTCATTTT	TCAGGGTTGG	TAAACATTTA	2520
	TGAGATGTCA	GTGACAAAGA	TGGCCTTATT	TTTTTCAGCC	TTTTCTTCTT	CCAAAATGTT	2580
	TCTTAAGGCA	ACTCTCTTAA	ATACATAAAC	ACAACAAATT	AAAATGAAAA	GTGACATGAG	2640
75	AGTAAATGAA	TCAAAGAGGA	AAAACATTGA	ACCAGAGGTG	AGGGCAGCAC	ATCCGAGCA	2700
	GCTGTCCAGG	CCTGAGCCAA	TGCAACCCCT	GGCGGGAAGG	CCAGCTCACC	GTGAGCAGGT	2760
	AGAAGCCAGC	GACCCACCCA	GGCAGGGACC	TTGGTTCTCC	CCACACACTC	CCAGGAGCAG	2820
	GGAACAGGGG	TGGAGTGGCC	TTTCCCAGAG	CTGGAGTTGG	CTGCAGCAGC	TTTCAATCA	2880
	GACCTGCCAA	GGTGAATGGG	GTCTGAGTTT	CACATCTGGG	CCCCCGTGA	CCCCACTGAG	2940
80	TCCTGACAGC	TAAGATGGG	CCACCTCCAC	AGCTCCGTCA	CTCGTACTTG	GGACAGGCCT	3000
	CTCATCTCT	GGGAAGGTCC	TCCTTGTTC	CTACCCAAC	AGAAGGGAAA	CAGTGGCATA	3060
	TTCTCATGGT	ACATGGTTGT	CTGAAAGCCT	TACCTAGGAA	GACGCAGGGT	CTAGATAGAA	3120
	GCTATAAGCA	AGCCACACAC	ATAACCCACA	TCCCCACACC	CCCAACATCC	CCCACTCTCC	3180
	CCACACCCCC	CACACCCCC	ACATCCCCAC	CATAATTACC	CCCACCTCCA	AATATCTCAT	

Seq ID NO: 264 Protein sequence
Protein Accession #: Eos sequence

5	1	11	21	31	41	51	
	MASTRSIELE	HFEERDKRPR	PGSRRGAPSS	SGGSSSSSGPK	GNGLIPSPAH	SAHCSFYRTR	60
	TLQALSSEKK	AKKARFYRNG	DRYFKGLVFA	ISSDRFRSFD	ALLIELTRSL	SDNVNLPQGV	120
	RTIYIDGSR	KVTSLEDELLE	GESYVCASNE	PFRKVDYTKN	INPNWSVNIK	GGTSRALAAA	180
	SSVKSEVKES	KDFIKPKLVT	VIRSGVKPRK	AVRILLNKKT	AHSFEQVLTD	ITEAIKXASG	240
10	VVKRLCTLDG	KQVRVTCVHL	PDFFGDDDFV	IACGPEKFRY	AQDDFVLDS	ECRVLKSSYS	300
	RSSAVKYSGS	KSPGFSRRSQ	ISAHGRSSSN	VNGGPELDRC	ISPEGVNGNR	CSESSTLLEK	360
	YKIGKVIDGD	NFAVVKECID	RSTKKEFALK	IDKAKCCGK	EHLIENEVSI	LRRVKHPNII	420
	MLVEEMETAT	ELFLVMELVK	GGDLFDAITS	STKYTERDGS	AMVYNLANAL	RYLHGLSIVH	480
15	RDIKPENLLV	CEYPDGTGKSL	KLGDFFGLATV	VEGPLYTVCG	TPTYVAPXII	AETGYGLKVD	540
	IWAAGVITYI	LLCGFPFPRS	ENNLQEDLFD	QILAGKLEFP	APYWDNITDS	AKELISQMLQ	600
	VNVEARCTAG	QILSHPWSD	DASQENMQA	EVTGKLQHF	NNALPKQNST	TTGVSVMVVS	660
	GRRQVWPCDG	AGLEVFEGLS	RELPSHGSWC	LP			

Seq ID NO: 265 DNA sequence
Nucleic Acid Accession #: AB020684.1
Coding sequence: 1..1744

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	TGGGTACCCG	ATTTATACCA	AAATAATGGA	CTTGATTGGT	ATTCAAACCA	AGATATGTTG	120
	GACGGTTACC	AGAGGAGAAG	GACTCAGTCC	TATTGAAAGC	TGTGAAGGAT	TGGGAGATCC	180
	TGCTTGCTTT	TATGTTGCTG	TAATTTTAT	TTTAAATGGA	CTAATGATGG	CATTATTCTT	240
	CATATATGCG	ACATATTTAA	GTGGCAGCCG	ATTAGGAGCG	CTGGTTACAG	TGTTGTGCTT	300
30	CTTTTTCAT	CATGAGAGAT	GTACCCGTGT	AATGTGGACA	CCACCTCTCC	GTGAAAGCTT	360
	CTCATATCCA	TTTCTTGTTT	TTCAGATGTT	GCTAGTGACT	CATATTCTCA	GGGCTACAAA	420
	ACTTTATAGA	GGAAGCTTGA	TTGCACCTCG	CATTTCCTCA	GTATTTTTC	TGCTTCCTTG	480
	GCAGTTTGCT	CAGTTTGTTT	TTCTTACTCA	GATTGCATCA	TTATTGTCAG	TATATGTTGT	540
	CGGGTACATT	GATATATGTA	AATTACGGAA	GATCATTAT	ATACACATGA	TTTCTCTTGC	600
35	ACTTTGTTTT	GTTTTGATGT	TTGGGAATCT	AATGTTATTA	ACTTCTTATT	ATGCTTCTTC	660
	TTTGGTAATT	ATTGSGGGTA	TTCTGGCAAT	GAAACACAT	TTCTGAAAA	TAAATGTATC	720
	TGAACCTAGT	TTATGGGTTA	TTCAAGGATG	TTTTGGTTA	TTTGGAACTG	TCATACTTAA	780
	ATACTTGACA	TCTAAAATTT	TTGGTATTGC	AGATGACGCT	CATATTGGCA	ACTTACTAAC	840
40	ATCAAAATTC	TTTAGTTATA	AGGATTTTGA	TACTTTATTG	TATACCTGTG	CAGCGGAGTT	900
	TGACTTTATG	GAAAAAGAGA	CTCCACTGAG	ATACACAAAG	ACATTATTGC	TTCCAGTTGT	960
	TCTTGTAGTG	TTTGTGTGCTA	TTGTTAGAAA	GATTATTAGT	GATATGTGGG	GTGCTCTTAGC	1020
	TAAACAACAG	ACACATGTAA	GAAAAACCA	GTTTGATCAT	GGAGAGCTGG	TTTACCATGC	1080
	ATTGCAATTG	TTAGCATATA	CAGCCCTTGG	TATTTTAATT	ATGAGACTAA	AACCTCTCTT	1140
45	GACACCACAT	ATGTGTGTTA	TGGCATCACT	GATCTGCTCA	AGACAGCTAT	TTGGATGGCT	1200
	CTTTTGCAAA	GTACATCTTG	GTGCTATTGT	GTTTGCTATA	TTAGCAGCAA	TGTCAATACA	1260
	AGGTTGAGCA	AATCTGCAAA	CCCAGTGGAA	TATTGTAGGG	GAGTTGAGCA	ATTGCCCCCA	1320
	AGAAGAACCT	ATAGAAATGA	TCAAATATAG	TACTAAACCA	GATGAGTGT	TTGCGGGTGC	1380
	CATGCCCCAG	ATGGCAAGTG	TTAAGCTCTC	TGCACCTCGG	CCCATTGTGA	ATCATCCACA	1440
50	TTATGAAGAG	GCAGGCTTGA	GAGCCAGAAC	AAAAATAGTA	TACTCAATGT	ATAGTCGGAA	1500
	AGCAGCCGAA	GAAGTGAAGC	GAGAAGTGA	AAAGTTAAAA	GTGAAGTATT	ACATTCTAGA	1560
	AGAGTCATGG	TGTGTAAGAA	GATCCAAGCC	TGGTTGCAGT	ATGCCGAAAA	TTTGGGATGT	1620
	AGAAGATCCT	GCCAACTGCT	GGAAAACTCC	CTTATGTAAC	CTCTTGGTGA	AGGATTCCAA	1680
	ACCTCACTTC	ACCACCTGT	TCCAGAACAG	TGTTTACAAA	GTCCTAGAAG	TTGTAAAAGA	1740
55	ATGACTGCTA	GATGACCTGC	TGCTACGGGA	GAACTACATC	TGTAATGGTT	TTAATGTTTT	1800
	GCTAAGTCAT	GTGTGTGTTT	TATCCCAAAA	ACTTTTATAG	GTAAGTGT	TCAAATAGAA	1860
	AACGTTTTAT	TTGGTCAATT	TGAATGTCAT	TCTAATTATA	AAAATGACTT	ACACCTTTAT	1920
	CAATTGGTTA	CTATTTCAAT	GCACCTTTA	AAATTTGCTA	TGCAAAATGAG	TATATGCTTG	1980
	TACTTGACTT	TAATATTGTT	GCTAAAGTGA	GCAAAGCTAC	CTGTATAAAG	AAAACACAGT	2040
60	GGGTTGTGAC	AAGGATGACA	TGAAAATACA	GGACAATTCT	GACAATGTAG	GGGCTGATTT	2100
	TATAGTGTA	GAAGTATTAA	TGCCCTTTC	TTCTTTTTC	TGCCTCTTGC	TCTTGTCTTT	2160
	TGGACATTTC	AGTGATTGTA	AGTTCTTCGG	TCATGTCAGC	CCCTGTCTATC	AACCTGAGTT	2220
	ACAGTAGATG	GGGCAGACAT	GGAGTGTGTT	CTATATAAAA	CTATCTGTTT	GTTTACTTTC	2280
	CTTGTGCGCT	TTTTGTTCTC	TGTTCTCTTG	TTAATGAAGC	TTTTCTCTGCC	CATTATTAAT	2340
65	CCAAACTCTT	GGACCTTGTG	GTTAGGAAAT	TCCCTTAAC	TCCAGCCATA	TGGCATTATC	2400
	GTGTCCTTTT	CTCTCTCTCT	CTTGCTCTCT	CTCTCTCTCT	CTTCCCCATA	TTTTCTGTCA	2460
	AATAAGTACT	GTTTACTCAT	TTAGTTGCTT	ATCAAGTACT	TATCTCTGGT	TTTTAAAAAA	2520
	ATTAATGGTA	ACTGTATTTT	TCTCATTTTT	AGCATTATTC	AAATGTTTAT	ATTTTAATAC	2580
	CTTTAAACCA	CTTTAAAGTT	TTTTCATGTT	TAATTATAGT	TTTAAGAAAA	ACTATTTTGA	2640
70	ACAACCCCAA	ATATAGTGCA	TCTAGAAACT	AATGTATATT	TGATTAGACA	TCATTTATAG	2700
	TGGAACAGTA	GAGCTGTAGTA	CATGGTAATT	TTTCTTTTAC	TATTAAGATA	CAATAAAACA	2760
	TGACTAAATT	TGCTGTCAAA	AATGTAAAGA	ATAATGATAA	ATGGAGTTTT	TTATATTTTA	2820
	CTTTTAAGAT	TGCTGTCTTT	TAATAAGACA	AAGCCTTAAG	CCTTATGTTA	TAATTTTGGT	2880
	TCTAAAAACC	ATCATTTTCAG	TATAAGGAAT	AAGTATATTT	CGTCCTCTCT	TTTAGTTTTT	2940
75	TTCTTCTTAT	TTATTTTAT	TTTGAAAAAT	TTCTACACCT	TCTTTGAATT	CCTTGTATGA	3000
	ATTTTGTGTT	CTTAGAAGTT	AATTTGTGTG	AAATGAGATT	CTTCAAAACG	ATGAAACCTC	3060
	ATAGCTCTGA	GAAAAGGTTT	TAGGGTTTTA	AATTTCTAAGC	AAAGCGTGAC	TATGGCTGAC	3120
	AGACTACACA	TTTAATTATA	CAGCTTCTCT	TTCTTAAACA	CAGGCAGATT	AACCTCATTG	3180
	TGGATTGTCC	TTACAGCTTT	AGTCTCTCAG	CATGGTTTCT	GGTGCCCACT	CCTGGAAGCC	3240
80	GCTGTGCTCT	TTTACCTTCT	TTACAGAGC	CCAAGGGCAG	GCCTGCTCCC	GGGGAAGCAG	3300
	CAGCTTGCTG	ACATAAGTCA	GCTGCAAAAG	CTGAGGAGTG	TGCCCTCAGA	GAAGCACCGC	3360
	CCCCCAGTCT	TGTGCGCAGC	CCTAGAGCCG	CAGCTCCAG	GGATGCTCCT	TCCCTGGAGG	3420
	CAGCCAGCA	GAGGACACTG	GGCAGCGTTC	TTTCAAGTTG	TGGCCACTGT	TTCTCATTTG	3480
	CTGGTTGACT	GTTTTTATTT	CTTAGGCTTT	TGCTAGTTT	AGAAAATAGG	GAAGCAGCCC	3540
	TTGATTGTG	GATTAAGAGC	AACATTGTAG	CGATGATGCA	CAACAGTCCA	GGAAAATGGG	3600

5 CGGTGGACAC TTGAGGCTGA GGATGGGAGT TGACATGAGC AGGGAGAGGG AGGTGCGCGC 3660
 TGCTTATCTG TGATTGTTGC TCACCTGAGT GTGGCTGATT GTGTACATCC AGCAGTTACA 3720
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 TTGCTACAAAC ATTTTCGAAA ACAAGTTGG GGCTGTATTT CTTTAAAAAG ATAAGCCTCT 4260
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 GAAAGTATGT ATCAGGAATA AAGTGATATT GCATAGGAGT ATTGTATTTT TATGAATTTT 4380
 15 ATGCCAGTTG TTTACATGTA CTATATATGT TAAATTAATA AAAATCATGA GAAATG

Seq ID NO: 266 Protein sequence
 Protein Accession #: BAA74900.1

20 1 11 21 31 41 51
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 ACFVAVVIFI LNGMMAFF IYGYLSGSR LGGLVTVLGF FNNHGECTRV MWTPLRESF 120
 SYPLVLQML LVTHILRATK LYRGLIALC ISNVFFMLPW QFAQFVLITQ IASLFVAVVV 180
 25 GYIDICKLRK IYIHMISLA LCFVLMFGNS MLLTSYYASS LVIIWGLAM KPHFLKINVS 240
 ELSLWVIQGC FWLFGTVILK YLTSKIFGIA DDAHIGNLLT SKFFSYKDFD TLLYTCAAEF 300
 DFMEKETPLR YTKILLPLPV LVVFVAIVRK IISDMWGLA KQOETHVRKHQ FDHGLVLYHA 360
 LQLLAYTALG ILIMRLKLEL TPHMCVMASL ICSRLFGWL FCKVHPGAIV FAILAAMSIQ 420
 GSNLQQTOWN IVGEFSNLPQ BELIEWIKYS TKPDVAFAGA MPTMASVKLS ALRPIVNHHPH 480
 30 YEDAGLRART KIVSMYSRK AAEVKKRELI KLVKNYYILE ESWCVRRSKP GCSMPEDW 540
 EDPANAGKTP LCNLLVKDSK PHFTTVFQNS VYKVLVVKE

Seq ID NO: 267 DNA sequence
 Nucleic Acid Accession #: U26744.1
 Coding sequence: 59..1600

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 40 GATGAGGGCT CAAGATCTGG ATCGCATCCG ACTCTCCACC TACAGAACAG CATGCAAGCT 180
 TAGGTTTGTG CAGAAGAAAT GCAATTGTCG CTGGTGGAC ATATGGAATG TCATAGAAGC 240
 ATTGCGGGAA AATGCTCTGA ACAACCTGGA CCCAAACACT GAACCTCAACG TGTCCCGCTT 300
 AGAGGCTGTG CTCTCCACTA TTTTTCACCA GCTCAACAAA CGGATGCCAA CCACTCACCA 360
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 45 GGAAGGCCAT GGTAAAATTT CAGTATTTGC TGTCAAAATG GCTTTAGCCA CATTGTGTGG 480
 AGGGAAGATC ATGGACAAAT TAAGATATAT TTTCTCAATG ATTTCTGACT CCAGTGGGGT 540
 GATGTTTTAT GGACGATATG ACCAATTCCT TCGGGAAGTT CTCAAACATC CCACGGAAGT 600
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 50 GAAAAAAGTG ACGTTAAATG GTTCTTGGGA CACGCTTATG TCAGATCCTC CCCCAGATG 720
 TCTGCTCTGG TTGCTCTTTC TGCATCGACT AGCAAAATGT GAAAAATGCT TCCATCCGGT 780
 TGAGTGTTC TACTGCCACA GTGAGAGTAT GATGGGATTT CGCTACCGAT GCCAACAGTG 840
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 CAACACGAC CAAATGAAAG AGTACACGTC ATGGAATCA CCTGCTAAGA AGCTGACTAA 960
 55 TGCAATAAGC AAGTCCCTGA GCTGTGCTTC CAGCCGTGAA CCTTTGCACC CCATGTTCCC 1020
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 TGTAACACAG ATGAACGACA CCTGTCTTC CCACTCTGTT CCCTCCTCAG GAAGTCTTT 1140
 TATTACCAG AGCATGCTTG AGAGTTCAAA CCGGCTTGAT GAAGAACACA GGCTAATTGC 1200
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 60 TGCTCCTGAC ATCTCTTTCA CCATCGATGC GAATAAGCAG CAAAGGCAGC TGATTGCTGA 1320
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 ACAAGCTTCT CAGCCACGCG CAGAGAAGGC ACAGCAAAC CCCACCCTGC TGGCAGAACT 1440
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 65 GAAGCAGGGA GTAAGTTATG TCCCCTACTG CAGGTCTTAA CTAACAGTGG AGGGGCTGCT 1620
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 70 TTAGAAAAGG GAACGAATTG TCATTTATTG GAAACATTTT AGATCCCCAG AGGTATAAGT 1860
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 TAACCTCTAC ACCACTCAC ACTGTGAGTA TTCAGTTCGS TTTCAATTTA CTGAAAAACCT 2040
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 75 ATAACGTACT ATTACGTGCC CATCTTTTGT GCTCTTCCCC AAAGCAGAAAT CCTTACTGTT 2220
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 TTCGGCTCCG GGAGACGAGA GGGTCATTAC ATACTTTTT TTTTCTGCG AAATAGGGGC 2340
 ATTGTGACTT TATAGCCTAA ACTGGAGCTG TCTGAACCTG TGCTCAGGCT CAAGAGCCAG 2400
 CAGGGGGAGC AGCAAACTC

Seq ID NO: 268 Protein sequence
 Protein Accession #: AAC50426.1

1 11 21 31 41 51
 | | | | |

MIEDSGKRGN TMAERRQLFA EMRAQDLDR IRLSTYRTACK LRFVQKKCNL HLVDIWNVIE 60
 ALRENALNNL DPNTLNVSR LEAVLSTIFY OLNKRMPETH QIHVEQSISL LLNPLLAFFD 120
 PEGHGKISVF AVKMALATLC GKGIMDKLRY IFSMISDSSG VMVYGRYDQF LREVLKLPTF 180
 VLEGPSEFGYT EQSARSCFSQ QKKVTLNGFL DTLMSDPPPO CLVWLPLLHR LANVENVFHP 240
 VECSYCHSES MMGFYRQCQ CHNYQLCQDC FWRGHAGGSH SNQHQMKEYT SWKSPAKKLT 300
 NALSKSLSCA SSREPLHPMF PDQPEKPLNL AHIVDTWPPR PVTSMNDTLF SHSVPSGSP 360
 FITRSMLESS NRLDEEHLRI AYAARLAAE SSSSQPPQOR SAPDISFTID ANKQQRQLIA 420
 ELENKREIL QEIQRLRLHEH EQASQPTPEK AQONPTLLAE LRLRLQRKDE LEQRMSALQE 480
 SRRELMVQLE GLMKLLKEEBE LKQGVSVVPY CRS

Seq ID NO: 269 DNA sequence
 Nucleic Acid Accession #: NM_001276.1
 Coding sequence: 127..1278

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 GCCAGAATGG GTGTGAAGGC GTCTCAAACA GGCTTTGTGG TCCTGGTGCT GCTCCAGTGC 180
 TGCTCTGCAT ACAAACTGGT CTGTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT 240
 GGGAGCTGCT TCCCAGATGC CCTTGACCGC TTCCTCTGTA CCCACATCAT CTACAGCTTT 300
 GCCAATATAA GCAACGATCA CATCGACACC TGGGAGTGGG ATGATGTGAC GCTCTACGGC 360
 ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTTGTC TGTGCGAGGA 420
 TGGAACTTTG GGTCTCAAAG ATTTTCCAAG ATAGCCTCCA ACACCCAGAG TCGCCGGACT 480
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 GCCGAATTTA TAAAGGAAGC CCAGCCAGGG AAAAGCAGC TCCTGCTCAG CGCAGCACTG 660
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 ATCTGTGACT TCTCCGCGG AGCCACAGTC CATAGAACC TCAGGACGCA GGTCCCTTAT 1080
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 CAGTACCTGA AGGATAGGCA GCTGGCAGGC GCCATGGTAT GGGCCCTGGA CCTGGATGAC 1200
 TTCCAGGGCT CCTTCTGCGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT 1260
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 GGCTCAGTCT CCTCCCTTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTTGAGCTCA 1440
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 TGGCAAGCTC TATACCAAG GAGCCAAACA TCCTACAAGA CACAGTGACC ATACTAATTA 1680
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 ACTTCCCTCT CTAATTTCCA CAGCTGCTCA ATAAAGTACA AGAGTTTAA AGTGTGTTGG 1800
 CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGGACTCAC CTCCCCATC 1860
 TCTTCTGGGT TCCTTCTCTT GAGCCTTGGG ACCCTGAGC TTGCAGAGAT GAAGGCCGCC 1920
 ATGTT

Seq ID NO: 270 Protein sequence
 Protein Accession #: NP_001267.1

1 11 21 31 41 51
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 KSVPPFLRTH GFDGLDLAWL YPGRRDKQHF TTLIKEMKAE FIKEAQPGKK QLLLSAALSA 180
 GKVTIDSSYD IAKISQHLDF ISIMTYDFHG AWRGTTGHHS PLFRGQEDAS PDRFSNTDYA 240
 VGYMLRLGAP ASKLVMGIPT FGSRFTLASS ETGVGAPISG PGIPGRFTKE AGTLAYYEIC 300
 DFLRGATVHR TLGQVVPYAT KGNQWVGYDD QESVKSQVQY LKDRQLAGAM VWALDLDDFQ 360
 GSFCGQDLRF PLTNAIPDAL AAT

Seq ID NO: 271 DNA sequence
 Nucleic Acid Accession #: NM_006474.1
 Coding sequence: 181..669

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 ATGTGGAAGG TGTGAGTCT GCTCTTCGTT TTGGGAAGCG CGTCGCTCTG GGTCTTGCCA 240
 GAAGGAGCCA GCACAGGCCA GCCAGAAGAT GACACTGAGA CTACAGGTTT GGAAGGCGGC 300
 GTTGCCATGC CAGGTGCCGA AGATGATGTG GTGACTCCAG GAACCAGCGA AGACCGCTAT 360
 AAGTCTGGCT TGACAACTCT GGTGGCAACA AGTGTCAACA GTGTAAACAG CATTGCAATC 420
 GAGGATCTGC CAACCTCAGA AAGCACATG CACGCGCAAG AACAAAGTCC AAGCGCCACA 480
 GCCTCAAACG TGGCCACCAG TCACTCCACG GAGAAAGTGG ATGGAGACAC ACAGACAACA 540
 GTTGAGAAAG ATGGTTTGTG AACAGTGACC CTGGTTGGAA TCATAGTTGG GGTCTTACTA 600
 GCCATCGGTT TCATTGTTGG AATCATCGTT GTGGTTATGC GAAAAATGTC GGAAGGTAC 660
 TCGCCCTAAA GAGCTGAAGG GTTACGCCCT GCTTGCCAAAC GTGCTTTAAA AAAAGACCGT 720
 TTCTGACTCT GTGGTGAAGT CCCTGAGCTC GTGGGGAGAA GATGACCCGT GAAACATTGT 780
 CGGGCCCAAT CAGATTCCAC GGTGACTTTC CGTTTGCCAA ATTAACCGAG GAAAGACCTT 840

TCACCAGATT TGGTTCTTAA ACTTT

Seq ID NO: 272 Protein sequence
Protein Accession #: NP_006465.1

1	11	21	31	41	51	
MWKVSALLFV	LGSASLWVLA	EGASTGQPED	DTETTGLEGG	VAMPGAEDDV	VTPGTSEDRY	60
KSLGLTLVAT	SVNSVTGIRI	EDLPTSESTV	HAQEQSPSAT	ASNVATSHST	EKVDGDTQTT	120
VEKDGSLSTVT	LVGIIVGVLL	AIGFIGGIIV	VVMRKMSGRY	SP		

Seq ID NO: 273 DNA sequence
Nucleic Acid Accession #: CAT cluster

1	11	21	31	41	51	
GCGGCCGCCA	GCTTGCAAAG	CCGAAGTCTG	GCCGCGCTCT	TCGACTCGCT	GCGCCACGTC	60
CCCCGGGGTG	CCGAGCCGCG	GGGGGTGAG	GTGGCTGCGC	CGGCGGCCGG	GCTAGGAGGT	120
GCGGGCACTG	GGGGCGCGGG	AGGGGACGTG	GCAGGCCCCG	CGGGGGCCAC	GGCGATCCCA	180
GGGGCCAGGA	AGGTCCCGCT	GCGGGCACGC	AATCTGCCTC	CGTCTTCTT	CACGGAGCCG	240
TCCCGGGCAG	GCGGCGGGGG	GTGTGGCCCG	TGCGGGCCGG	ACGTGAGCTT	GGGCGACCTG	300
GAGAAGGGCG	CGGAGGCCGT	GGAGTCTTCT	GAGCTGTGCG	GGCCCGACTA	CGGCGCCGGC	360
ACGGAGGGCG	CAGTCTTGCT	TGCCGCCGAG	CCTCTCGACG	TGTTCCCGCG	CGGAGCCTCC	420
GTACTGCGGG	GACCCCGCGA	GCTGGAGCCC	GGCCTCTTTG	AGCCGCGGCC	GGCAGTGGTG	480
GGAAACCTAC	TGTACCCCGA	GCCCTGGAGC	GTCCCGGGCT	GCTCCCCGAC	CAAAAAGAGC	540
CCCTTGACTG	CCCTCCGGGG	CGGGTTGACC	TGGAACGAGC	CCTTGAGCCC	CCTGTACCCC	600
GCCGCTGCGA	ATTTCTCCCG	GCGGGGAGGA	CGGGCCGGGC	CATTGCGCTT	CTTTCGCCCC	660
CTTCTTTCCA	GACTGCGCTT	TGC				

Seq ID NO: 274 DNA sequence
Nucleic Acid Accession #: Eos sequence

1	11	21	31	41	51	
CAAAGAGGCC	GGGCTCCAGC	TCCGGGGGTC	CCCGCAGTAC	GGAGGCTCCG	GCGGGGAACA	60
CGTCGAGAGG	CTCGGGCGGA	AGCAAGACTG	CGCCCTCCGT	GCGGCGCCCG	TAGTCGGGCC	120
CAGACAGCTC	AAAGAACTCC	ACGGCCTCCG	CGCCCTTCTC	CAGGTCGCCC	AAGCTCACGT	180
CCGGCCCCGA	CGGGCCACAC	CCGCGCCGCG	CTGCCCGGGA	CGGCTCCGTG	AAGAAGGACG	240
GAGGCAGATT	GCGTGCCCGC	AGCGGGACCT	TCTTGCCCCC	TGGGATCGCC	GTGGCCCCCG	300
CGGGGCTGCG	CACGTCCCCCT	CCCGCGCCCC	CAGTGCCCCG	ACCTCCTAGC	CCGGCCGCCG	360
GCGCAGCCAC	CTCACCCCCC	GCGCGCTCGG	CACCCCGGGG	GACGTGGCGC	AGCGAGTCGA	420
AGAGCGCGGC	CAGACTTCGG	CTTGCAAGC	TGGCGGCCGC			

Seq ID NO: 275 DNA sequence
Nucleic Acid Accession #: NM_001118.1
Coding sequence: 74..1651

1	11	21	31	41	51	
AGCCCAGAGA	CACATTGGGG	CTGACCTGCC	GCTGCTGTCA	GTGGGAGGCC	AGTGGTGCTG	60
GCCAAAGAAGT	GTGATGGCTG	GTGTCGTGCA	CGTTTCCCTG	GCTGCTCACT	GCGGGGCCCTG	120
TCCGTGGGGC	CGGGGCGAGC	TCCGCAAGAG	ACGCGCAGCC	TGCAAGTCCG	CGCCCCAGAG	180
ACACATTGGG	GCTGACCTGC	CGCTGCTGTC	AGTGGGAGGC	CAGTGGTGCT	GGCCAAAGAAG	240
TGTCATGGCT	GGTGTGCTGC	ACGTTTCCCT	GGCTGCTCTC	CTCCTGCTGC	CTATGGCCCC	300
TGCCATGCAT	TCTGACTGCA	TCTCAAGAA	GGAGCAAGCC	ATGTGCTTGG	AGAAGATCCA	360
GAGGGCCAAT	GAGCTGATGG	GCTTCAATGA	TTCCTCTCCA	GGCTGTCTTG	GGATGTGGGA	420
CAACATCACG	TGTTGGAAGC	CCGCCCATGT	GGGTGAGATG	GTCTTGGTCA	GCTGCCCTGA	480
GCTCTTCCGA	ATCTTCAACC	CAGACCAAGT	CTGGGAGACC	GAAACCATTG	GAGAGTCTGA	540
TTTTGGTGAC	AGTAACCTCT	TAGATCTCTC	AGACATGGGA	GTGGTGAGCC	GGAACTGCAC	600
GGAGGATGGC	TGGTCGGAAC	CCTTCCCTCA	TTACTTTGAT	GCCTGTGGGT	TTGATGAATA	660
TGAATCTGAG	ACTGGGGACC	AGGATTATTA	TACCTGTGCA	GTGAAGGCCC	TCTACACGGT	720
TGGCTACAGC	ACATCCCTCG	TACCCCTCAC	CAGTGCCATG	GTGATCCTTT	GTGCTTCCG	780
GAAGCTGCAC	TGCACACGCA	ACTTCATCCA	CATGAACCTG	TTTGTGTCGT	TGATGCTGAG	840
GGCGATCTCC	GTCTTCATCA	AAGACTGGAT	TCTGTATGCG	GAGCAGGACA	GCAACCACTG	900
CTTCATCTCC	ACTGTGGAAT	GTAAGGCCGT	CATGGTTTTC	TTCCACTACT	GTGTTGTGTC	960
CAACTACTTC	TGGCTGTTCA	TGAGGGGCC	GTACCTCTTC	ACTCTGCTGG	TGGAGACCTT	1020
CTTCCCTGAA	AGGAGATACT	TCTACTGGTA	CACCATCATT	GGCTGGGGGA	CCCCAACTGT	1080
GTGTGTGACA	GTGTGGGACT	CGCTGAGACT	CTACTTTGAT	GACACAGGCT	GCTGGGATAT	1140
GAATGACAGC	ACAGCTCTGT	GGTGGGTGAT	CAAAGGCCCT	GTGGTTGGCT	CTATCATGGT	1200
TAACTTTGTG	CTTTTATTTG	GCATTATCGT	CATCCTTGTC	CAGAAACTTC	AGTCTCCAGA	1260
CATGGGAGGC	AATAGTCCCA	GCACTACTTT	GCGACTGGCC	CGGTCCACCC	TGCTGCTCAT	1320
CCCACTATTC	GGAATCCACT	ACACAGTATT	TGCCTTCTCC	CCAGAGAATG	TCAGCAAAAG	1380
GGAAAGACTC	GTGTTTGAGC	TGGGGCTGGG	CTCCTTCCAG	GGCTTTGTGG	TGGCTGTTCT	1440
CTACTGTTTT	CTGAATGGTG	AGGTACAAGC	GGAGATCAAG	CGAAAAATGG	GAAGCTGGAA	1500
GGTGAACCGT	TACTTCGCTG	TGGACTTCAA	GCACCGACAC	CCGTCTCTGG	CCAGCAGTGG	1560
GGTGAATGGG	GGCACCCAGC	TCTCCATCCT	GAGCAAGAGC	AGCTCCCAAA	TCCGATGTC	1620
TGGCTTCCCT	GCTGACAATC	TGGCCACCTG	AGCCATGCTC	CCCT		

Seq ID NO: 276 Protein sequence
Protein Accession #: NP_001109.1

1	11	21	31	41	51	
MAGVVHVSIA	AHCACPWGR	GRLRKGRAAC	KSAAQRHIGA	DLPLLSVGQ	WCWPRSVMAG	60

VHVSLAALL LLLPAPAMHS DCIFKKEQAM CLEKIQRANE LMGFNDSSPG CPGMWDNITC 120
 WKPAHVGEVM LVSCPELFRI FNPQVWETE TIGESDFGDS NSLDLSDMGV VSRNCTEDGW 180
 SEFPFPHYFDA CGFDEYESTI GDQDYVYLSV KALYTVGYST SLVTLTAMV ILRCRFRKLHC 240
 TRNFIHMLNF VSEMLRAISV FIKDWILYAE QDSNHCFFIST VECKAVMVVF HYCVVSNYFW 300
 LFIEGLYLF LTVETFFPER RYFYWYTIIG WGTPTVCVTV WATLRLYFDD TGCWDMNDST 360
 ALWWVIKGPV VGSIMVNFVL FIGIIVILVQ KLQSPDMGNN ESSIIYLRLLAR STLLLIPLFG 420
 IHYTVFAFSP ENVSKRERLV FELGLGSFQG FVVAVLYCFL NGEVQAEIKR KWRSWKVNRY 480
 FAVDFKHRHP SLASSGVNGG TQLSILSKSS SQIRMSGPLA DNLAT

Seq ID NO: 277 DNA sequence
 Nucleic Acid Accession #: NM_004000.1
 Coding sequence: 36..1193

1 11 21 31 41 51
 AGAAGAAGCT GGCCAAGGAT ATGGGAGCAA CCACCATGGA CCAGAAGTCT CTCTGGGCAG 60
 GTGTAGTGGT CTGTGCTGCT CTCCAGGGAG GATCTGCCTA CAAACTGGTT TGCTACTTTA 120
 CCAACTGGTC CCAGGACCGG CAGGAACCCAG GAAAATTCAC CCCTGAGAAAT ATTGACCCCT 180
 TCCTATGCTC TCATCTCATC TATTCATTCG CCAGCATCGA AAACAACAAG GTTATCATCA 240
 AGGACAAGAG TGAAGTGATG CTCTACCAGA CCATCAACAG TCTCAAAACC AAGAATCCCA 300
 AACTGAAAAT TCTCTGTGCC ATTGGAGGGT ACCTGTTTGG TTCCAAAGGG TTCCACCCTA 360
 TGGTGGATTCT TTCTACATCA CGCTTGAAGT TCATTAATCT CATAATCCTG TTTCTGAGGA 420
 ACCATAACTT TGATGGACTG GATGTAAGCT GGATCTACCC AGATCAGAAA GAAAACACTC 480
 ATTTCACTGT GCTGATTCAT GAGTTAGCAG AAGCCTTTC GAAGGACTTC ACAAAATCCA 540
 CCAAGGAAAG GCTTCTCTTG ACTGCGGGCG TATCTGCAGG GAGGCAAAATG ATTGATAACA 600
 GCTATCAAGT TGAGAAACTG GCAAAAGATC TGGATTTCAT CAACCTCCTG TCCTTTGACT 660
 TCCATGGGTC TTGGGAAAAG CCCCTTATCA CTGGCCACAA CAGCCCTCTG AGCAAGGGGT 720
 GGCAAGACAG AGGGCCAAAG TCCTACTACA ATGTGGAATA TGCTGTGGGG TACTGGATAC 780
 ATAAGGGAAT GCCATCAGAG AAGGTGGTCA TGGGCATCCC CACATATGGG CACTCCTTCA 840
 CACTGGCCTC TGAGAAACCC ACCGTGGGGG CCCCTGCCTC TGGCCCTGGA GCTGCTGGAC 900
 CCATCAGAGA GTCTTCAGGC TTCTTGGCCT ATTATGAGAT CTGCCAGTTC CTGAAAGGAG 960
 CCAAGATCAC GCGCCTCCAG GATCAGCAGG TTCCCTACGC AGTCAAGGGG AACCAAGTGG 1020
 TGGGCTATGA TGATGTGAAG AGTATGAGA CCAAGGTTCA GTTCTTAAAG AATTTAAACC 1080
 TGGGAGGAGC CATGATCTGG TCTATTGACA TGGATGACTT CACTGGCAAA TCCTGCAACC 1140
 AGGGCCCTTA CCCTCTTGTC CAAGCAGTCA AGAGAAGCCT TGCTCTCTTG TGAAGGATTA 1200
 ACTTACAGAG AAGCAGGCAA GATGACCTTG CTGCTGGGG CCTGCTCTCT CCCAGGAATT 1260
 CTCATGTGGG ATTCCCTTGG CCAGGCTGGC CTTTGGATCT CTCTTCCAAG CCTTCTCTGA 1320
 CTTCTCTTCA GATCATAGAT TGGACCTGGT TTTGTTTTCC TGCAGCTGTT GACTTGTGTC 1380
 CCTGAAGTAC AATAAAAAAA ATTCATTTTG CTCCAGTA

Seq ID NO: 278 Protein sequence
 Protein Accession #: NP_003991.1

1 11 21 31 41 51
 MDQKSLWAGV VLLLLLQGGG AYKLVCYFTN WSQDRQEPGK FTPENIDPFL CSHLIYSFAS 60
 IENNKVLIKD KSEVMLVQTI NSLTKNPKL KILLSIGGYL FSGKGFHPMV DSSTSRLEFI 120
 NSIILFLRNH NFDGLDVSWI YPDQKENTHF TVLIHELAEAFQKDFTKSTK ERLLLTAGVS 180
 AGRQMDNSY QVEKLAKDLI FINLSFDFH GSWEKPLITG HNSPLSKGWQ DRGPSSYINV 240
 EYAVGYWIHK GMPSEKVVMG IPTYGHSTFL ASAETTVGAP ASGPAAAGPI TESSGFLAYY 300
 EICQFLKGAK ITRLDQDQVP YAVKGNQWVG YDDVKSMETK VQFLKNLNLG GAMIWSIDMD 360
 DFTGKSCNQG PYPVLQAVKR SLGSL

Seq ID NO: 279 DNA sequence
 Nucleic Acid Accession #: NM_015166.1
 Coding sequence: 116..1249

1 11 21 31 41 51
 TGCTGGAAGT CCCTCACCCA GAGACCAGTG CTCCCAACGG CAGAGCAGCG GGGGAGATAA 60
 AGAACTGGTG ACACGTGGCT GTACATTGAG CACAGCTGTG GTGTCCCAA GTGCCATGAC 120
 CCAGGAGCCA TTCAGAGAGG AGCTGGCCTA TGACCGGATG CCCACGCTGG AGCGGGGCGG 180
 GCAAGACCCC GCCAGCTATG CCCAGACGCG GAAGCCGAGC GACCTGCAGC TGTGGAAGAG 240
 ACTGCCCCC TGCTTCAGCC ACAAGACGTG GGTCTTCTCT GTGCTGATGG GGAGCTGCCT 300
 CCTGGTGACC TCGGGGTTTT CGCTGTACCT GGGGAACGTG TTCCCGGCTG AGATGGATTA 360
 CTTGCGCTGT GCTGCAGGCT CTTGCATCCC CTCGCAATT GTGAGCTTCA CCGTCTCCAG 420
 GAGGAACGCC AATGTGATTC CCAACTTTCA GATATTGTTT GTTTCCAGT TGTGCTGTGAC 480
 CACTACGTGT TTAATTTGGT TTGGATGCAA ACTAGTCTTG AACCCTATCAG CAATAAACAT 540
 CAACTTCAAC CTCATCCTGC TGCTCCTGCT GGAGCTGCTC ATGGCGGCCA CGGTGATCAT 600
 CGCTGCAGG TCCAGCGAGG AGGACTGCAA GAAAAGAAG GGTCCATAGT CTGACAGCGC 660
 CAACATTCTG GACGAAGTGC CATTTCCTGC TCGGGTCTTG AAATCTTACT CAGTGTGCGA 720
 GGTAAATCGA GGCATCTCTG CCGTCTCTCG GGGGATCATT GCCCTGAACG TGGATGACTC 780
 AGTTTTCAGG CCACACCTCT CAGTGACGTT CTTTGGATC CTAGTGGCCT GCTTTCCAAG 840
 TGCCATTGCC AGTCATGTGG CAGCAGAGTG TCCCAGCAAG TGTCTGGTGG AGGTCTCTGAT 900
 TGCCATAAGC AGCCTCACGT CTCCGCTGCT GTTCAAGGCC TCTGGATATC TGTCAATCAG 960
 CATCATGAGA ATCGTGGAGA TGTTTAAGGA TTACCCGCCA GCCATAAAAC CATCCTACGA 1020
 TGTGCTGCTG CTGCTGCTGC TGCTAGTGTCT CCGTCTGAGC GCCCGGCTCA ACACGGGCAC 1080
 CGCCATCCAG TCGGTGCGCT TCAAGTCTAG TGCAAGGCTG CAGGGTGCAAT CTTGGGACAC 1140
 CCAGAACGGC CCGCAGGAGC GCCTGGCTGG GGAGGTGGCC AGGAGCCCCC TGAAGGAGTT 1200
 CGACAGGAG AAAGCCTGGA GAGCCGTCGT GGTGCAATG GCCCAGTGAC CCCAGAGCGC 1260
 GGAACCCGGG TGGCAGCGCC CAGCCTGGCC CCAAGCATGG AAACGCACAA CCCCTAATCG 1320
 CCCTGAGCTA CTGCTTCTAA CACCTCTTTT CCCTTGTGTG AGGGCAAACC AGGTCTCAGG 1380
 TGGGTTTTTC ACTTCTTAGG GTAGTTTAAT TTTAAATAG GCCAATGTTG GCTAGTCTGT 1440
 GCCTCAGTGA GATCAGTCAG CTCCGAGTGG CTCCGCTGTC GTAACAGCAG GAGCATGGCC 1500

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GCAACTTCCC AGGCCGAGGA AGGGCCCCCG GCTCGGCCTC TTGAGAGCCC CACCCCTGAA 1560
 CTGGCCCCAG CTCTCTTCC TGCTCTCTC ATGGCTTGGG CTGGAGTGGG CTCTCTGGAC 1620
 CTGACCAGAC TGTGGGTCCC TGCGTCTCCT GCCCACTCTG ACCGGGCTTC CTCCCTCCAC 1680
 GCTTAGGGTC TGTCCCGGGT ACTCAGTCAG CCCAGTGGGA TCTTACCCAC TTCCCTGCAA 1740
 GGTGCACCTC CCCAGGCTC AGGCTGCCCA GCGGCTCTTC CTGGACAGTG AGAGCAGGGC 1800
 TTGGCGCCTC TGTCTTGGCC CGGGAGCCGC AGGGGCCCCCT CCTCCAGAGC CTGGGCGCAA 1860
 GCGACACAGG CTGCCGCTGC TCTCCAGGT GAAATCCACA CCAGTCCACG CCGGCTCGCC 1920
 TGCCCTGTCT CCCTACTTAG ACCCAGTCAT TCTAGAGGGA TCCACCGCCA CACTGGCCGG 1980
 CCCACGTCCT GGTGTCTGTC ATGCCAGCT TGGAGTGCCA CGTGGCCGCT GCCACGTC 2040
 CGGGCACTGT CATGCCAGC TTGGAGTGCC ACATGGCCGC TGCCACGTC CCGGGCACTG 2100
 TCATGCCAGC CTGGAGTGC CAGTGGCCG CTGCTGTGAC AGGCAGTGT CTGGGGGTG 2160
 GGGCTGCATC CAAGGCTTTG TAAACCGGCT GGACCACTG TCCTGGCCG CAGTGACCGG 2220
 GGAAGCTGA GCCCTCCCT CCTGTGTTG CTCCATTAC TCAAAATGCA GGACAGATCA 2280
 GGTGAGAGCC CAGGAATCT CACAGGTCA CCCAGCGCCC TCTACCTCCT AGCAAGTACT 2340
 TTGTCTTGT CCTCAGTGA AAGGCCAGG GGCAGCGGT TCTCCATCT CCGCTGTTTT 2400
 GGGGTCTTAG GGTACAGCCC AGGCGGTGAC TGCCACCTG CCAGGCTGCA GGGACAGTTG 2460
 GGTGTGAGAA TAACACTGGC TTTGGGTAGT GCCATGGCCA GGAGTGGGT TCCTGCGTC 2520
 TCCTGCTCCC GAGGGCGCCT GGTCTCTCCC AGCTGACGGC AGTAAATCCA CAGTGAGTTG 2580
 GGGCGACTGT GAAACTGGAA TGCTGTACT TTGATAATTA CTTCCAGCA GGTGTTTTCC 2640
 TTCACAATGG TTTGTTTCT TTCCTTCTGA TCTGAGAAGA CATGAACGTT TTCTCTTAC 2700
 CGCCGTGGG TGTATTGACT GGTCCCCAT GGGCTGCTGG AAAGGCCGG AGATGCATCT 2760
 GTGGCCTGGG GCCATCAAGA TCAAGAACC AGGAGGCTG GGAGATGAG CTGGATGGGG 2820
 CGGCCTGCAG ACCCTGTCAG GGGGTTGAG GACCCTCCA GGTTCCTCC TGCGGAACAG 2880
 GAGTGACTCT GGCTGCCAAG ATACCTTCAT GGTGTTTATG ACAAGTGGAA TCATTATTTT 2940
 CAACCTTTGA AGGGGGATGC AGGCAAGACA CCTTCCAGC TGCTCCTAGA GGGACAAAGC 3000
 CAGGCCCTCT CTGCAGTCTC CGGCAGCTCC GGAAGGACAC AGTCAGGGGC CGGGCAAACA 3060
 CTTTGGCCAC AGCCCCAAC AAGCGCCACC GTGGGAGAGG AGAGGCTGCT GTCACCTGTA 3120
 CCGGATGCAG ACCCCACCCT GTCTGCAGGC CACCCCCACC TCCTGTCAGC TTTGAGGCTG 3180
 GCGGGGTCTG CTCTGCGGAA TGGGGTGGGA GCCACAGGGA CGACCCGGGG CGGGCTGATG 3240
 TCTTCTTGGG GGCAGACCA AGAGCTCAAG TTTGAGATC AGAATTAGGC ACTTGGAAACG 3300
 TTTTGTCTGG CTTGACTTTT CTTATTTTCT TATTTTAGAG CGCTTAAAA ATCCGAAAA 3360
 ATGGGGTTTA AAAGAACTGT CTCCTTCAGT CTACATTTTT GTTTAATACG CTTGAGCAAT 3420
 AAACGCTGAC TTGCAGAGCT G

Seq ID NO: 280 Protein sequence
 Protein Accession #: NP_055981.1

1 11 21 31 41 51
 | | | | |
 40 MTQEPFREEL AYDRMPTLER GRQDPASYAP DAKPSDLQLS KRLPPCFPSHK TWVFSVLMGS 60
 CLLVTSGFSL YLGNVFPDEM DYLRCAAGSC IPSAIVSFTV SRRNANVIPN FQILFVSTFA 120
 VTTTCLIWFG CKLVNPSAI NINFNILLLL LLELLMAATV IIAARSSEED CKKKKGSMSD 180
 SANILDEVFP PARVLKSYEV VEVIAGISAV LGGIIALNVD DSVSGPHLSV TFFWILVACF 240
 45 PSATASHVAA ECPSPKLVSEV LIAISSLTSP LLFTASGYLS FSIIMRIVEMF KDYPPIAIKPS 300
 YDVLVLLLLL VLLQAGLNT GTAIQCVRFK VSARLQGASW DTQNGPQERL AGEVARSPK 360
 EFDKEKAWRA VVVQMAQ

Seq ID NO: 281 DNA sequence
 Nucleic Acid Accession #: NM_004518.1
 Coding sequence: 43..2577

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1 11 21 31 41 51
 | | | | |
 GCTGAGCCTG AGCCCGAGCC GGGGCGCCTC CCGCCAGGCA CCATGGTGCA GAAGTCGCGC 60
 AACCGCGCGG TATACCCCGG CCCGAGCGGG GAGAAGAAGC TGAAGGTGGG CTTCGTGGGG 120
 CTGAGACCCG GCGCGCCCGA CTCCACCCGG GACGGGGCGC TGCTGATGCG CGGCTCCGAG 180
 GCCCCCAAGC GCGGCAGCAT CCTCAGCAA CCTCGCGCGG GCGGCGCGGG CGCCGGGAAG 240
 CCCCCCAAGC GCAACGCTT CTACCGCAAG CTGCAGAAAT TCCTCTACAA CGTGCTGGAG 300
 CGGCGCGCGG GCTGGGCGTT CATCTACCAC GCCTACGTGT TCCTCCTGGT TTTCTCTGTC 360
 60 CTGCTGCTGT CTGTGTTTTT CACCATCAAG GAGTATGAGA AGAGCTCGGA GGGGGCCCTC 420
 TACATCCTGG AAATCGTGAC TATCGTGTG TTTGGCGTGG AGTACTTCGT GCGGATCTGG 480
 GCGCGAGGCT GCTGTGCGG GTACCGTGGC TGGAGGGGGG GGCTCAAGTT TGCCCGGAAA 540
 CCGTTCTGTG TGATTGACAT CATGGTGCTC ATCGCCTCCA TTGCGGTGCT GGCCGCGCGC 600
 TCCAGGGGCA ACGTCTTTGC CACATCTGCG CTCGGAGACC TGCGCTTCCT GCAGATTCTG 660
 65 CGGATGATCC GCATGGACCG GCGGGGAGGC ACCTGGAAGC TGCTGGGCTC TGTGGTCTAT 720
 GCCCACAGCA AGGAGCTGGT CACTGCTTGG TACATCGGCT TCCTTGTCT CATCCTGGCC 780
 TCGTTCTCTG TGTACTTGGC AGAGAAGGGG GAGAACGACC ACTTTGACAC CTACGCGGAT 840
 GCACCTCTGT GGGGCTGAT CACGCTGACC ACCATTGGCT ACGGGGACAA GTACCCCCAG 900
 70 ACCTGGAACG GCAGGCTCCT TCGGCAACC TTCACCTCA TCGGTGTCTC CTTCTTCGCG 960
 CTGCCTGCA GCATCTTGGG GTCTGGGTTT GCCCTGAAGG TTCAGGAGCA GCACAGGCGAG 1020
 AAGCACTTTG AGAAGAGGGC GAACCCGGCA GCAGGCTTGA TCCAGTCGGC CTGGAGATTC 1080
 TACGCCACCA ACCTCTCGAG CACAGACCTG CACTCCACGT GGCAGTACTA CGAGCGAAGC 1140
 GTACCGTGC CACTGTACAG ACTTATCCCC CCGCTGAACC AGCTGGAGCT GCTGAGGAAC 1200
 75 CTCAAGAGTA AATCTGGACT CGCTTTCAGG AAGGACCCCC CGCCGGAGCC GTCTCCAAGC 1260
 CAGAAGGTCA GTTTGAAAGA TCGTGTCTTC TCAGCCCCC GAGGCGTGGC TGCCAAGGGG 1320
 AAGGGGTCCC CGCAGGCCCA GACTGTGAGG CGGTCAACCA GCGCCGACCA GAGCCTCGAG 1380
 GACAGCCCA GCAAGGTGCC CAAGAGCTGG AGCTTCGGGG ACCGAGCCG GGCACGCCAG 1440
 GCTTTCGCGA TCAAGGGTGC CGGTCACGG CAGAACTCAG AAGAAGCAAG CCTCCCCGGA 1500
 80 GAGGACATTG TGGATGACAA GAGCTGCCCC TGCGAGTTTG TGACCGAGGA GTCTGCCCG 1560
 GGCCTCAAAG TCAGCATCAG AGCCGTGTGT GTCATGCGGT TCCTGGTGTG CAAGCGGAAG 1620
 TTCAAGGAGA CCGTGGCGGC CTACGACGTG ATGGACGTCA TCGAGCAGTA CTCAGCCGGC 1680
 CACCTGGACA TGCTGTCCCC AATTAAGAGC CTGCAGTCCA GAGTGGACCA GATCGTGGGG 1740
 GGGGGCCAG CGATCACGGA CAAGGACCGC ACCAAGGGCC CGGCGAGGC GGAGCTGCC 1800
 GAGGACCCCA GCATGATGGA ACGGCTCGGG AAGGTGGAGA AGCAGGTCTT GTCCATGGAG 1860

	AAGAAGCTGG	ACTTCCTGGT	GAATATCTAC	ATGCAGCGGA	TGGGCATCCC	CCCGACAGAG	1920
	ACCGAGGCCCT	ACTTTGGGGC	CAAAGAGCCG	GAGCCGGGCG	CGCCGTACCA	CAGCCCGGAA	1980
	GACAGCCGGG	AGCATGTCTGA	CAGGCACGGC	TGCATTGTCA	AGATCGTGGC	CTCCAGCAGC	2040
5	TCACAGGGCC	AGAAGAAGTT	CTCGGCGCCC	CCGGCCGCGC	CCCTGTCCA	GTGTCCGCCC	2100
	TCACCTCTCT	GGCAGCCACA	GAGCCACCCG	CGCCAGGGCC	ACGGCACCTC	CCCCGTGGGG	2160
	GACCACGGCT	CCCTGGTGGC	CATCCCGCCG	CCGCTGCCCC	ACGAGCGGTC	GCTGTCCGCC	2220
	TACGGCGGGG	GCAACCCGCG	CAGCATGGAG	TTCTGCGGCG	AGGAGGACAC	CCCGGGCTGC	2280
	AGGCCCCCGG	AGGGGACCTT	GCGGGACAGC	GACACGTCCA	TCTCCATCCC	GTCCGTGGAC	2340
10	CACGAGGAGC	TGAGAGCTTC	CTTCAGCGGC	TTAGCATCTT	CCAGTCCAA	GGAGAACCTG	2400
	GATGCTCTCA	ACAGCTGCTA	CGCGGCCGTG	GCGCCTTGTG	CCAAAGTCAG	GCCCTACATT	2460
	GCGGAGGGAG	AGTCAGACAC	CGACTCCGAC	CTCTGTACCC	CGTGGGGGCC	CCCGCCACGC	2520
	TCGGCCACCG	GCGAGGGTCC	CTTTGGTGAC	GTGGGCTGGG	CCGGGCCCCG	GAAGTGAGGC	2580
	GGCGCTGGGC	CAGTGGACCC	GCCCGCGGCC	CTCCTCAGCA	CGGTGCCTCC	GAGGTTTGA	2640
	GGCGGGAACC	CTCTGGGGCC	CTTTCTTAC	AGTAACTGAG	TGTGGCGGGA	AGGGTGGGCC	2700
15	CTGGAGGGGC	CCATGTGGGC	TGAAGGATGG	GGGCTCCTGG	CAGTGACCTT	TTACAAAAGT	2760
	TATTTTCCAA	CAGGCGACTC	CAGGCCCTTG	TCGCCATTGA	GGTGCCCTCC	CTGGGCTGTC	2820
	TCCTCACCCC	TCCTGTGTCT	GGAGCCTGTC	CCAAAAGGTT	GCCAACTGGG	AGGCCTCGGA	2880
	AGCCACTGTC	CAGGCTCCCA	CTGCCTGTCT	GCTCTGTTC	CAAAGGCAGC	GTGTGTGGCC	2940
20	TCGGGCCCTG	CGGTGGCATG	AAGCATCCCT	TCTGGTGTGG	GCATCGCTAC	GTGTTTTGGG	3000
	GGCAGCGTTT	CACGGCCGTG	CCCTTGCTGT	CTCCCTTGGG	CTGGCTCGAG	CCTGGGGTCC	3060
	ATGTCCCTTT	GCCGTCCCGT	CATGGGGCAG	GGAATCCATA	GCGGGGCCCA	CAGGCAGGGG	3120
	TATGAGTGGC	TCCACCCCAA	CGCAGCACCA	GCCCGGCCCA	CCGTCCCCCG	TGTCCCCAGT	3180
	TCCGTCTCAG	CTACTCTGGC	TCCAGGACCC	TGGAGAAGGG	AGACCTGGCA	GTGGAGGGAG	3240
25	GCTGTGCTGT	GTGTCCCTCT	GCAGGTGTGA	CCCCGCTGTC	TCTTCTCTCC	CCCGCCAGGT	3300
	GTGGCCCGGC	CTGTCTTTTC	CTCCCCCACC	AGTATGGCCC	CACCTGCTCT	TTCTNCCCC	3360
	CCCAAGGTGT	GGCCCCACCT	GTTCTTTCTT	CCCCTGCGGA	GGTGTGACCC	CACCTGCTCT	3420
	TTCTTCCCTC	CCAGTATGGC	CCCACCTGCT	CTTTCTCTCC	CCGAGGTGAG	GGCCCGCTCT	3480
	CTCTTTCTCT	CCATGGGAGC	CGCTGAGGCG	TGCGCACCTG	GGCAGAGGTT	GGGGCTCTGC	3540
30	AGGATGAGGA	AGACAGGCCA	ATCCCTTCCC	TCCAGAAAGC	TGGCCGCCCA	GCAGGAGGGA	3600
	CTGAGGCCAG	ACTCATGTCC	AGCAAGGAAC	GTGTGGTGTG	TCCCTTGGGA	AGTCTCTGGG	3660
	CCCTGGGAAG	AGGGAAGGTG	CACGTCCTGG	GATGGTTGCG	GGGCCCTGTT	TTGGGAGACA	3720
	AAGGGGTAGA	GGGTCTGTCT	TGNGCCCCCC	CAGACTCTAG	CCCAGAGAGT	GCAGCCACCT	3780
	ACTGCCCCAC	CTCAGAGAAG	TGCAGCGGGA	AGGAGGCTGG	AGGTGGTGCG	CGCGTGCCTC	3840
35	GGGTGTCTGC	GTGAATGAGC	GTGGCCAAGG	ACCAGTGCCA	CCTCATGGCA	AAGAGCTCCC	3900
	GCAGTGTTTG	TTAGAGTGCA	CATCCTACGT	GCCCACTGGC	ACACACACGT	GCTCACATAC	3960
	ANGTCNGNCT	ACAGGNGTAC	ACATGCANGC	TTGCACACAT	GCACACAGAC	CACATAGCAC	4020
	ACATGTGCAC	TGACACACAT	TGTATAGACC	ATGCACAGTA	CACATACGTG	CATACACATG	4080
	CCTGCATACA	GGCATACACA	TGCACGCTTA	CATGTACACG	TGCACAGATC	ACACACATGC	4140
40	ACACACGTGT	AGCTCACACA	CAGTATACAC	ATACACAAGT	GCACAGACCA	CACACAGCAC	4200
	TAACACATGC	ACACACAAAG	TGCATAGGCC	ACACAGCACA	TGCACACAGG	TGCACAGACC	4260
	ACACAGCACA	CACAAGTGCA	CAGAGCACAC	TGCACACATG	CACACACACA	CGCGTGCATG	4320
	CACACTCCTC	CGACTTCCAG	CCTTGAGGCC	CTTCTGTCTC	TGGTCTTTCT	CTTTGACCCT	4380
	GCTGAGTGTA	AGCTGCCTGG	GGAGGGGCTA	CAAGGAGTAA	TTGTGGCTTT	AGGGGTCTGT	4440
45	GTGATGCTGG	AATGTCAAGC	GCCGTCTGTG	GGTATCCGAC	TGTCCGGGCT	CCTGGTCCGC	4500
	AGTGGCAGAG	CGCCAGGCAG	AGCCAAATCAG	GGTCTCGTGC	TGCCCTTCCC	CCCCACAGCC	4560
	TGGCAGCCAT	CCAGAGGAGG	GGCTCTACCA	GATGCCAAGG	TGCCCCGGTG	TCTGTATGGG	4620
	TGTCCGGTTG	GGTCTCTGT	TTGGTCTGCC	CTGGAGGTGG	CTGGGCCCTC	CTGGGATGGG	4680
	TGGCTCAGCC	TGGAATCCCA	GGCCCCAGCC	CAGGCAGGTG	CTGCTGCCTG	TTGTGGTTTC	4740
50	CTGGCCCGAG	TTCTCTCTCT	CCCTCTGCAT	AAAATCACAG	TCCGTGAGTC	TTCCAGCTGC	4800
	CACACCGGCT	GGGACACGCT	GGGGGAGGGC	TCCTCCCATG	CCTCTGTCAC	ACAGCCGTCT	4860
	GAGCAGGGCA	GGTGCCAACA	CCCCCACCCG	GAGACACGCT	GCCCCCTCAGC	GATGCCCTTA	4920
	CCTTTGGGGG	GGCCTCGTCT	CAAGCCCCCC	CTTGGAGGCT	GAATACACCC	CAGGCACTGT	4980
	GAGGGCTTCT	CCAGGGGGAC	ACCCTTTGAG	CTGTGGGTCT	GATCACCCCA	AGTCCCGCAC	5040
55	ACGGAGGAGA	GGCAGAGCCA	GGGCGTGTGG	TTTAATGTTT	GCCCCCTCGG	GGCTGGAGGT	5100
	CTCAGTGTTC	CTAGATTCCA	GACCCTGCTG	CCAGAGAGAC	CTGCTGCCGG	AGAGAAGGGG	5160
	AGGAGGACTC	CAGCTGGGCT	CGGTCCCCCA	CAGTCAGGGA	CCCCCATAAA	GGACACCCCC	5220
	TTCTCTCTAG	AAAGAGCTGG	GCTCTCAGCT	ATTCTTAGTT	GCTTCCAGTA	AGCCGAGGAG	5280
	CAGAAGGAGC	TGTGAGAGCT	TTGCAGAAAC	GCCCTTGTCC	CCGCCCTCCT	GAGCTATGAA	5340
60	TGCCGTACAG	AGCAGAGGCT	GGGCGATTGG	CAAGATCACA	GGTGTATGCT	GCACAGCCCC	5400
	ATTGACACAA	ACCCTCAAAG	CAGACGTGAG	AGGGACGGTT	CACAAAGCTT	GGACCTGCCG	5460
	TGGAGGGTGC	CCGCAGACCG	TGGCGTGAGA	GGGACGGCTC	ACGAGGCTTG	GACCTGCTGT	5520
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	GGGTGCCCGG	CAGACGTGGT	GTGAGAGGGA	CGGCTCACAG	GGCTTGGACC	GGAGAGAGAT	5640
65	GGCTCATGAG	ACTTGGACCT	GCCGTGGAGG	GTGCCAGCA	GACGTGGTAT	GAGAGGGATG	5700
	GCTCACGAGG	CTTGGACCTG	GTGGAGGGTG	CCCGGCAGAC	GTGTGAGAGG	GACGGTTTAC	5760
	AAGGCTTGGA	CCTGCCATGG	AGGGTGCCCA	GCAGACGTGG	TGTGAGAGGG	ACAGCTCACG	5820
	AGGCTTGAGC	CTGCCGTGGA	GGGTGCCCAG	CAGGGGGCTG	AGCTCTGAGG	GGTGGGTGCT	5880
	CAGTGCAOCC	GTGCCCCAG	TGTCTCTGTA	TCTGTCTCGG	TGCCTCCCCC	AACCCCCACA	5940
70	CCCATGCAGA	ACTCCCAGGT	CACATGCACG	TATGTCCAGG	GCATGGGGGT	GGCGTGAAGA	6000
	GGCCTGGTCA	GGGCCCTTAG	GGGCTGCAGG	ACGGAATGGC	CACCTGGGGA	GCCTGTGTGG	6060
	CTGTGCCGGG	CAGCCATCCT	GCAITCCCCAC	CCAGCGCGCA	GTCTCCACCT	CGGCCCCAGC	6120
	AAAGCGCTAA	GCAGCCGGAG	AGACAGCCAG	GGCGGCTTCC	TGAAGGATGT	GGGATGGTGG	6180
	ACTCCGGGGT	CGAGGGAATA	CGCAGGTTCC	TGTCTCCCGG	GAGACCTAGA	GAAGCTGCAC	6240
75	ACCCAGGAGC	TTTCCATGAC	CCGGGAGCAT	GAGTGAATGG	GGGGTTCCAG	TTTGTGAAC	6300
	TTTGCTGTCT	TGTAAGGGTG	GGGGCTGACG	GCCGACCCCTG	GGAGGAGGTG	ACACCCGAGG	6360
	GGGAGGTTGT	GGGCAACGGT	GGAGGAGGAG	AGACGGGAGG	GGACCATTTG	GGATGGAGGG	6420
	GCCTCTCAG	AGTTTAAAAA	GGCGTTTGTG	GGGTGGAGTT	GAGTGTGCTC	TGGGCTTGA	6480
	CACTTGCCCT	GGTGCCCCCTG	GCTGGCCGAG	GAGACTGGCT	CTGGCCAGGG	CCCCGTCTCTG	6540
80	AGAGGTCCCT	AGCGTCTGAC	TCTCGGCCAG	GCGCCAGCAA	GGAGGGGCCG	GTCCCCGGGG	6600
	CTACCAGGCA	GGCAGCTGCA	CATCGCCATC	GCCACAGCCC	AACTCCGCTT	GGGTTTATCA	6660
	AAGTCGTTGC	CTTAATGTCAT	GTGGACAGGA	ACTCCCTGAG	GTGCCCCCAT	GGCCCCCTGGC	6720
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Seq ID NO: 282 Protein sequence
 Protein Accession #: NP_004509.1

1 11 21 31 41 51
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 SSEGALYILE IVTIVVFGVE YFVRIWAAGC CCRYRGWRGR LKFARKPFCV IDIMVLIASI 180
 AVLAAGSQGN VFATSLRSL RFLQILRMIR MDRRGGTWKL LGSVVYAHSK ELVTAWYIGF 240
 LCLILASFLV YLAEKGENDH FDTYADALWV GLITLTITIGY GDKYPQTWNG RLLAATFTLI 300
 GVSFFALPAG ILGSGFALKV QEOHRQKHE KRRNPAAGLI QSAWRFYATN LSRTDLHSTW 360
 QYYERTVTVP MYRLIPPLNQ LELLRLNLSK SGLAFRKDPP PEPSPSQKVS LKDRVFSPPR 420
 GVAAGKKGSP QAQTVRSPS ADQSLSDSPS KVPKSWFSGD RSRARQAFRI KGAASRQNSE 480
 EASLPGEDIV DDKSCPCBEV TEDLTPGLKV SIRAVCMVRF LVSKRKFKES LRPYDVM DVI 540
 EQYSAGHLDM LSRIKSLQSR VDIIVGRGPA ITDKDRTKGP AEAELPEDPS MMGRLGKVEK 600
 QVLSMEKKLD FLVNIYMQRM GIPPTETEAY FGAKEPEPAP PYHSPEDSRE HVDHRHCIVK 660
 IVRSSSTGQ KNFSAPPAAP PVQCPPSTSW QPQSHPRQGH GTSPVGDHGS LVRIPPPFAH 720
 ERSLSAYGGG NRASMEFLRQ EDTPGCRPPE GTLRSDTSI SIPSDHEEL ERSFSGFSIS 780
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 GPRK

Seq ID NO: 2838 DNA sequence
 Nucleic Acid Accession #: AF152496.1
 Coding sequence: 1..2391

1 11 21 31 41 51
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 GCGAGGGGGG CCCAAGTTGT GTCCAAAGGG AACAAACAGC ATTTTCAGCT CAGTCATCAG 240
 ACAGGTGATT TGCTCCTGAA TGAGAAATTG GACCGGGAGG AGCTATGCGG CCCCACAGAA 300
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 CTCCTGATCA TAGATGTAAA TGACCATTTCT CCGGTATTCT TTGAAAATGA AATGCATCTG 420
 AAAATCTTAG AAAGCACTCT GCCAGGAACA GTAATTCCTT TGGGAAATGC TGAGGACTTG 480
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 CTCCTCGCA GTCGTAGGGA CGGAAGGAAG TACCCGGAAC TAGTACTGGA TAAAGCGCTC 600
 GATCGGGAGG AGCAGCCGGA ACTCAGCTTA ACGCTCACCG CGCTGGACGG CGGCTCTCCC 660
 CCTCGTCTG GACAGGCCCA GATAAACATC CAGGTCTTAG ATATAAACGA CAATGCACCA 720
 GAATTGTCAC AGCCGCTCTA TGAGGTTGCA GTTCTAGAGA ATACCCCGGT TAACTCTGTC 780
 ATTGTCACTG TCTCGGCTTC TGACTTAGAT ACAGGAAGTT TTGGGACAAT ATCATATGCA 840
 TTTTTCATG CTCTGGAAGA AATTCGCAAA ACTTTTCAGC TAAATCCAAT TACTGGTGAT 900
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 AACGACAACC CACCGGAAC TACCTTGTCT TCAGTAAACA GCCCTATTCC TGAGAACTCG 1080
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Seq ID NO: 284 Protein sequence
 Protein Accession #: AAD43757.1

1 11 21 31 41 51
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 5 EFAQPLYEVA VLENTPVNSV IIVTASASDL TGSFGTISYA FFHASEEIRK TFQLNPITGD 300
 MQLVKYLNEF AINSYFVDIE AKDGGGLSGK STVIVQVVDV NDNPPELTSL SVNSPIPIENS 360
 GETVLAVFSV SLDLSDGNGR VMCSIENMLP FFLKPSVENF YTLVSEGLD RETRSEYNIT 420
 ITITDLGTPR LKTKYNITVL VSDVNDNAPA FTQISYTLFV REMNSPALHI GSVSATDRDS 480
 GTNAQVTYSL LPPQDPHLPL SSLVSNADN GHLFALRSLD YEALQAFEFV VGATDRGSPA 540
 10 LSSEALVRVL VLDANDNSPF VLYPLONGSA PCTELVPRAA EPGYLVTKVV AVDGDGSGQA 600
 WLSYQLLKAT EPLFLGVWAH NGEVRTARLL SERDAAKHRL VVLVKDNGEP PRSATATLHV 660
 LLVDGFSQPY LPLPEAAPAQ AQADLLTVYL VVALASVSSL FLFSVLLFVA VRLCRRSRAA 720
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Seq ID NO: 285 DNA sequence
 Nucleic Acid Accession #: NM_001794.2
 Coding sequence: 15..2765

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 35 AGGTGGAGAA TACAGCTGAC CTGTACATCT ACCTCATCGA CATGAATGAC AACCCTCTG 840
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 AGACTGGAGA TATCGTCAAC GTGGCGGCTG GCCTGGACCG AGAGAAAGTT CAGCAGTACA 1080
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 40 CCACAGCCAT CATCACGGTG ACAGATGTGA ATGACAACCC GCCAGAATTT ACCGCCAGCA 1200
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 65 ACCCCACGGC ACCCCCTAT GACTCCCTGC TGGTCTTCGA CTACGAGGGG AGCGGCTCCA 2640
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 AAG

Seq ID NO: 286 Protein sequence
 Protein Accession #: NP_001785.2

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 80 VAQTSSPSPHK HKPQKGKKVV ALDPSPPPKD TLLPWPQHQN ANGLRRRKRD WVIPPINVE 180
 NSRGPPFPQQL VRRISDKDND IPIRYSITGV GADQPPMEVF SIDSMSGRMY VTRPMDREEH 240
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 ANDADDSTTA NGMVRYRIVT QTPQSPSQNM FTINSETGDI VTVAAGLDRE KVQYTVIVQ 360

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 LQIYLIDIND NApELLPKEA QICEKPNLNA INITAADADV DPNIGPYVFE LPFVPAVRK 660
 NWTITRLNGD YQSLRLRILY LEAGMYDVPI IVTDSGNPPL SNTSIKVKV CPCDDNGDCT 720
 TIGAVAAAGL GTGAIVAILI CILILLTMVL LFMVMMKRRE KERHTKQLLI DPEDDVRDNI 780
 LKYDEEGGGE EDQDYDLSQL QQPEAMGHVP SKAPGVRRVD ERPVGAEPQY PIRPMVPHFG 840
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 PRFKKLADMY GGGEBD

Seq ID NO: 287 DNA sequence
 Nucleic Acid Accession #: AF152495.1
 Coding sequence: 1..2397

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 AGGCAGACCG GGAATTGTGT GTTAAATGAG AAATTGGACC GGGAGGAGCT GTGCGGCCCC 300
 ACAGAGCCCT GTGTCTTACC TTTCAGGTG TTAAGAGAAA ATCCCTTGA GTTTTTCAG 360
 GCGGAGCTAC GGATTAGGGA CGTAAATGAT CATTCCCCAG TTTTCTAGA CAAAGAAATA 420
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 GACTCGGGCA CCAACGCCCA GGTACCTAC TCGCTGCTGC CGCCCCAGGA CCGCACCTG 1500
 CCCTCGCCT CCCTGGTCTC CATCAACGCG GACAACGCGC ACCTGTTGCG TCTCCAGTCG 1560
 CTGGACTAG AGGCCCTGCA GCGGTTGAG TTCCGCTGG GCGCCGAGA CCGCGGCTCC 1620
 CCGCGGTTGA GCAAGGAGGC GCTGGTGCGC GTGCTGGTGC TGGACGCCAA CGACAACCTG 1680
 CCCTTCTGTC TGTACCGCTC GCAGAACGCG TCCGCGCCTC GCACCGAGCT GGTGCCCGG 1740
 GCGGCGGAGC CCGGCTACT GGTGACCAAG GTGGTGGCGG TGGACGGCGA CTCGGGCGCA 1800
 AACGCCTGGC TGTGCTACCA GCTGCTCAAG GCCACGGAGC CCGGCTGTT CCGGCTGTG 1860
 GCGCACATG GCGAGGTGCG CACCGCCAGG CTGCTGAGG AGCGCGAGC TGCCAAGCAG 1920
 AGGCTGGTGG TCGAGGTCAA GGACAATGGC GAGCCTCCGC GCTCGGCCAC CGCCACGCTG 1980
 CACGTGCTCC TGGTGGACGG CTTCTCCAG CCCTACCTGC TGTCTCCGGA GCGGCGACCG 2040
 GCCAGGCCC AGGCCGACTT GCTCACCGTC TACCTGGTGG TGGCGTTGGC CTCGGTGTCT 2100
 TCGCTCTTCC TCTTCTCGGT GCTCCTGTTT GTGGCGGTGC GGCTGTGAG GAGGAGCAGG 2160
 GCGGCTCGG TGGGTGCTGT CTCGGTGCCC GAGGCGCCCT TTCAGGGCA GATGGTGGAC 2220
 GTGAGCGGCA CCGGACCGCT GTCCAGAGC TACCAGTACG AGGTGTGTCT GACTGGAGGC 2280
 TCCGGGACAA ATGAGTTCAA GTTCTGAAG CCAATTATCC CCAACTTCGT TGCTCAGGGT 2340
 GCAGAGAGGG TTAGCGAGGC AAATCCAGT TTCAGGAAGA GCTTTGAATT CACTTAA

Seq ID NO: 288 Protein sequence
 Protein Accession #: AAD43756.1

1 11 21 31 41 51
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 MEAGEGKERV PKQRQVLIFV VLLGIAQASC QPRHYSVAEE TESGSFVANL LKDLGLEIGE 60
 LAVRGARVVS KGKMHLPQFD RQTGDLLENE KLDREELCGP TEPCLVPFQV LLENPLQFFQ 120
 AELRIRDVND HSPVFLDKIE LLKIPESITP GTTFLIERAQ DLDVGTNSLQ NYTISPNEHF 180
 HLNLDQSLDG IILPQLVLNR ALDREEQPEI RLTLTALDGG SPFRSGTALV RIEVDINDN 240
 VPEFAKLLYE VQIPEDSPVG SQVAIVSARD LDIGTNGEIS YAFSQASEDI RKTFRLSAKS 300
 GELLRLQKLD FESIQTYTVN IQATDGGGLS GTCVVFVQVM DLNDNPPELT MSTLINQIPE 360
 NLQDTLIAVF SVSDPDSDGN GRMVCISIQDD LPFFLKPSVE NFYTLVISTA LDRETRSEYN 420
 ITITVDFGT PRKTEHNIT VLVSDVNDNA PAFTQTSYTL FVRENNSPAL HIGSVSATDR 480
 DSGTNAQVTV SLPLPDQPHL PLASLVISINA DNHGLFALQS LDYEAQAFE FRVGAADRG 540
 PALSSEALVR VLVLDANDNS PFVLYPLQNG SAPCTELVPR AAEPGYLVTK VVAVDGDSGQ 600
 NAWLSYQLLK ATEPGLFGVW AHNGEVRTAR LLRERDAAKQ RLVVLVKDN EPPRSATATL 660
 HVLLVDGFSQ PYLLLEPAAP AQQAQDLTLV YLVVALASVS SLFLFSVLLF VAVRLCRRSR 720
 AASVGRCSVP EGFPPGQMD VSGTGLTSQS YQYEVCLTGG SGTNEFKFLK PIIPNFVAQG 780
 AERVSEANPS FRKSFEFT

Seq ID NO: 289 DNA sequence
 Nucleic Acid Accession #: NM_018674.1
 Coding sequence: 390..2009

1 11 21 31 41 51
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	CGGAGCACAT	GCTGAGCGGA	GCGGCTGGGG	CTGCGCGGCG	TGGCGGAGCA	GCGCTCGCTC	60
	CCTCGCTCAC	TGCTCGCTC	GCAGGGACAC	ACGCAGGGGC	TGACAGCTGT	GCTGGTGCTG	120
	ATAAGGGAAG	CCACAGAGGAG	ACGATCGAGG	AGAGAGACAA	GCGGCAGCAG	AGGCAGCAGC	180
5	GGCAGAGGCA	GCACCAGGGC	TGCGGAGCTG	CTGGGAGTGG	GAGTGACTCC	CCCACCTCGG	240
	GCCCCACCC	TGTCCTGTTC	CTCTTCCC	TGCCCCGAG	TTTAGAAGAG	CAGCCGCTGC	300
	CACCACTGCC	ACTCGGGAGG	GCACCAGGGC	TGCTGGCTAG	GGAGGGACAG	GGCAGGGAGG	360
	CTCTGGCCAG	TCCAGCAGC	CGGGACAGA	TGCCGATCGA	GATTGTGTGC	AAAATCAAAT	420
	TTGCTGAGGA	GGATGCGAAA	CCCAAGGAGA	AGGAGGCAGG	GGATGAGCAG	AGCCTCCTCG	480
10	GGGCTGTTGC	CCCTGGAGCA	GCCCCCGGAG	ACCTGGCCAC	CTTTGCCAGC	ACCAGCACCC	540
	TGCATGGACT	GGGCCGGGCC	TGTGGCCAG	GCCCCACGG	ACTGCGCAGA	ACCCTGTGGG	600
	CACTGGCCCT	ACTCACTCG	CTGGCTGCCT	TCCTGTACCA	GGCGCTGGC	CTGGCCCGGG	660
	GCTACCTGAC	CCGGCCTCAC	CTGGTGGCAA	TGGACCCCGC	TGCCCCAGCC	CCAGTGGCGG	720
	GCTTCCCGGC	TGTCACCCCT	TGCAATATCA	ACCGCTTCCG	GCATTGCGCA	CTCAGCGATG	780
	CCGACATCTT	CCACCTGGCC	AATCTGACAG	GGCTGCCCCC	CAAAGACCGG	GATGGGCACC	840
15	GTGCGGCTGG	CTGCGCTAC	CCAGAGCCTG	ACATGGTAGA	CATCTCAAC	CGCACTGGCC	900
	ACCAGCTCGC	CGACATGCTT	AAGAGCTGCA	ACTTCAGTGG	GCATCACTGC	TCCGCCAGCA	960
	ACTTCTCTGT	GGTCTATACT	CGCTATGGGA	AGTGTACAC	CTTCAACGCG	GACCCGCGGA	1020
	GCTCGCTGCC	CAGCCGGGCA	GGGGGCATGG	GCAGTGGCCT	GGAGATCATG	CTGGACATCC	1080
20	AGCAGGAGGA	GTACCTGCCC	ATCTGGAGGG	AGACAAATGA	GACGTCGTTT	GAGGCAGGTA	1140
	TTGCGGTGCA	GATCCACAGC	CAGGAGGAGC	CGCCCTACAT	CCACCAGCTG	GGGTTCGGGG	1200
	TGTCCCCAGG	CTTCAGAGCC	TTTGTGTCTT	GCCAGGAACA	GCGGCTGACC	TACCTGCCCC	1260
	AGCCCTGGGG	CAACTGCCCG	GCAGAGAGTG	AGCTCAGGGA	GCCTGAGCTT	CAGGGCTACT	1320
	CGGCCCTACG	TGTGTCTGCC	TGCGGCTGCG	GCTGTGAAAA	GGAGGCCGTG	CTTCAGCGCT	1380
25	GCCACTGCCG	GATGCTGCAC	ATGCCAGGCA	ATGAGACCAT	CTGCCACCA	AATATCTACA	1440
	TGGAGTGTGC	AGACACACAC	CTGGACTCCC	TGGGTGGGGG	CCCTGAGGGC	CCGTGCTTCT	1500
	GCCCCACCCC	CTGCAACCTG	ACACGCTATG	GGAAAGAGAT	CTCCATGGTC	AGGATCCCCA	1560
	ACAGGGGCTC	AGCCCCGGTAC	CTGGCGAGGA	AGTACAACCG	CAACGAGACC	TACATACGGG	1620
	AGAACTTCTT	GGTCTTAGAT	GTCTTCTTTG	AGGCCCTGAC	CTCTGAAGCC	ATGGAGCAGC	1680
30	GAGCAGCCTA	TGGCTGTGTA	GCCCTGCTGG	GAGACCTCGG	GGGACAGATG	GGCCTGTTC	1740
	TTGGGGCCAG	CATCTCACG	TTGCTGGAGA	TCCTCGACTA	CATCTATGAG	GTGTCTGGG	1800
	ATCGACTGAA	GCGGGTATGG	AGGCGTCCCA	AGACCCCTC	GCGGACCTCC	ACTGGGGGCA	1860
	TCTCCACTTT	GGGGCTTCAG	GAGCTGAAGG	AACAGAGTCC	CTGCCCGAGC	CTGGGCCGAG	1920
	CGGAGGGTGG	GGGGGTTCAG	AGTCTGCTCC	CCAATCACCA	CCACCCCCAC	GGTCCCCCAG	1980
35	GAGGTCTCTT	TGAAGATTTT	GCTTGCTAGG	ACGGTGTCTG	GACTGAAAGG	ACCCAGGAGT	2040
	CTGGGACCCC	TCTTGGGATC	CCCAGCACAT	TCTCTGCTC	CTGGGAGAGG	CCTGGGGGCG	2100
	GTGCTCACTG	GGAGGGCCAG	GACTCAGTTC	CTGCTCTCAT	CCTCCCTGCG	CCTGATGTCA	2160
	GCTGCTTTGC	ACAAAGGTCC	TTCTTGTCCA	CACCCCTTAT	CCCCAGGCTG	GTGCCCCGGG	2220
	AGGGCTGGAG	ACCCAGCCAT	GGGCCCCAC	GGAGAGGAAG	GGAAGGAAGG	AGAGGGAGGG	2280
40	GGAGGATAGA	GCCCATCCCA	GCCGGGGAGG	GGGAGCCCTC	TGTACATTTG	TAAATATTTA	2340
	GGGAAAGCCG	GGTGGGGGGA	GGGGATACAG	ATGTAGAAGG	TGGGTAGGGC	TACAGGGGTG	2400
	GGTGATTTAG	GGACAGCCAG	GGTCCCAGCC	CCAATGTCAG	CAGGATAGGG	AGAGCCCCAG	2460
	GACTCAGGAG	TGCTGGGCTG	GTCTACTTTC	CTGCCCTCT	CCAGGCCCGG	CTCCCTCTT	2520
	GGCAGGGGGA	GGGATGGCTC	CAGCAGGCCT	GGCCAGCTC	CCAGTTCCCC	CTGCACCAAG	2580
45	CCCAACCCCTA	GAGTCCCTTC	TATAGGAGG	GGGCAGGAGA	CCTTCCAGAC	TTCCGGCTGAG	2640
	CTTGAGGGGT	GGGAAGGGAG	CCTTCTCAGT	CCTCTCTCCC	TCCAGTCTGA	TTTTATAAAG	2700
	TGCTGACGAG						

Seq ID NO: 290 Protein sequence
Protein Accession #: NP_061144.1

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	MPIEIVCKIK	FAEEDAKPKE	KEAGDEQSL	GAVAPGAAPR	DLATFASTST	LHGLGRACGP	60
	GPHGLRRLTW	ALALLTSLAA	FLYQAAGLAR	GYLTRPHLVA	MDPAAAPAPVA	GFPVAVTLN	120
55	NRFRHSALSD	ADIFHLANLT	GLPPKDRDGH	RAAGLRYPEP	DMVDILNRTG	HQLADMLKSC	180
	NFSGHHCSAS	NFVVVYTRYG	KCYTFNADPR	SSLPSRAGGM	SGGLEIMLDI	QOEYLPFIWR	240
	ETNETSFPEAG	IRVQIHSQEE	PPYIHQLQFG	VSPGFQTFVS	CQEQLRITYLP	QPWGNCRAES	300
	ELREPELQGY	SAYSVSACRL	RCEKEAVLQR	CHCRMVHMPG	NETICPPNIY	IECADHTLDS	360
60	LGSGPEGPCF	CPTPCNLTRY	GKEISMVRIP	NRGSARYLAR	KYNRNETYIR	ENFLVLVDVFF	420
	EALTSEAMEG	RAAYGLSALL	GDLGGQMLF	IGASILTLLE	ILDYIYEVSW	DRLKRVWRRP	480
	KTPRLRTSTGG	ISTLGLQELK	EQSPCPSLGR	AEGGGVSSLL	PNHHHPHGP	GGLFEDFAC	

Seq ID NO: 291 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62..895

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	TATGATCATC	TTAATTTACT	TATTTCTCTT	GCTATGGGAA	GACACTCAAG	GATGGGGATT	120
70	CAAGGATGGA	ATTTTTCATA	ACTCCATATG	GCTTGAACGA	GCAGCCGGTG	TGTACCACAG	180
	AGAAGCAGCG	TCTGGCAAT	ACAAGCTCAC	CTACGCAGAA	GCTAAGGCGG	TGTGTGAATT	240
	TGAAGGCCGC	CATCTCGCAA	CTTACAAGCA	GCTAGAGGCA	GCCAGAAAAA	TTGATTTC	300
	TGTCTGTGCT	GCTGGATGGA	TGGCTAAGGG	CAGAGTTGGA	TACCCCATTG	TGAAGCCAGG	360
75	GCCCAACTGT	GGATTTGAA	AAACTGGCAT	TATTGATTAT	GGAATCCGTC	TCAATAGGAG	420
	TGAAAGATGG	GATGCTTATT	GCTACAACCC	ACACGCAAG	GAGTGTGGTG	GCGTCTTAC	480
	AGATCCAAG	CAAATTTT	AATCTCCAGG	CTTCCCAAT	GAGTACGAAG	ATAACCAAT	540
	CTGCTACTGG	CACATTAGAC	TCAAGTATGG	TCAGCGTATT	CACCTGAGTT	TTTATGATT	600
	TGACCTTGAA	GATGACCCAG	GTTGCTTGGC	TGATTATGTT	GAAATATATG	ACAGTTACGA	660
80	TGATGTCCAT	GGCTTTGTGG	GAAGATACAT	TGGAGATGAG	CTTCCAGATG	ACATCATCAG	720
	TACAGGAAT	GTCATGACCT	TGAAGTTTCT	AAGTATGCT	TCAGTGACAG	CTGGAGGTTT	780
	CCAAATCAAA	TATGTTGCAA	TGGATCCTGT	ATCCAAATCC	AGTCAAGGAA	AAAATACAA	840
	TACTACTTCT	ACTGGAAATA	AAAACGTTT	AGCTGGAAGA	TTTAGCCACT	TATAAAAAA	900
	AAAAAAGGA	TGATCAAAAC	ACACAGTGTT	TATGTTGGAA	TCTTTTGGAA	CTCCTTTGAT	960

CTCACTGTGA TTATTAACAT TTATTTATTA TTTTCTAAA TGTGAAAGCA ATACATAATT 1020
 TAGGGAAAAT TGGAAAATAT AGGAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC 1080
 ACTGCATAGA AATAACAAGC GTTAACATTT TCATATTTTT TTCTTTTCAGT CATTITTTCTA 1140
 TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTTGCGAT TTGAAATTTT GGAATCCTGC 1200
 TCTATGTACA GTTTGTATAT ATACTTTTA AATCTTGAAC TTTATAAACA TTTTCTGAAA 1260
 TCATTGATTA TTCTACAAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA 1320
 TGTTTTATGC ATTATTTAAG CCGTCTCTTA TTGTTGGAAT TTCAGGTCAT TTTTATAAAT 1380
 ATTGTTGCAA TAAATATCCT TGAACACACA AAAAAAAAAA AA

Seq ID NO: 292 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
 EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCGFQKGTI IDYGI RLNRS 120
 ERWDAYCYNP HAKECGGVFT DPKQIFKSPG FPNEDYDNI QYWHIRLKYG QRIHLSFLDF 180
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDDIIS TGNVMTLKF L SDASVTAGGF 240
 QIKYVAMDPV SKSSQKNTS TTSTGNKNFL AGRFSLH

Seq ID NO: 293 DNA sequence
 Nucleic Acid Accession #: NM_007115.1
 Coding sequence: 69..902

1 11 21 31 41 51
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 CTGACGATAT GATCATCTTA ATTTACTTAT TTCTCTTGCT ATGGGAAGAC ACTCAAGGAT 120
 GGGGATTCAA GGATGGAATT TTTTATAACT CCATATGGCT TGAACGAGCA CCGGGTGTGT 180
 ACCACAGAGA AGCAGCGTCT GGCAAAATACA AGCTCACCTA CGCAGAAGCT AAGCGGTGTG 240
 GTGAATTTGA AGGCGGCCAT CTCGCAACTT ACAAGCAGCT AGAGCCAGCC AGAAAAATTG 300
 GATTTCATGT CTGTGCTGCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA 360
 AGCCAGGGCC CAACGTATGA TTTGGAAAAA CTGGCATTAT TGATTATGGA ATCCGTCCTCA 420
 ATAGGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAAGGAG TGTGGTGGCG 480
 TCTTTACAGA TCCAAAGCGA ATTTTAAAT CTCCAGGCTT CCCAAATGAG TACGAAGATA 540
 ACCAAATCTG CTACTGGCAC ATTAGACTCA AGTATGGTCA GCGTATTAC CTGAGTTTCT 600
 TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA 660
 GTTACGATGA TGTCCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA 720
 TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG 780
 GAGGTTTCCA AATCAAAATAT GTTGCAATGG ATCTCTGTAT CAAATCCAGT CAAGGAAAAA 840
 ATACAAGTAC TACTTCTACT GGAATAAATA ACTTTTATAG TGAAGATTT AGCCACTTAT 900
 AAAAAAAAAA AAGGATGATC AAAACACACA GTGTTTATGT TGGAATCTTT TGGAACCTCT 960
 TTGATCTCAC TGTATTATT AACAATTATT TATTATTTT CTAATATGTA AAGAAATACA 1020
 TAATTATAGG AAAATTGGAA AATATAGGAA ACTTTAAACG AGAAATGAA ACCTCTCATA 1080
 ATCCCACTGC ATAGAAATTA CAAGCGTTAA CATTTTCATA TTTTCTCTT TCAGTCATT 1140
 TTGTATTGT GGTATATGTA TATATGTACC TATATGTATT TGCAATTTGAA ATTTTGGAAAT 1200
 CCTGCTCTAT GTACAGTTT GTATTATACT TTTTAAATCT TGAACCTTAT GAACATTTC 1260
 TGAAATCATT GATTATTCTA CAAAAACATG ATTTTAAACA GCTGTAATAAT ATTCATATGAT 1320
 ATGAATGTTT TATGCATTAT TTAAGCCTGT CTCTATTGTT GGAATTTTCA GTCATTTTCA 1380
 TAAATATTGT TGCAATAAAT ATCCTTCGGA ATTC

Seq ID NO: 294 Protein sequence
 Protein Accession #: NP_009046.1

1 11 21 31 41 51
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 MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
 EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNXGFQKGTI IDYGI RLNRS 120
 ERWDAYCYNP HAKECGGVFT DPKRIFKSPG FPNEDYDNI QYWHIRLKYG QRIHLSFLDF 180
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDDIIS TGNVMTLKF L SDASVTAGGF 240
 QIKYVAMDPV SKSSQKNTS TTSTGNKNFL AGRFSLH

Seq ID NO: 295 DNA sequence
 Nucleic Acid Accession #: NM_001218.2
 Coding sequence: 116..1180

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 CCGGCGCAGC CTGCACCGCG CGGCCGTGCT CCTGCTGGTG ATCTTAAAGG AACAGCCTTC 180
 CAGCCCGGCC CAGTGAACG GTTCCAAGTG GACTTATTTT GGTCTGTATG GGGAGAATAG 240
 CTGGTCCAAG AAGTACCCGT CGTGTGGGGG CCTGCTGCAG TCCCCATAG ACCTGCACAG 300
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 TGCCAACAAG CAGTTTCTCC TGACCAACAA TGGCCATTCA GTGAAGCTGA ACCTGCCCTC 420
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 GGGGAACCCG AATGACCCG ACAGCTCTGA GCACACCGTC AGCGGACAGC ACTTCGCCG 540
 CGAGCTGCAC ATTGTCCATT ATAACCTAGA CCTTATCTT GACGCCAGCA CTGCCAGCAA 600
 CAAGTCAGAA GGCTCGCTG TCCTGGCTGT TCTCATTTGAG ATGGGCTCCT TCAATCCGTC 660
 CTATGACAAG ATCTTCAGT ACCTTCAACA TGTAAAGTAC AAAGGCCAGG AAGCATTCGT 720
 CCGGGATTCC AAGTCAAG AGCTGCTTCC GGAGAGGACC GCTGAATATT ACCGCTACCG 780
 GGGTCCCTG ACCACACCCC CTTGCAACCC CACTGTGCTC TGGACAGTTT TCCGAAACCC 840
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GGACGACCCT TCCCCAGAG AAATGATCAA CAACTTCCGG CAGGTCCAGA AGTTCGATGA 960
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GGGCATCATC CTCTCACTGG CCCTGGCTGG CATTCCTTGGC ATCTGTATTG TGGTGGTGGT 1080
GTCCATTGGG CTTTTCAGAA GGAAGAGTAT CAAAAAAGGT GATAACAAGG GAGTCATTTA 1140
CAAGCCAGCC ACCAAGATGG AGACTGAGGC CCACGCTTGA GGTCCCGGGA GCTCCCGGGC 1200
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CACTTCTGCA GGTATCCCTAC TGCCAACTCT GAATGGAGAG TTTTATCTAC TTCCTCTCT 2280
CTGAAGATGT CAAATCGTGG TTTAGATCAA ATATATTTC AACTATAAAA GCAGGAGGTT 2340
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ATACTCCATA TTCTTCCCGC AATCACACAG ACAGTTTCTG ACAGGCGCAA CTCCTCCATT 2460
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ACCCCTAGTT GAGAGCACTT TGCACTTCCC CGAGAACTTT CTGATTCACA GTCTCATTTT 2580
GACAGCATGA AATGTCTCT TGAAGCATAG CTTTTTAAAT ATCTTTTTC TTCTACTCCT 2640
CCCTCTGACT CTAAGAATTC TCTCTCTGG AATCGCTTGA ACCCAGGAGG CGGAGGTTGC 2700
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AAAAA AAAA

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Seq ID NO: 296 Protein sequence
Protein Accession #: NP_001209.1

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HSDILQYDAS LTPLEFQGVN LSANKQFLLT NNGH5VKLNL PSDMHIQGLQ SRYSATQLHL 120
HWGNPNDPHG SBHTVSGQHF AAEHLIVHYN SDLYPDASTA SNKSEGLAVL AVLIEMGSFN 180
PSYDKIFSHL QHVKYKGQEA FVPGFNIEEL LPERTAERYR YRGSLLTPPC NPTVLWTVFR 240
NPVQISQEQ LLALETALYCT HMDDPSPREM INNFRQVQKF DERLVTYSFS QVQVCTAAGL 300
SLGIILSLAL AGILGICIVV VVSIWLFRRK SIKKGDNKG V IYKPAKMET EAHA

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Seq ID NO: 297 DNA sequence
Nucleic Acid Accession #: NM_006632.1
Coding sequence: 377..1582

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CGGCGCGTGC TGGAGCACCT GACCGCGGAG ATCCTGGAGC TGGCTGGCAA CCGCGCCGCG 120
GACAAGAAGA CCCGCATCAT CTGCGGCAC CTGTAGCTGG CCATTGCGAA CGGCGAGGAG 180
CTTAACAAGC TGCTGGGCGA AGTCACCATC GCGCAGGGCG GTGTCTGCC CAACATTCAG 240
GGCGTGCTTC TGCCCCAGAA GACCAAGAGC CACCACAAGG CCAAGGGTGA AAACCATTC 300
CTAGGAGAGG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCACAG CAAGGGAGAG 360
CAAGAAGCGA CAAGATATGC AAGTGGATGA GACACTGATC CCCAGGAAAG GTCCAAGTTT 420
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ACAAAAATGC ATCATGAACA TCACCATGGT AGCCATGGTC AACAGCACAA GCCCTCAATC 540
CCAGCTCAAT GATTCCTCTG AGGTGCTGCC TGTGACTCA TTTGGTGGCC TAAGTAAAGC 600
CCCAAAGAGT CTTCTGCAA AGTCTCAAT ACTTGGGGGT CAGTTTGCAA TTTGGGAAAA 660
GTGGGGCCCT CCACAAGAAC GAAGCAGACT CTGCAGCATT GCTTTATCAG GAATGTTACT 720
GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTCAATAGT GAAACCCCTG GGTGGCCCTT 780
TGTCTCTAT ATCTTTGGAG GTGTGGCTG TGTCTGTGC CTTCTCTGTT TGTGTTGAT 840
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CTCCTTGAAA CAACAGGTCG GGTCTTCTAA GCAGCCTCT CCCATCAAAG CTATGCTCAG 960
ATCTCTACCC ATTTGGTCCA TATGTTTAGG CTGTTTCAGC CATCAATGGT TAGTTAGCAC 1020
AATGGTTGTA TACATACCAA CTTACATCAG CTCTGTGTAC CATGTTAACA TCAGAGACAA 1080
TGGACTTCTA TCTGCCCTTC CTTTATTGTT TGCCCTGGTC ATAGGCATGG TGGGAGGCTA 1140
TCTGGCAGAT TTCCTTCTAA CCAAAAAGTT TAGACTCATC ACTGTGAGGA AAATTTGCCA 1200
AATTTTAGGA AGTCTCCCTT CTTGAGCACT CATTGTGTCT CTGCCTTACC TCAATTCCGG 1260
CTATATCACA GCAACTGCCT TGCTGACGCT CTCTTGCGGA TTAAGCACAT TGTGTAGTC 1320
AGGGATTTAT ATCAATGCTC TAGATATTGC TCCAAGGTAT TCCAGTTTTC TCATGGGAGC 1380
ATCAAGAGGA TTTTCGAGCA TAGCACTGT CATTGTACCC ACTGTACGCG GATTCTCTCT 1440
TAGTCAGGAC CCTGAGTTTG GGTGGAGGAA TGTCTTCTTC TTGCTGTTG CCGTTAACTT 1500
GTTAGGACTA CTCTTCTACC TCATATTTGG AGAAGCAGAT GTCCAAGAAAT GGGCTAAAGA 1560
GAGAAACTCT ACTCGTTTAT GAAGTTATCC CACCTTGGAT GGAAAAGTCA TTAGGCACCG 1620
TATTGCATRA AATAGAAGGC TTCCGTGATG AAAATACCAG TGAAAAGAT TTTTCTTCTT 1680
GTGGCTCTTT TCAATTATGA GATCAGTTCA TTATTTTAT CAGACTTTT TTTGAGAGAA 1740
ATGTAAGATG AATAAAAT CAAATAAAT GATAACTAAG AAAAAA AAAA

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Seq ID NO: 298 Protein sequence
Protein Accession #: NP_006623.1

1 11 21 31 41 51
 5 MQVDETLIPR KGPSLCSARY GIALVLHFCN FTIAQNVIM NITMVMVNS TSPQSQLNDS 60
 SEVLVPDSFG GLSKAPKSLP AKSSILGGQF AIWEKWGPPQ ERSRLCSIAL SGMLLGCPFA 120
 ILIGGFISSET LGWPFVIFYF GVGVCVCCLL WFWVIYDDPF SYPWISTSEK EYIISSLKQK 180
 VGSSKQPLPI KAMLRSLPIW SICLGCFSHQ WLVTMVVYI PTYISSVYHV NIRDNGLLSA 240
 LPFIVAWVIG MVGGYLDLFL LTKKFRITV RKIATILGSL PSSALIVSLP YLNSGYITAT 300
 10 ALLTLSCGLS TLCQSGIYIN VLDIAPRYSS FLMGASRGFS SIAPVIVPTV SGFLLSQDPE 360
 FGWRNVFFLL FAVNLLGLLF YLIFGEADVQ EWAKERKLTR L

Seq ID NO: 299 DNA sequence
 Nucleic Acid Accession #: NM_003058.1
 Coding sequence: 145..1812

1 11 21 31 41 51
 20 GGCCCTGCCC TGAAGGCTGG TCACTGTCAG AGGTAAACTC CCCTCTTTGA CTCTGCGCCA 60
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 TCGGGCCCTC CTGCTGTCAG GATCATGCCC ACCACCGTGG ACGATGTCCT GGAGCATGGA 180
 GGGGAGTTTC ACTTTTTCCTT GAAGCAAATG TTTTCTCTCT TGGCTCTGCT CTCGGCTACC 240
 TTCGCGCCCA TCTACGTGGG CATCGTCTTC CTGGGCTTCA CCCTGACCA CCGCTGCCGG 300
 AGCCCGGAG TGGCCGAGCT GAGTCTGCGC TCGCGCTGGA GTCTGTCAGA GGAAGTGAAC 360
 25 TACACGGTGC CGGGCCGAGG ACCTGCGGGC GAAGCCTCCC CAAGACAGTG TAGGCGCTAC 420
 GAGGTGGAGT GGAACCCAGG CACCTTTGAC TCGGTGGACC CCCTGGCCAG CCTGGACACC 480
 AACAGGAGCC GCCTGCCACT GGGCCCTGCG CGGGACGGCT GGGTGTACGA GACGCTGGC 540
 TCGTCCATCG TCACCGAGTT TAACCTGGTA TGTGCCAACT CTGGATGTT GGACCTATT 600
 CAGTCATCAG TGAATGTAGG ATTCTTTATT GGCTCTATGA GTATCGGCTA CATAGCAGAC 660
 30 AGGTTTGGCC GTAAGCTCTG CCTCCTAACT ACAGTCTCTA TAAATGCTGC AGCTGGAGTT 720
 CTCATGGCCA TTTCCCAAC CTATACGTGG ATGTTAATTT TTCGCTTAAT CCAAGGACTG 780
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 TATCGGAGAA CAGTGGGGAT TTTTACCAA GTTGCCTATA CAGTTGGGCT CTGGTGCTA 900
 GCTGGGGTGG CTTACGCACT TCCTCACTGG AGGTGGTTGC AGTTCACAGT TGCTCTGCCC 960
 35 AACTTCTTCT TCTTGCTCTA TTACTGGTGC ATACCTGAGT CTCCAGGTG GCTGATCTCC 1020
 CAGAATAAGA ATGCTGAAGC CATGAGAATC ATTAAGCACA TCGCAAAGAA AAATGGAAAA 1080
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 45 ATGTGTGACA TTGGTGGCAT CATCACGCCA TTCCTGGTCT ACCGGCTCAC TAACATCTGG 1620
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 CCAATGAAGT AAGAAGAGAG ACCGTTGCTG CTGTATGAC CTAGCTTTGA TGGCAGCAAG 1860
 50 ACCAAAAGTA GAAATCCCTG CACTCATCAC AAAGCCCATC CAACTCAACC AAATTTACCC 1920
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 CATTGGACAT TGGTTTTCTG GAGGTTTTTT TTTCCGATCT TTGTATTTT TTAATTTGA 2100
 55 TTCTTTTCTT TGCAATGCTA GCAACCAGAA TACATAGGGG AACTGTGGGC TAGGCAANA 2160
 AAATAGAAAA AGTGTGAAAA ACAGTAAAGT TGGGAGAGGA GCATCTATTT TCTTAAGAA 2220
 ATAAACACC NAAACAAAA AAAAAAATA AAAAAA

Seq ID NO: 300 Protein sequence
 Protein Accession #: NP_003049.1

1 11 21 31 41 51
 60 MPTTVDDVLE HGGEFHFQK QMFFLLALLS ATFAPYVGI VFLGFTPDHR CRSPGVAELS 60
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 65 PCRDWVYET PGSSIVTEFN LVCANSWMLD LFQSSVNVGF FIGSMSIGYI ADRFGRKLCL 180
 LTTVLINAAA GVLMAISPTY TWMLIFRLIQ GLVSKAGWLI GYILITEFVG RRYRRTVGIF 240
 YQVAYTVGLL VLAGVAYALP HWRWLQFTVA LPNFFFLYY WCIPESPRWL ISQNKNAEAM 300
 RIKHIAKKN GKSLEPASLQR LRLEETGKK LNPSFLDLVR TPQIRKHTMI LMYNWFTSSV 360
 LYQGLIMHMG LAGDNIYLDY FYSLVEFPA AFMIILTIDR IGRYPWAAS NMVAGAACLA 420
 70 SVFIPGDLQW LKIIISCLGR MGITMAYEIV CLVNAELYPT FIRNLGVHIC SSMCDIGGII 480
 TPFLVYRLTN IWLEPLMVF GVLGLVAGGL VLLLPEKTKG ALPETIEEAE NMQRPRKNKE 540
 KMILYQVQKL DIPLN

Seq ID NO: 301 DNA sequence
 Nucleic Acid Accession #: NM_012206.1
 Coding sequence: 52..1131

1 11 21 31 41 51
 80 GTTACCCAGC ATTGTGAGTG ACAGAGCCTG GATCTGAACG CTGATCCCAT AATGCATCCT 60
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 GTTGGTGGAG AGGCAGTCC ATCTGTACA CTACCTGCC ACTACAGTGG AGCTGTACA 180
 TCAATGTGCT GGAATAGAGG CTCATGTTCT CTATTCACAT GCCAAATGG CATGTCTGG 240
 ACCAATGGAA CCCACGTAC CTATCGGAAG GACACACGCT ATAAGCTATT GGGGGACCTT 300
 TCAAGAAGGG ATGTCTCTTT GACCATAGAA AATACAGCTG TGTCTGACAG TGGGTATAT 360

TGTGTCCGTG TTGAGCACCG TGGGTGGTTC AATGACATGA AAATCACCGT ATCATTTGGAG 420
 ATTGTGGCAC CCAAGGTCAC GACTACTCCA ATTGTACAAA CTGTTCCAAC CGTCACGACT 480
 GTTCGAACGA GCACCACTGT TCCAACGACA ACGACTGTTC CAACGACAAC TGTTCACAACA 540
 ACAATGAGCA TTCCAACGAC AACGACTGTT CCGACGACAA TGACTGTTTC AACGACAACG 600
 AGCGTTCCAA CGACAACGAG CATTTCAACA ACAACAAGTG TTCCAGTGAC AACAACGGTC 660
 TCTACCTTTG TTCTTCCAAT GCCTTTGCCC AGGCAGAAC ATGAACCACT AGCCACTTCA 720
 CCATCTTCAC CTCAGCCAGC AGAAACCCAC CCTACGACAC TGCAGGAGC AATAAGGAGA 780
 GAACCCACCA GCTCACCATT GTACTCTTAC ACAACAGATG GGAATGACAC CGTGACAGAG 840
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 ACGGCCAATA CCACTAAGG AATCTATGCT GGAGTCTGTA TTTCTGTCTT GGTGCTTCTT 960
 GCTCTTTTGG GTGTCATCAT TGCCAAAAAG TATTTCTTCA AAAAGGAGGT TCAACAACATA 1020
 AGTGTTCAT TTAGCAGCCT TCAAATTAAG GCTTTGCAAA ATGCAGTTGA AAAGGAAGTC 1080
 CAAGCAGAAG ACAATATCTA CATTGAGAAT AGTCTTTATG CCACGGACTA AGACCCAGTG 1140
 GTGCTCTTTG AGAGTTTACG CCCATGACTG CAGAAGACTG AACAGGTATC AGCACATCAG 1200
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 AATGTAGTCC TAATTTGTTT TGCTAAAACT GGCTCAATCC TTCTGATCAT TGCAAGTCTT 1380
 TCTCTCAAC ATGAACACTT TAGAATTGTA TGTCTCTTCT AGACCCCAT AATCCTGTAT

Seq ID NO: 302 Protein sequence
 Protein Accession #: NP_036338.1

1 11 21 31 41 51
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 MHPQVVLISL ILHLADSVAG SVKVGGEAGP SVTLPCHYSG AVTSMCWNRG SCSLFTCQNG 60
 IVWNGTHVT YRKTRYKLL GDLRRDVSLS TIENITAVSDS GYVCCRVEHR GWFNDMKITV 120
 SLEIVPPKVT TPIVITVTPT VTTVRTSTTV PTTTIVPTTT VPTTMSIPTT TTVPTTMTVS 180
 TTTSVPTTTS IPTTTSVPTV TTVTFVFPFM PLPRQNHPEV ATSPSSPQPA ETHPTTLQGA 240
 IRREPTSSPL YSYTTDNDNT VTSSDGLWN NNQTLFLFH SLLTANTTKG IYAGVCISVL 300
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Seq ID NO: 303 DNA sequence
 Nucleic Acid Accession #: NM_001044.1
 Coding sequence: 129..1991

1 11 21 31 41 51
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 TCCAGCTGCT GCACAGACAC CGTGAGCTCT TCACGCTCTT CATCGTCTCT GCGACCTTCC 1500
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 ACAAGTTCTG CAGCCTGCCT GGGTCTTTTC GAGAGAACT GGCCTACGCC ATTGCACCCG 1920
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 TCAAGGTGTA GAGGGAGCAG AGACGAAGAC CCCAGGAAGT CATCCTGCAA TGGGAGAGAC 2040
 ACGAACAAAC CAAGGAATC TAAGTTTCGA GAGAAAGGAG GGCAACTTCT ACTCTTCAAC 2100
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5 AGGAGCATGT CCTATCCCTG GACGCATGCA GGGCCCCCAC AGGAGCGTGT ACTACCCACG 2880
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 GCGGCTTCCC ATGTGCTTC TGGGGAGGGA CACAGAGGAC AGTTTCCCCA TGCCTTCTG 3780
 GTTGTGAAG ACAGCACAGA GAGCGGCTTC CCCATCGCCT TCTGGGGAGG GGCTCCGTGT 3840
 AGCAACCCAG GTGTTGTCCG TGTCTGTGA CCAATCTCTA TTCAGCATCG TGTGGGTCCC 3900
 20 TAAGCACAAT AAAAGACATC CACAATGGAA AAAAAAAG GAATTC

Seq ID NO: 304 Protein sequence
 Protein Accession #: NP_001035.1

25 1 11 21 31 41 51
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 30 GQFNREGAAG VWKICPILKG VGFTVILISL YVGFYFNVII AWALHYLFSS FTTELPIWIC 180
 NNSWNSPNCB DAHPGSSGD SSGLNDTFGT TPAAEYFERG VLHLHQSHGI DDLGPPRWQL 240
 TACLVLVIVL LYFSLWKGVK TSGKVVNITA TMPYVVLTA LRGVTLPGA IDGIRAYLSV 300
 DFYRLCEASV WIDAATQVCF SLGVGFGVLI AFSSYNKFTN NCVDAIVTT SINSLSFS 360
 GFVVFSFLGY MAQKHSVPIG DVAKDGPGLI FIYPEAIAT LPLSSAWAVV FFIMLLTLGI 420
 DSAMGMESV ITGLIDEFQL LHRHRELFTL FIVLATFLLS LFCVTNGGIY VFTLLDHFAA 480
 35 GTSILFGVLI EAIGVAFYFG VQGFSDDIQ MTGQRPSLYW RLCWKLVSPC FLFFVWVSI 540
 VTRFRPHYGA YIFPDWANAL GWVIATSSMA MVPIYAYKF CSLPGSFREK LAYIAPEKD 600
 RELVDRGEVR QFTLRHWLKV

Seq ID NO: 305 DNA sequence
 Nucleic Acid Accession #: NM_001216.1
 Coding sequence: 43..1422

45 1 11 21 31 41 51
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 CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCAGAGGT TGCCCCGGAT GCAGGAGGAT 180
 50 TCCCTCTGGG GAGGAGGCTC TTCTGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCC 240
 AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGAG AGGAGGATCT ACCTGGAGAG 300
 GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAATACAGA AGAAGAGGGC 360
 TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCAG 420
 AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480
 55 CCGCCCTGGC CCGGGGTGTC CCCAGCTGC CGGGGCGCT TCCAGTCCC GGTGGATATC 540
 CGCCCCCAGC TCGCCGCTT CTGCCCGGCC CTGGCGCCCC TGGAACTCCT GGGCTTCCAG 600
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 CCTCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT CTGACTGCAT 720
 60 CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC 780
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 TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAA 1080
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 65 GAGGCCTCCT TCCCTGTGCG AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
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 GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA 1440
 70 TGTGAGAAAG CAGCCAGAGG CATCTGAGG GAGCCCGGTA ACTGCTCTGT CTGCTCATT 1500
 ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTTATA AT

Seq ID NO: 306 Protein sequence
 Protein Accession #: NP_001207.1

75 1 11 21 31 41 51
 MAPLCPSPWL PLLIPAPAPG LTVQLLSLL LMPVHPQRL PRMQEDSPLG GSSGEDDPL 60
 GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPFVKP KSEBEGSLKL EDLPVEAPG 120
 DPQEPQNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180
 80 ELLGQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240
 VEGHRFPABE HVVHLSTAFR RVDEALGRPG GLAVLAAFLB EGPEENSAYE QLSRLLEIA 300
 EEGSETQVPG LDISALLPSD FSRFYQYEGS LTPPCAQGV IWTVFNQTV LSAKQLHTLS 360
 DTLWGPDSR LQLNFRATPD LNRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420
 GLLFAVTSVA FLVQMRQRH RGTGKGVSYR PAEVAETGA

Seq ID NO: 307 DNA sequence
Nucleic Acid Accession #: NM_003039.1
Coding sequence: 76..1581

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5      1      11      21      31      41      51
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GTGCTTGCCC TGGCAACCCCT GATAGCTGCC TTTGGGTCTC CCTTCCAGTA TGGGTACAAC 180
10    GTGGCTGCTG TCAACTCCCC AGCACTGCTC ATGCAACAAT TTACAATGA GACTTACTAT 240
GGTAGGACCG GTGAATTCAT GGAAGACTTC CCCTTGACGT TGCTGTGGTC TGTAAACCGTG 300
TCCATGTTTC CATTGTGAGG GTTTATCGGA TCCTCTCTGG TCGGCCCTCT GGTGAATAAA 360
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15    GGAATATGTG CAGGTGTATC TTCCAACGTG GTCCCCATGT ACTTAGGGGA GCTGGCCCCCT 540
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CTGGGGCTGA CCGGGGCTCC CGCGGCGCTG CAGCTCCTTC TGCTGCCCTT CTCCCCGAG 720
20    AGCCCCAGGT ACCTGCTGAT TCAGAAGAAA GACGAAGCGG CCGCCAAGAA AGCCCTACAG 780
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25    GTGGAGCTCC TGGGTCCGAG GCTGCTGCTG CTGCTGGGCT TCTCCATCTG CCTCATAGCC 1140
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AGCATCGTCT GTGTCACTCT CTACGTCATA GGACATGCCC TCGGGCCCGG TCCCATACCC 1260
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30    GGCCTCGGCC CGTACAGCTT CATGTCTTTC GCCGTGATCT GCCTCCCTAC CACCATCTAC 1440
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ACCAAGATGA ATAAGGTGTC TGAAGTGTAC CCGGAAAAGG AGGAACGTAA AGAGCTTCCA 1560
CCTGTCACTT CGGAACAGTG ACTCTGGAGA GGAAGCCAGT GGAGCTGGTC TGCCAGGGGC 1620
35    TTCCCACTTT GGCCTATTTT TCTGACTTCT AGCTGTCTGT GAATATCCAG AAATAAAACA 1680
ACTCTGATGT GGAATGCAGT CCTCATCTCC AGCCTCCCCA CCCCAGTGGG AACTGTGCAA 1740
AGGGCTGCCT TGCTGTCTCT GAAGCTGGGC TGTCTCTCTC CATGTTGGCC TGTCAACAGA 1800
CCCGAGTCAA TTAACAGCTT GGTCTCCAC TTTGCTGGTT CAGCCTTCGT GTGGCTCTG 1860
GTAACGTGGC TCCACCTTGA TGGGTCAACC TTTGTGTGGC TCCTGGTAAC ATAACAACA 1920
40    CAGTTACTAT AGTGGTGAGA TGAAGGAAT CAAATTTTGC CAGAGAAACT AACTCGGTGG 1980
CCCCAACAGG TCTTCCGGGG CCATGGGCAT TTGTTTAGAG CCAAAATCAT CCTCTTACCA 2040
GATCCTTTTC CAGAAATACC TGTCTAGGAA GGTGTGATGT CAGAAACAAT AACATCCAGA 2100
AAGCTGAGGA ACAGGTTCTT GTGGAGACAC TGAGTCAGAA TTCTTCATCC AAATATTTT 2160
GTTAGTGAA AATGGAATTG CTTCTGTGTA GTCATAAAA TGAACCTGAT CACTTTTC

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Seq ID NO: 308 Protein sequence
Protein Accession #: NP_003030.1

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1      11      21      31      41      51
|      |      |      |      |      |
MEQQDQSMKE GRLTLVLALA TLIAAFGSSF QYGVNVAAVN SPALLMQQFY NETYYGRTGE 60
FMEDFPLTLL WSVTVSMPEF GGFIGSLLVG PLVNKFGRRK ALLFNNIFS I VPAILMGC SR 120
VATSFELIII SRLLVGICAG VSSNVVPMYL GELAPKNLRG ALGVVPQLFI TVGILVAQIF 180
GLRNLLANVD GWPILLGLTG VPAALQLLLL PFFPESPRYL LIQKDEAAA KKALQTLRGW 240
55    DSVDRVAAEI RQEDBAEKAA GFISVLKFLR MRSRLRWQLS IIVLMGGQQL SGVNAIYYA 300
DQIYLSAGVP BEHVQYVMTF TGAVNVMTF CAVFVVELLG RRLLLLLGFS ICLIACCVLT 360
AALALQDTSV WMPYISIVCV ISYVIGHALG PSPIPALLIT EIFLQSSRPS AFMVGGSVHW 420
LSNFTVGLIF PFIQGLGPHY SFIVFAVICL LTTIYIFLIV PETKAKTFIE INQIFTRMKN 480
VSEVPEKEEE LKELEPPVTSE Q

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Seq ID NO: 309 DNA sequence
Nucleic Acid Accession #: NM_001252.1
Coding sequence: 138..719

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1      11      21      31      41      51
|      |      |      |      |      |
GGCTGGTCCC CTGACAGGTT GAAGCAAGTA GACGCCAGG AGCCCCGGA GGGGGCTGCA 60
GTTTCCTTCC TTCCTTCTCG GCAGCGCTCC GCGCCCCAT CGCCCTCTCT GCGCTAGCGG 120
AGGTGATCGC CGCGGCGATC CCGGAGGAGG GTTCGGGCTG CTCGGTGCGG CGCAGGCCCT 180
70    ATGGGTGCGT CTGCGGGGCT GCTTTGGTCC CATTGGTTCG GGGCTTGGTG ATCTGCCTCG 240
TGGTGTGCTC CCAGCGCTTC GCACAGGCTC AGCAGCAGCT GCCGCTCGAG TCACTTGGGT 300
GGGAGCTAGC TGAGCTGTCG CTGAATCACA CAGGACCTCA GCAGGACCCC AGGCTATACT 360
GGCAGGGGGG CCAGGACTG GCGCGCTCCT TCCTGCATGG ACCAGAGCTG GACAAGGGGC 420
AGCTACGTAT CCATCGTGAT GGCATCTACA TGGTACACAT CCAGGTGACG CTGGCCATCT 480
GCTCCTCCAC GACGGGCTCC AGGCACCACC CCACCACCCT GGCCGTGGGA ATCTGCTCTC 540
75    CCGCCTCCCG TAGCATCAGC CTGCTGCGTC TCAGCTTCCA CCAAGGTTGT ACCATTGCCT 600
CCAGCGCCTT GACGCCCCG GCCCGAGGGG ACACACTCTG CACCAACCTC ACTGGGACAC 660
TTTTGCCTTC CCGAAACACT GATGAGACCT TCTTTGGAGT GCAGTGGGTG CGCCCTGAC 720
CACTGCTGCT GATTAGGGTT TTTTAAATTT TATTTTATTT TATTTAAGTT CAAGAGAAAA 780
80    AGGTGACACA CAGGGGCCAC CCGGGGTTGG GGTGGGAGTG TGGTGGGGGG TAGTGGTGGC 840
AGGACAAGAG AAGGCATTGA GCTTTTTCTT TCATTTTCCT ATTAAAAA

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Seq ID NO: 310 Protein sequence
Protein Accession #: NP_001243.1

1	11	21	31	41	51	
MPEEGSGCSV	RRRPFYGCVL	AALVPLVAGL	VICLVVCIQR	FAQAQQQLPL	ESLGWDVAEL	60
QLNHTGFPQD	PRLYWQGGPA	LGRSFLHGP	LDKGQLRIHR	DGIYMVHIQV	TLAICSSTTA	120
SRHPHTTLAV	GICSPASRSI	SLRLSLFHQ	CTIASQRLTP	LARGDTLCTN	LTGTLLPSRN	180
TDETFPGVQW	VRF					

Seq ID NO: 311 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..3978

1	11	21	31	41	51	
ATGGTGGGTG	AAGGACCCTA	CCTTATCTCA	GATCTGGACC	AGCGAGGCCG	GCGGAGATCC	60
TTTGACAGAA	GATATGACCC	CAGCCTGAAG	ACCATGATCC	CAGTGCGACC	CTGTGCAAGG	120
TTAGCACCCA	ACCCGGTGGG	TGATGCCGGG	CTACTCTCCT	TGCGCACATT	TTCTTGCTCT	180
ACGCCGGTGA	TGGTGAAAGG	CTACCGGCCA	AGGCTGACCG	TAGACACCC	GCCCCATTG	240
TCGACATATG	ACTCATCTGA	CACCAATGCC	AAAAGATTTC	GAGTCCTTTG	GGATGAAGAG	300
GTAGCAAGGG	TGGTCTCTGA	GAAGGCTCT	CTGAGCCACG	TGGTGTGGAA	ATTCCAGAGG	360
ACACGCGTGT	TGATGGACAT	CGTGGCCAAC	ATCCTGTGCA	TCATCATGGC	AGCCATAGGG	420
CCGACAGTTT	TCATTACCA	AATCCTCCAG	CAGACTGAGA	GGACCTCTGG	GAAAGTCTGG	480
GTGGGCAATT	GACTGTGCAT	AGCCCTTTTT	GCCACCGAGT	TTACCAAAAGT	CTTCTTTTGG	540
GCCTTGCCT	GGCCCATCAA	CTACCGCACG	GCCATCCGGT	TGAAGGTGGC	GCTCTCCACC	600
TTGGTTTTTG	AAAACCTAGT	GTCTTCAAG	ACATTGACCC	ACATCTCTGT	TGGCGAGGTG	660
CTCAATATAC	TGTCAAGTGA	TAGCTATTCT	TTGTTTGAAG	CTGCCTTTGT	TTGTCTTTTG	720
CCAGCCACCA	TCCCGATCCT	AATGGTCTTT	TGTGCGCGGT	ACGCTTTTTT	CATTCTGGGG	780
CCACAGCTC	TCATCGGGAT	ATCAGTGTAT	GTCTATTCTA	TACCCGTCCA	GATGTTTATG	840
GCCAAGCTCA	ATTGAGCTTT	CCGAAGGTCA	GCAATTTTGG	TGACAGACAA	GCGAGTTCAG	900
ACAATGAATG	AGTTTCTTGAC	CTGCATCAGG	CTGATCAAAA	TGTATGCCCT	GGAGAAATCT	960
TTTACCAACA	CTATCCAAGA	TATAAGAAAG	AGGGAAGAAA	AATTACTGGA	AAAAGCTGGA	1020
TTTGTCCAAA	GTGGAAACTC	TGCCCTGGCC	CCCATCGTGT	CCACCATAGC	CATCGTGTCT	1080
ACATTATCCT	GCCACATCCT	CCTGAGACGC	AAACTCACCG	CACCCGTGGC	ATTTAGTGTG	1140
ATTGCCATGT	TTAATGTAAT	GAAGTTTTC	ATTGCAATCT	TGCCCTTCTC	CATCAAAGCA	1200
ATGGCTGAAG	CGAATGTCTC	TCTAAGGAGA	ATGAAGAAAA	TTCTCATAGA	TAAAAGCCCC	1260
CCATCTTACA	TCACCCAACC	AGAAGACCCA	GATACGTCT	TGCTTTTAGC	AAATGCCACC	1320
TTGACATGGG	AGCATGAAGC	CAGCAGAAA	AGTACCCCAA	AGAAATTGCA	GAACAGAAA	1380
AGGCATTAT	GCAGAAACCA	GAGGTGAGAG	GCATACAGTG	AGAGGAGTCC	ACCAGCCAAG	1440
GGAGCCACTG	GCCGAGAGGA	GCAAGGTGAC	AGCCTCAAAT	CGGTTCTGCA	CAGCATAAGC	1500
TTTGTGGTGA	GAAAGTTATG	TGCTTATCCC	GAAAGCCAGC	TCTGTGCTTG	GAGGTGGCCA	1560
GCAGTGTGTT	TTGGGAGAAT	CATCAGAGGA	TACAGGCCCTC	ATGGATTTTC	TGCTAAAGAC	1620
AAGGATGAAT	CTAGAAGGCT	TCTTACTTGG	CCCCAAGAAG	TGGATAGGAC	TCAAAAGGCA	1680
GCCAAATACC	TGGGGAAGAT	CTTGGGAATA	TGTGGGAATG	TGGGAAGTGG	AAAGAGCTCC	1740
CTCCTTGCA	CTCTCCTAGG	ACAGATGCAG	CTGCAGAAAG	GGGTGGTGGC	AGTCAATGGA	1800
ACTTTGGCT	ACGTTTCA	GCAGGCATGG	ATCTTTCATG	GAAATGTGAG	AGAAAAATA	1860
CTCTTTGGAG	AAAAGTATGA	TCACCAAGAG	TATCAGCACA	CAGTCCCGCT	CTGTGGCCTC	1920
CAGAAGGACC	TGAGCAACCT	CCCCTATGGA	GACCTGACTG	AGATTGGGGA	GCGGGGCTC	1980
AACCTCTCT	GGGGGACAGG	GCAGAGGATT	AGCCTGGCCC	GCGCTGTCTA	CTCCGACCTG	2040
CAGCTCTACC	TGCTGGACGA	CCCCTGTCTG	GCCGTGGACG	CCCACGTGGG	GAAGCACGTC	2100
TTTGAGGAGT	GCATTAAGAA	GACGCTCAGG	GGAAGACAG	TGCTCCTGGT	GACCCACGAC	2160
CTACAGTTCT	TAGAGTCTTG	TGATGAAGTT	ATTTTATTAG	AAGATGGAGA	GATTTTGTGA	2220
AAGGGAACCC	ACAAGGAGTT	AATGGAGGAG	AGAGGGCGCT	ATGCAAAAC	GATTCAACAAC	2280
CTGCGAGGAT	TGCAGTTCAA	GGATCTTGAA	CACCTTTACA	ATGCAGCAAT	GGTGGAGGCC	2340
TTCAAGGAGA	GCCCTGCTGA	GAGAGAGGAA	GATGCTGGTA	TAATCGGGTA	CCTCCTTTCT	2400
CTCTTCACTG	TGTTCTCTCT	CCTCCTGATG	ATTGGCAGCG	CTGCCTTCAG	CAACTGGTGG	2460
CTGGGTCTCT	GGTTTGGACAA	GGGCTCACGG	ATGACCTGTG	GGCCCCAGGG	CAACAGGACC	2520
ATGTGTGAGG	TCCGCGCGGT	GCTGGCAGAC	ATCGGTACGC	ATGTGTACCA	GTGGGTGTAC	2580
ACTGCAAGCA	TGGTGTTCAT	GCTGGTGTTC	GGCGTCACCA	AAGGCTTCGT	CTTCAACCAAG	2640
ACCACACTGA	TGGCATCTCT	CTCTCTGCAT	GACACGGTGT	TTGATAAGAT	CTTAAAGAGC	2700
CCAATGAGTT	TCCTTGACAC	GACTCCCACT	GGCAGGCTAA	TGAACCGTTT	TTCCAAGGAT	2760
ATGGACGAGC	TGGATGTGAG	GCTGCCGTTT	CACGCAGAGA	ACTTCTGCA	GCAGTTTTTT	2820
ATGGTGGTGT	TTATTCTCGT	GATCTTGGCT	GCTGTGTTTC	CTGCTGTCTC	TTTAGTGTGT	2880
GCCAGCCTTG	CTGTAGGCTT	CTTCATTCTG	TTACGCATTT	TCCACAGAGG	AGTCCAGGAG	2940
CTCAAGAAGG	TGGAGAAATG	CAGCCGGTCA	CCCTGGTTCA	CCCACATCAC	CTCCTCCATG	3000
CAGGCGCTGG	GCATCATTCA	CGCCTATGGC	AAGAAGGAGA	GCTGCATCAC	CTATACTTCA	3060
TCCAAAGGCC	TGTCATTGTC	ATACATCATC	CAGCTGAGCG	GACTGCTCCA	AGTGTGTGTG	3120
CGAACGGGAA	CAGAGACGCA	AGCCAAATTC	ACCTCCGTGG	AGCTGCTCAG	GGAATACATT	3180
TCGACCTGTG	TTCTCTGAAT	CACCTATCCC	CTCAAAGTGG	GGACCTGTCC	CAAGGACTGG	3240
CCAGCTGTG	GGGAGATCAC	CTTCAGAGAC	TATCAGATGA	GATACAGAGA	CAACACCCCC	3300
CTTGTTCCTG	ACAGCCTGAA	CTTGAACATA	CAAAGTGGGC	AGACAGTCGG	GATTGTTGGA	3360
AGAACAGGTT	CCGGAAGTTC	ATCGTTAGGA	ATGGCTTTGT	TTGCTCTGGT	GGAGCCAGCC	3420
ATTGGCAACA	TCCTTATTGA	TGAGGTGGAT	ATCTGCATTC	TCAGCTTGGG	AGACCTCAGA	3480
ACCAAGCTGA	CTGTGATCCC	ACAGGATCCT	GTCTGTGTTG	TAGGTACAGT	AAGGTACAAC	3540
TTGATCCCT	TTGAGAGTCA	CACCGATGAG	ATGCTCTGGC	AGGTTCTGGA	GAGAACATT	3600
ATGAGAGACA	CAATAATGAA	ACTCCAGAAA	AAATTACAGG	CAGAAGTCAC	AGAAAAATGA	3660
GAAAACTTCT	CAGTAGGGGA	ACGTGAGCTG	CTTTGTGTGG	CCCGAGCTCT	TCTCCGTAAT	3720
TCAAAGATCA	TTCTCTTTGA	TGAAGCCACC	GCCTCTATGG	ACTCCAAGAC	TGACCACTGT	3780
GTTCAAGACA	CCATCAAAGA	TGCCTTCAAG	GGCTGCACTG	TGCTGACCAT	CGCCACCCGC	3840
CTCAACACAG	TTCTCAACTG	CGATCAGGTC	CTGTTTATGG	AAAATGGGAA	GGTGATTGAG	3900
TTTGACAAGC	CTGAAGTCTT	TGCAGAGAAG	CCAGATTCTG	CATTTGCGAT	GTTACTAGCA	3960
GCAGAAGTCA	GATTGTAG					

Seq ID NO: 312 Protein sequence
 Protein Accession #: Eos sequence

	1	11	21	31	41	51	
	MVGEQPYLIS	DLDQGRRRRS	FAERYDPSLK	TMIPVRPCAR	LAPNPVDDAG	LLSFATFSWL	60
5	TPVMVKGYRQ	RLTVDTLPL	STDSSDTNA	KRFRVLWDEE	VARVGPEKAS	LSHVVKFQR	120
	TRVLMDIVAN	ILCIIMAAIG	PTVLIHQILQ	Q'ERTSGKVM	VGIGLCIALF	ATEFTKVFFW	180
	ALAWAINYRT	AIRLKVALLST	LVFENLVSK	TLTHISVGEV	LNILSSDSYS	LFEAALFCPL	240
	PATIPILMFV	CAAYAFFILG	PTALIGISVY	VIFIPVQMF	AKLNSAFRRS	AILVTDKRVQ	300
	TMNEFLTCIR	LKIMYAWEKS	FTNTIQDIRR	RERKLEKAG	FVQSGNSALA	PIVSTIAIVL	360
10	TLSCHILLRR	KLTAPEVAFSV	IAMFNVMKFS	IAILPFSIKA	MAEANVSLRR	MKKILIDKSP	420
	PSYITQPEEP	DTVLLANAT	LTWEHEASRK	STPKKLQNK	RHLCKQRSE	AYSERSPPAK	480
	GATGPEEQSD	SLKSVLHSIS	FVVRKLCRYP	EAQLLAWRWP	AVFVGRIIRG	YRPHGFSAD	540
	KDESRLTLTW	PQEVDRTOQA	AKYLGKILGI	CGNVGSGKSS	LLAALLGQMQ	LQKGVAVANG	600
	TLAYVQQAW	IFHGNVRENI	LFGEKYDHQR	YQHTVRVCG	QKDLNLPG	DLTEIGERGL	660
15	NLSGGQRQRI	SLARAVYSR	QYLLDDPLS	AVDAHVGKHV	FEECIKTLR	GKTVVLVTHQ	720
	LQFLESCDEV	ILEDGEICE	KGTHKELMEE	RGRYAKLIHN	LRGLQFKDPE	HLNNAAMVEA	780
	FKESPAEREE	DAGIIGYLLS	LFTVFLFLM	IGSAAFSNW	LGLWLDKGS	MTGCPQGNRT	840
	MCEVGAFLAD	IQGHVQWVY	TASMVFMVLF	GVTKGFVFTK	TTLMASSSLH	DTVFDKILKS	900
	PMSFFDTTPT	GRLMNRFSDK	MDLVDRLPF	HAENFLQKFF	MVVFILVILA	AVFPAVLLV	960
20	ASLAVGFFIL	LRIFHRGVQE	LKKVENVRS	PWFTHITSSM	QGLGIIHAYG	KKESCITYTS	1020
	SKGLSLSYII	QLSGLLQVCV	RTGTETQAKF	TSVELLEREYI	STCVPECTHP	LKVGTCPKDW	1080
	PSCGEITFRD	YQMYRDNTPT	LVLDLNLNI	QSGQTVGIVG	RTGSGKSSLG	MALFRLVEPA	1140
	SGTIFIDEVD	ICILSLEDLR	TKLTVIPQDP	VLFGVTVRYN	LDPFESHTDE	MLWQVLERTF	1200
	MRDTIMKLPE	KLQAEVTENG	ENFSVGERQL	LCVARALLRN	SKIILLDEAT	ASMDSKDTTL	1260
25	VQNTIKDAFK	GCTVLTIAHR	LNTVLNCDHV	LVMENGKVIE	FDKPEVLAEK	PDSAFAMLLA	1320
	AEVRL						

Seq ID NO: 313 DNA sequence
Nucleic Acid Accession #: Z31560
Coding sequence: 1-966

	1	11	21	31	41	51	
	CACAGCGCCC	GCATGTACAA	CATGATGGAG	ACGGAGCTGA	AGCCGCCGGG	CCCGCAGCAA	60
35	ACTTCGGGGG	GCGCGCGCGG	CAACTCCACC	GCGCGCGCGG	CCCGCGGCAA	CCAGAAAAAC	120
	AGCCCGGACC	GCGTCAAGCG	GCCCATGAAT	GCCTTCATGG	TGTGGTCCCG	CGGGCAGCGG	180
	CGCAAGATGG	CCCAGGAGAA	CCCCAAGATG	CACAACCTCG	AGATCAGCAA	GCGCCTGGGC	240
	GCCGAGTGG	AACCTTTTGT	GGAGACGGAG	AAGCGGCCGT	TCATCGACGA	GGCTAAGCGG	300
	CTGCGAGCGC	TGCACATGAA	GGAGCACCCG	GATTATAAAT	ACCGGCCCGG	CCGGAAAACC	360
40	AAGACGCTCA	TGAAGAAGGA	TAAGTACACG	CTGCCCGCG	GGCTGCTGGC	CCCGCGCGG	420
	AATAGCATGG	CGAGCGGGGT	CGGGGTGGGC	GCCGGCCTGG	GCGCGGGCGT	GAACGAGGCG	480
	ATGACAGGTT	ACGCGCACAT	GAACGGCTGG	AGCAACGGCA	GCTACAGCAT	GATGCAGGAC	540
	CAGCTGGGCT	ACCGCGAGCA	CCCGGGCCTC	AATGCGCACG	GCGCAGCGCA	GATGCAGCCC	600
	ATGCACCGCT	ACGACGTGAG	CGCCCTGCAG	TACAACCTCA	TGACACGCTC	GCAGACCTAC	660
45	ATGAACGGCT	CGCCACCTTA	CAGCATGTCC	TACTCGCAGC	AGGGCACCCC	TGGCATGGCT	720
	CTTGGCTCCA	TGGGTTCGGT	GGTCAAGTCC	GAGGCCAGCT	CCAGCCCCCC	TGTGGTTACC	780
	TCTTCTCTCC	ACTCCAGGGC	GCCCTGCCAG	GCCGGGGACC	TCCGGGACAT	GATCAGCATG	840
	TATCTCCCGG	GCGCCGAGGT	GCCGGAACCC	GCCGCCCCCA	GCAGACTTCA	CATGTCCAG	900
	CACTACCAGA	GCGGCCCGGT	GCCCGGCACG	GCCATTAAACG	GCACACTGCC	CCTCTCACAC	960
50	ATGTGAGGGC	CGGACAGCGA	ACTGAGGGGG	GGAGAAATTT	TCAAGAGAAA	ACGAGGGAAA	1020
	TGGGAGGGGT	GCAAAAGAGG	AGAGTAAGAA	ACAGCATGGA	GAAACCCCGG	TACGCTCAAA	1080
	AAAAA						

Seq ID NO: 314 Protein sequence
Protein Accession #: CAA83435

	1	11	21	31	41	51	
	HSARMYNMME	TELKPFPGPQ	TSGGGGNGST	AAAAGNQKN	SPDRVKRPMN	AFMVVSRGQR	60
60	RKMAQENPKM	HNSEISKRLG	AEWKLLSETE	KRPFIDEAKR	LRALHMKEHP	DYKYRPRRKT	120
	KTLMKKDKYT	LPGLLAPGG	NSMASGVGVG	AGLGAGVNQR	MDSYAHMNGW	SNGSYMMQD	180
	QLGYPPHPLG	NAHGAAQMQP	MHRYDVSAHQ	YNSMTSSQTY	MNGSPYYSMS	YSQQGTPGMA	240
	LGSMGSVVKS	EASSSPVVT	SSSHSRAPCQ	AGDLRDMISM	YLPGEVPEP	AAPSRIHMSQ	300
	HYQSGFVPGT	AINGTLPLSH	M				

Seq ID NO: 315 DNA sequence
Nucleic Acid Accession #: U91618
Coding sequence: 29..541

	1	11	21	31	41	51	
70	CGGACTTGGC	TTGTTAGAAG	GCTGAAAGAT	GATGGCAGGA	ATGAAAATCC	AGCTTGTATG	60
	CATGCTACTC	CTGGCTTTCA	GCTCCTGGAG	TCTGTGCTCA	GATTCAAGAA	AGGAAATGAA	120
	AGCATTAGAA	GCAGATTTCT	TGACCAATAT	GCATACATCA	AAGATTAGTA	AAGCACATGT	180
75	TCCCTCTTGG	AAGATGACTC	TGCTAAATGT	TTGCAGTCTT	GTAATAAATT	TGAAACGCCC	240
	AGCTGAGGAA	ACAGGAGAGG	TTTCATGAAGA	GGAGCTTGTT	GCAAGAGGGA	AACTTCTCTAC	300
	TGCTTTAGAT	GGCTTTAGCT	TGGAAGCAAT	GTTGACAATA	TACCAGCTCC	ACAAAATCTG	360
	TCACAGCAGG	GCTTTTCAAC	ACTGGGAGTT	AATCCAGGAA	GATATTCTTG	ATACTGGAAA	420
	TGACAAAAAT	GGAAAGGAAG	AAGTCATAAA	GAGAAAAAAT	CCTTATATTC	TGAAACGGCA	480
80	GCTGTATGAG	AATAAACCCA	GAAGACCCTA	CATACTCAAA	AGAGATTCTT	ACTATTACTG	540
	AGAGAATAAA	TCATTTATTT	ACATGTGATT	GTGATTCATC	ATCCCTTAAT	TAAATATCAA	600
	ATTATATTTG	TGTGAAAATG	TGACAAACAC	ACTTATCTGT	CTCTTCTACA	ATTGTGGTTT	660
	ATTGAATGTG	TTTTTCTGCA	CTAATAGAAA	TTAGACTAAG	TGTTTTCAAA	TAAATCTAAA	720
	TCTCAAAAAA	AAAAAAAATA	AAATGGGGCC	GCAATT			

Seq ID NO: 316 Protein sequence
Protein Accession #: AAB50564

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MMAGMKIQLV CMLLLAFSSW SLCS DSEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60
VCSLVNNLNS PAETGEVHE EELVARRKLP TALDGFSLTA MLTIYQLHKI CHSRAFAQHWE 120
LIQEDILD TG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYYY

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Seq ID NO: 317 DNA sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109..2940

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15      1      11      21      31      41      51
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ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120
AGCATTGCAG GTCCCTATTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180
GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAGACA ATGGGTATAA TGGATTGCTC 240
ATTGCAATTA ATCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG 300
ATAACTGAAG CTTCAATTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTGAGAAAT 360
ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
TCATATGAAA AGGCAAAATG CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
TACACCTCAT AATACAGAGG GTGTGGAAAA GAGGGAAAT ACATTCATTT CACACCTAAT 540
25      TTCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT 600
GAATGGGCCC ACCTCCGTTG GGGTGTGTTC GATGAGTATA ACAATGACAA ACCTTTCTAC 660
ATAAATGGGC AAAATCAAAAT TAAAGTGACA AGGTGTTTAT CTGACATCAC AGGCATTTTT 720
GTGTGTGAAA AAGGTCTCTG CCCCAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
30      AGTTTATCTT CTGTGTTTGA ATTTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC 900
CTACAGAAAC AGATGTGCAG CCTCAGAAAT GCATGGGATG TAATCAGAGA CTCTGTGCAG 960
TTTCACCACA GCTTTCCCAT GAATGGGACT GAGCTTCCAC CTCTCCACAT ATTCTCGCTT 1020
GTACAGGCTG GTGACAAAGT GGTCTGTGTTA GTCTGGATG TGTCCAGCAA GATGGCAGAG 1080
GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAAATTT ATTTGATGCA GATTGTTGAA 1140
35      ATTCAATCTT TCGTGGGCAT TGCCAGTTTC GACAGCAAAAG GAGAGATCAG AGCCAGCTA 1200
CACCATAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
TCAGCTAAAA CAGACATCAG CATTGTGTTA GGGCTTAAGA AAGGATTGTA GGTGGTTGAA 1320
AAACTGAATG GAAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG 1380
CTTCTTGCCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTC A CTCCATTGCC 1440
40      CTGGGTTTAT CTGCAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500
TTCTTTGTTC CAGATATATC AAATCTCAAT AGCATGATTG ATGCTTTTCA TAGAATTTCC 1560
TCTGGAAGTG GAGACATTTT CCAGCAACAT ATTCACTTG AAAGTACAGG TGAAAATGTC 1620
AAACCTCACC ATCAATTGAA AAAACACAGT ACTGTGGATA ATACTGTGGG CAACGACACT 1680
ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCTGAGA TTATATTATT TGATCTGTAT 1740
45      GGACGAAAAA ACTACACAAA TAAATTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT 1800
TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCCTGAACAA TACCCATCAT 1860
TCTCTGCAAG CCCTGAAAGT GACAGTGACC TCTCGCGCCT CCAACTCAGC TGTGCCCCCA 1920
GCCACTGTGG AAGCTTTTGT GGAAAGAGAG AGCCTCCATT TTCCTCATCC TGTGATGATT 1980
TATGCCAATG TGAAACAGGG ATTTTATCCC ATTTCTAATG CCACCTGTCA TGCCACAGTT 2040
50      GAGCCAGAGA CTGGAGATCC TGTTACGCTG AGACTCCTTG ATGATGGAGC AGTGTCTGAT 2100
GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTCTCT CCTTTGCTGC AAATGGTAGA 2160
TATAGCTTGA AAGTGCAATG CAATCACTCT CCCAGCATAA GCACCCAGC CCACCTCTAT 2220
CCAGGGAGTG ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280
GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340
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Seq ID NO: 318 Protein sequence
Protein Accession #: NP_006527.1

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Seq ID NO: 319 DNA sequence

Nucleic Acid Accession #: NM_000228.1

Coding sequence: 82..3600

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Seq ID NO: 320 Protein sequence
 Protein Accession #: NP_000219.1

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 30 VLRPAEKLVV SMTKQLGDFW TRMEELRHQA RQQGAEAQQA QQLAEGASEQ ALSAQEGFER 1080
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Seq ID NO: 322 Protein sequence
 Protein Accession #: NP_001935.1

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Seq ID NO: 324 Protein sequence
 Protein Accession #: P39900

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 YTPDMNRDVE DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAHGD PHAFDGGKGI 180
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 EPNYPKSIHS FGFNPNFKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420
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Seq ID NO: 325 DNA sequence
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 Coding sequence: 64..2590

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	TACACAGCCA	GGGCTGTTGC	GCTGTCTGAT	AAGAAAAGAT	CATTTACCAT	ATGGCTTTCT	360
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10	TCGAAGACAA	GACACACTAG	AGAACTGTGT	CTCAGGCGTG	CCAAGAGGAG	ATGGGCACCT	480
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	GAATCTGATG	CAGCACAGAA	CTATACTGTC	TTCTACTCAA	TAAGTGGACG	TGGAGTTGAT	600
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	CCTGTGGATC	GTGAAGAATA	TGATGTTTTT	GATTTGATTG	CTTATGCGTC	AACTGCAGAT	720
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	CTGAAATACA	GCATTTTGCA	GCAGACACCA	AGGTCACCTG	GGCTCTTTTC	TGTGCATCCC	960
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	CCAAGATTAT	GTCCCTCACT	ATAACTATGA	GGGAAGAGGA	TCTCCAGCTG	GTTCTGTGGG	2700
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	CTGTTTCAAG	ATTTCTGCAT	CCACAAGTTA	GTAGCAAACT	GGGAATACT	CGCTGCAGCT	3720
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	CTGAAGCTCT	CGCCTCCCGG	GTTTATGCCA	TTCTCCTGCC	TCAGCCTCCT	GAGTAGCTGG	4920
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Seq ID NO: 326 Protein sequence
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Seq ID NO: 327 DNA sequence
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 Coding sequence: 64..2754

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 65 C T G A C C C T C G T G A T C T T C A G T C G T G A T G G T G A A G C C T G C A A A A A G G T G A T A C T T A A T G T A 180
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 A A A G A A C C T T T A A A T T T G T T T T A T A T A G A A A G A G A C A C T G G A A A T C T A T T T T G C A C T C G G 660
 75 C C T G T G G A T C G T G A A G A A T A T G A T G T T T T T G A T T T G A T T G C T T A T G C G T C A A C T G C A G A T 720
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 C A C C C T G T T T T C A C A G A A G C A A T T T A T A A T T T T G A A G T T T T G G A A A G T A G T A G A C C T G G T 840
 A C T A C A G T G G G G G T G G T T T G T G C C A C A G A C A G A G A T G A A C C G G A C A C A A T G C A T A C G C G C 900
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	GTTCATGTGA	GGGATCTGGA	TGAGGGGCCT	GAATGCACCT	CTGCAGCCCA	ATATGTGCGG	1500
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	CCCAAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
	ACTGGAACAC	TTGCTGTGAA	CATTGAAGAT	GTAAATGATA	ATCCACCAGA	AATACTTCAA	1800
10	GAATATGTAG	TCATTTGCAA	ACCAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCAGTTTGC	CCAATACTTC	TCCAGAAATC	1920
	AGTAGACTGT	GGAGCCTCAC	CAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGAATA	TACCATTCCCT	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
	GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGCG	2100
15	ACTTCAAGGA	GTACAGGAGT	AATACTTGGG	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCCTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTTTTG	TGCAACTAAA	2220
	GGGAAACGTT	TTCCGTGAAG	TTTAGCACAG	CAAACTTAA	TTATATCAAA	CACAGAAAGCA	2280
	CCTGGAGAGC	ATAGAGTGTG	CTCTGCCAAT	GGATTATGA	CCCAAACTAC	CAACAACTCT	2340
	AGCCAAGGTT	TTTGTTGTAC	TATGGGATCA	GGAATGAAAA	ATGGAGGGCA	GGAAACCATT	2400
20	GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCCTGGACT	CCTGACAGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTACTCG	2520
	GAGTGGCACA	GTTTACTACA	ACCCGCTCTC	GGTGAAAAAT	TGCATCGATG	TAATCAGAAT	2580
	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
	CCAGCTGGTT	CTGTGGGCTG	CTGCAGTGAA	AAGCAGGAAG	AAGATGGCCT	TGACTTTTTA	2700
25	AATAAATTGG	AACCCAAAAT	TATTACATTA	GCAGAGCAT	GCACAAAGAG	ATAATGTCAC	2760
	AGTGCTACAA	TTAGGTCCTT	GTGACACATT	CTGGAGGTTT	CCAAAAATAA	TATTGTAAAG	2820
	TTCAATTCTA	ACATGTATGT	ATATGATGAT	TTTTTTCTCA	ATTTTGAATT	ATGCTACTCA	2880
	CCAATTTATA	TTTTTAAAGC	CAGTTGTTGC	TTATCTTTTC	CAAAAAGTGA	AAAATGTTAA	2940
	AACAGACAAC	TGGTAAATCT	CAAACTCCAG	CACCTGGAAT	AAGGTCTCTA	AAGCATCTGC	3000
30	TCCTTTTTTT	TTTTCAGGAT	ATTTTAGTAA	TAAATATGCT	GGATAAATAT	TAGTCCAAAC	3060
	ATAGCTAAGT	TATGCTAATA	TCACATTATT	ATGTATTAC	TTTAAGTGAT	AGTTTAAAAA	3120
	ATAAACAAAG	AATATTGAGT	ATCACTATGT	GAAGAAAGTT	TTGAAAGAGA	AACAATGAAG	3180
	ACTGAATTA	ATTAAAAATG	TTGCAGCTCA	TAAAGAATTG	GGACTCACCC	CTACTGCAC	3240
	ACCAAAATTC	TTTGACTTTG	GAGGCAAAAT	GTGTTGAAGT	GCCTATGAA	GTAGCAATTT	3300
35	TCATATGGCA	TATAGTTGGA	AATAAATGTG	TGTGTGTATA	TTATTATTA	TCAATGCAAT	3360
	ATTTAAAAAT	AAATGAGAAC	AAAGAGGAAA	ATGGTAAAAA	CTTGAATGA	GGCTGGGGTA	3420
	TAGTTTGTCC	TACAAATAGA	AAAAGAGAGA	GCTTCCTAGG	CCTGGGCTCT	TAAATGCTGC	3480
	ATTATAACTG	AGTCTATGAG	GAATAGTTTC	CTGTCCAATT	TGTGTAATTT	GTTTAAATTT	3540
	GTAAATAAAT	TAAACTTTTC	TGGTTTCTGT	GGGAAGGAAA	TAGGGAATCC	AATGGAACAG	3600
40	TAGCTTTGCT	TTGCAGTCTG	TTTCAAGATT	TCTGCATCCA	CAAGTTAGTA	GCAAACTGGG	3660
	GAATACTGCT	TGCAGCTGGG	GTTCCCTGCT	TTTTGGTAGC	AAGGGTCCAG	AGATGAGGTG	3720
	TTTTTTTCGG	GGAGCTAATA	ACAAAAACAT	TTTTAAACTT	ACCTTTACTG	AAGTTAAATC	3780
	CTCTATTGCT	GTTCTATATC	TCTCTTATAG	TGACCAACAT	CTTTTAAAT	TAGATCCAAA	3840
	TAACCATGTC	CTCCTAGAGT	TTAGAGGCTA	GAGGGAGCTG	AGGGGAGGAT	CTTACTGAAA	3900
45	GCACCTGGG	GAGATTGAAT	GTCCCTTAAAC	CTAAGCCCCA	CAAACTTGAC	ACCTGATCAG	3960
	GTCTGGGAGC	TACAAAATTT	CATTTTCTC	CTCACTGCCC	TTCTTCTGAG	TGGCATTGGC	4020
	CTGAATCAAG	GAAAGCCAGG	CCTTGTGGGC	CCCCTTCTTT	CGGCTTCTG	CTAAGCAAC	4080
	ACCTCCAGCA	GAGATTCCTT	TAAAGTACTC	CAGGTTTTCC	ACCATCCTTC	AGCGTGAATT	4140
	AATTTTAAAT	CAGTTTGCTT	TCTCCAGAGA	AATTTTAAAA	TAATAGAAGA	AATAGAAATT	4200
50	TTGAATGTAT	AAAAGAAAAA	GATCAAGTTG	TCATTTTAGA	ACAGAGGGAA	CTTTGGGAGA	4260
	AAGCAGCCCA	AGTAGGTTAT	TTGTACAGTC	AGAGGGCAAC	AGGAAGATGC	AGGCCTTCAA	4320
	GGGCAAGGAG	AGGCCACAAG	GAATATGGGT	GGGAGTAAAA	GCAACATCGT	CTGCTTCATA	4380
	CTTTTTCCTA	GGCTTGGCAC	TGCCTTTTCC	TTTCTCAGGC	CAATGGCAAC	TGCCATTTGA	4440
	GTCCGGTAGC	GGATCAGCCA	ACCTCTTCTC	TATGGCTCAC	CTTATTTGGA	GTGAGAAATC	4500
55	AAGGAGACAG	AGCTGACTGC	ATGATGAGTC	TGAAGGCATT	TGCAGGATGA	GCCTGAACCTG	4560
	GTTGTGCAGA	ACAAACAAGG	CATTCAATGG	AATTGTTGTA	TTCTTCTGTC	AGCCCTCCTT	4620
	CTGGGCCTTA	AGAAGGCTCTA	TGAATTAAT	GCCTATCTAA	AATTCTGATT	TATTCCTACA	4680
	TTTTCTGTTT	TCTAATTTTG	CCCTAAAAATC	TATGTGTTTT	AGACTTAGAC	TTTTTATTGC	4740
	CCCCCCCCC	TTTTTTTTTG	AGACGGAGTC	TCGCTCTGAC	GCACAGGCTG	GAGTGCAGTG	4800
60	GCTCCGATCT	CTGCTCACTG	AAAGCTCCGC	CTCCCGGTTT	CATGCCATTTC	TCCTGCCTCA	4860
	GCCTCCTGAG	TAGCTGGGAC	TACAGGCGCC	CACCACCACG	CCCGGCTAAT	TTTTTGTATT	4920
	TTTAATAGAG	ACGGGGTTTC	ACTGTGTTAG	CCAGGATGGT	CTCGATCTCC	TGACCTCGTG	4980
	ATCCGCTGCT	CTCGGCTTCC	CAAAGTGCTG	GGATTACAGG	CATGACCCAC	CGCTCCCGGC	5040
	CTTGTTTTCC	GTTTAAAGTC	GTCTTCTTTT	AATGTAATCA	TTTTGAACAT	GTGTGAAAGT	5100
65	TGATCATACG	AATTGGATCA	ATCTTGAAT	ACTCAACCAA	AAGACAGTCG	AGAAGCCAGG	5160
	GGGAGAAAAG	ACTCAGGGCA	CAAAATATTG	GTCTGAGAAT	GGAAATCTCT	GTAAGCCTAG	5220
	TTGCTGAAAT	TTCTGTCTGT	AACCAGAAGC	CAGTTTATATC	TAACGGCTAC	TGAAACACCC	5280
	ACTGTGTTTT	GCTCACTCCC	TCACTCACCG	ATCAAAACCT	GCTACCTCCC	CAAGACTTTA	5340
	CTAGTGCCGA	TAAACTTTCT	CAAAGAGCAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACCTC	5400
70	TAACCATCTC	TTTGTCTTTT	GAACATGCTG	AAAACACCTT	GGTCTGCATG	TATGCCCGAA	5460
	TTTGTAATCT	TTTTCTCTCA	AATGAAAATT	TAATTTTAGG	GATTCAATTC	TATATTTTCA	5520
	CATATGTAGT	ATTATTATTT	CCTTATATGT	GTAAGGTGAA	ATTATGGTGA	TTTGAGTGTG	5580
	CAAGAAAATA	TATTTTAAAA	GCTTTTCAAT	TTCCCCAGT	GAATGATTTA	GAATTTTTTA	5640
	TGTAAATATA	CAGAATGTTT	TTTCTTACTT	TTATAAGGAA	GCAGCTGTCT	AAAAATGCAGT	5700
75	GGGGTTTGT	TTGCAATGTT	TTAAACAGAG	TTTTAGTATT	GCTATTAAAA	GAAGTTACTT	5760
	TGCTTTTAAA	GAAACTTGGC	TGCTTAAAA	AAGCAAAAAT	TGGATGCATA	AAGTAATATT	5820
	TACAGATGTG	GGGAGATGTA	ATAAAACAAT	ATTAACTTGG	TTTCTTGT	TTGCTGTATT	5880
	TAGAGATTAA	ATAATTCTAA	GATGATCACT	TTGCAAAAAT	ATGCTTATGG	CTGGCATGGA	5940
	AATAGAAATA	CTCAATTTATG	TCCTTGTGTG	ATTAAATGGG	AATATTTTGG	ACAATGTTTC	6000
80	ATTATCAAAAT	TGCTGACATC	ATTAAATATAT	ATTGTAATGT	TGGGAAGAGA	TCACTATTTT	6060
	GAAGCACAGC	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAAT	TTGATCGGGT	6120
	ATTAAAAAGTA	TTAGAAGGGT	GTTATAATTG	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180
	AGGGGTTTTA	TCTTGAAGAC	CAGTGTAGTC	AAGGGAAAAAC	ATGAGTTAAA	AAGAAAAGCA	6240
	GGCAATATTG	CAGTCTTGTAT	TCTGCCACTT	ACAGGATAGA	TAATGCCTGA	ACTTTAATGA	6300
	CAAGATGATC	CAACCATAAA	GGTGCTCTGT	GCTTCACAGT	GAATCTTTTC	CCCATGCAGG	6360

AGTGTGCTCC CCTACAAACG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420
 AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAATT CCAGTAACTT CTATTGTAAC 6480
 CATTATTTTT GTGTATGTC TCAAGAATGT TCATTGGATT TTTGTTTGTA ATAGTAAAT 6540
 ACCGGATACA TTTCAGTGT CCTTCAGTAT TGATTGGGT GAATATTTGG TCATAATGGT 6600
 TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGTCACTTAC 6660
 TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCTCTCTTA GCTTCTCAT TAAATCAAT 6720
 GAACAATGCC AGCCTCATGG GGTGTGTGAA TGATTAAAT AGTTAATATA CCTAAAGTAC 6780
 ATAGAACACT GCCTGCACAT AGTAAAAGAA TTATAAGTGT GAGGTAGTTG GTAAAATTAT 6840
 GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTTT AGGGAATAA AGTTTGTGCA 6900
 TATATATAAT CCCGAAACAT G

Seq ID NO: 328 Protein sequence
 Protein Accession #: NP_001932.1

1 11 21 31 41 51
 | | | | |
 MAAAGPRRSV RGAVCLHLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60
 ADLIRSDPD FRVLNDGSVY TARAVALSDK KRSFTIWLSD KRKQTQKEVT VLEHQKQVS 120
 KTRHRTRETV RRAKRRWAPI PCSMQENSLG PFPLFLQOVE SDAAQNYTVF YSISGRGVDK 180
 EPLNLFYIER DTGNLFCRTP VDREYDVFD LIAYASTADG YSADLPLPLP IRVEDENDNH 240
 PVFTEAIYNF EVLESSRPGT TVGVVCATDR DEPDTHMTRL KYSILQOTPR SPGLFSVHPS 300
 TGVITTVSHY LDREVVDKYS LIMKVQDMDG QFFGLIGTST CIITVTDSND NAPTFRQNAV 360
 EAFVEENAFN VEILRIPIED KDLINTANWR VNFTILKNE NGHFKISTDK ETNEGVLSVV 420
 KPLNYEENRQ VNLEIGVNEE APPARDIPRV TALNRALVTV HVRDLDEGPE CTAAQYVRI 480
 KENLAVGSKI NGYKAYDPEN RGNGLRYKK LHDPKGWITI DEISGSITS KILDREVETP 540
 KNELYNITVL AIDKDDRSCT GTLAVNIEDV NDNPPAILQE YVICKPKMG YTDILAVDPD 600
 EPVHGAPFYF SLPNTSPEIS RLWSLTKVND TAARLSYQKN AGFQBYTIPI TVKDRAGQAA 660
 TKLLRVNLCE CTHPTQCRAT SRSTGVILKG WAILAILGI ALLFSVLLTL VCGVFGATKG 720
 KRFPEDLAQO NLIISNTPEAP GDDRVCSANG FMTQTTNNS QGFCGTMSGG MNKGQETIE 780
 MMKGGNQILE SCRAGHHHT LDSCRGGHTE VDNCRITYSE WHSFTQPRLG EKLHRCNQNE 840
 DRMPSQDYVL TYNYEGRGSP AGSVGCCSEK QEEDGLDFLN NLEPKFITLA EACTKR

Seq ID NO: 329 DNA sequence
 Nucleic Acid Accession #: NM_016583.2
 Coding sequence: 72..842

1 11 21 31 41 51
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 GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC 60
 TAAGAGCAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCGAGA 120
 CCATGGCCCA GTTTGGAGGC CTGCCGTGC CCCTGGACCA GACCCGTGCC TTGAATGTGA 180
 ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA 240
 ATGGCCTGCT GTCTGGGGGC CTGTTGGGCA TTCTGGAAAA CCTTCCGCTC CTGGACATCC 300
 TGAAGCCTGG AGGAGGTACT TCTGTTGGCC TCCTTGGGGG ACTGCTTGGA AAAGTGACGT 360
 CAGTGATTCC TGGCCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG 420
 AACTTGGCCT TGTGCAGAGC CCTGATGGCC ACCGTCTCTA TGTCAACATC CCTCTCGGCA 480
 TAAAGCTCCA AGTGAATACG CCCCTGGTCG GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC 540
 TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC 600
 TTGTTGACTG CACCATTCCT CTGGAAGGCC TGCAAATTTT TCTGCTTGAT GGAAGTGGCC 660
 CCCTCCCCAT TCAAGTCTCT CTGACAGGCC TCACAGGGAT CTGAATAAA GTCCCTGCCTG 720
 AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGGACATCA 780
 CCCTGGTGCA TGACATTGTT AACATGCTGA TCCACGGACT ACAGTTTGTC ATCAAGGTCT 840
 AAGCCTTCCA GGAAGGGGCT GGCCTCTGCT GAGCTGCTTC CCAGTGCTCA CAGATGGCTG 900
 GCCCATGTGC TGAAGATGA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCTCTCCTT 960
 TCCACACAGG CGTGTGTAAC ATCCCATGTG CCTCACCTAA TAAATGGCT CTCTCTCTGC 1020
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 330 Protein sequence
 Protein Accession #: NP_057667.1

1 11 21 31 41 51
 | | | | |
 MFQTGGLIVF YGLLAQTMQ FGGLPVPLDQ TLPLNVNPAL PLSFTGLAGS LTNALSNGLL 60
 SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL 120
 VQSPDGHRLY VTIPLGILKQ VNTPLVGASL LRLAVKLDIT AEILAVRDKQ ERIHLVLGDC 180
 THSPGSLQIS LLDGLGLPLI QGLLDSLITGI LNKVLPVLVQ GNVCPVNEV LRGLDITLVH 240
 DIVNMLIHGL QFVIKV

Seq ID NO: 331 DNA sequence
 Nucleic Acid Accession #: NM_004363.1
 Coding sequence: 115..2223

1 11 21 31 41 51
 | | | | |
 CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60
 TCCTGGAAC CTAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
 TCTCCCTCGG CCCCTCCCCA CAGATGTTGC ATCCCTGGC AGAGGCTCCT GCTCACAGCC 180
 TCACTTCTAA CCTTCTGAA CCCGCCACC ACTGCCAAGC TCACTATTGA ATCCACGCCG 240
 TTCAATGTCG CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT 300
 TTTGGTACA GCTGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360
 GTAATAGGAA CTAAACAAGC TACCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC 420
 CCCAATGCAT CCTGCTGAT CCAGAATATC ATCCAGAATG ACACAGGATT CTACACCTTA 480

5 CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCCG 540
 GAGCTGCCCC AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600
 GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAA 660
 CAGAGCCTCC CGGTCACTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
 TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT 780
 GCCAGGCGCA GTGATTCAGT CATCCTGAAT GTCTCTATG GCCGGATGTC CCCCACCATT 840
 TCCCCTCTAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCCTG CCACGCAGCC 900
 TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
 10 GAGCTCTTTA TCCCCACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
 AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080
 CCCAAACCCCT TCATCACCAG CAACAACCTC AACCCTGCTG AGGATGAGGA TGCTGTAGCC 1140
 TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
 CTCCCGGTCA GTCCAGGCT GCAGCTGTCC AATGACAACA GGACCTCAC TCTACTCAGT 1260
 15 GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTGAC 1320
 CACAGCGACC CAGTCATCCT GAATGTCTCT TATGGCCAG ACGACCCAC CAATTCCCCC 1380
 TCTATACCTT ATTACCTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC 1440
 CCACCTGCAC AGTATTCTTG GCTGATTGAT GGGAACTACC AGCAACACAC ACAAGAGCTC 1500
 TTTATCTCCA ACATCACTGA GAAGAACAGC GGAATCTATA CTGCGCAGGC CAATAACTCA 1560
 20 GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCAGAG TCTCTGCGGA GCTGCCCCAAG 1620
 CCCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGTCTG GGCCTTCACC 1680
 TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
 GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTCA 1800
 AGAAATGAGC CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1860
 25 GACCCAGTCA CCCTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTT CCCCCCAGAC 1920
 TCGTCTTACC TTTCCGGAGC GAACCTCAAC CTCTCCTGCC ACTCGGCCTC TAACCCATCC 1980
 CCGCAGTATT CTTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040
 GCCAAATCA CGCCAAATAA TAACGGGACC TATGCCTGTT TTGCTCTTAA CTGCGTACT 2100
 GGCCGCAATA ATTCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCCTGGT 2160
 30 CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA 2220
 TAGCAGCCCT GGTGTAGTTT CTTCAATTTA GGAAGACTGA CAGTTGTTT GCTTCTCTCT 2280
 TAAAGCATTT GCAACAGCTA CAGTCTAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA 2340
 AGACTCTGAC CAGAGATCGA GACCATCTTA GCCAACATCG TGAAACCCCA TCTCTACTAA 2400
 AAATACAAA ATGAGCTGGG CTGTGTGGCG CGCACTCTGA GTCCAGTTA CTCGGGAGGC 2460
 35 TGAGGCAGGA GAATCGCTTG AACCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520
 ACTGCACTCC AGTCTGGCAA CAGAGCAAGA CTCATCTCA AAAAGAAAAG AAAAGAAAGAC 2580
 TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA 2640
 AACTTTAATG AACTAATCGA CAGCTTCATG AAAGTGTCCA CCAAGATCAA GCAGAGAAAA 2700
 TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTTCTTA AATGTCTTGT 2760
 40 TTCCAGATT TCAGGAAACT TTTTCTCTT TAAGCTATCC ACTCTTACAG CAATTGATA 2820
 AAATATACCT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC 2880
 AGACTTGGGA AACTATTCTA GAATATTTAT ATTGTATGTT AATATAGTTA TTGCACAAGT 2940
 TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

Seq ID NO: 332 Protein sequence
 Protein Accession #: NP_004354.1

1 11 21 31 41 51
 | | | | |
 50 MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLVHNLPO 60
 HLEFGYSWKY ERVDGNRQII GYVIGTQOAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY 120
 TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTCEPE TQDATYLWVW 180
 NNQSLVPSPR LQLSNGNRTL TLFNVTRNDT ASYKCEQNP VSARRSDSVI LNVLYGPDAP 240
 TISPLNTSYR SGENLNLSC AASNPPAQYS WFNVTGQQS TQELFIPNIT VNNSGSYTCQ 300
 55 AHNSDTGLNR TTTVTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTLYLWVWVN 360
 QSLPVSPLRQ LSNDRNLTL LSVTRNDVGP YECGIONELS VDHSDPVLN VLYGPDPTI 420
 SPSYTYRPG VNLSSLSCA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480
 NSASGHSRTT VKTITVSAEL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWVWNGQS 540
 LPVSPRLQLS NGNRTLFLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPTIISP 600
 60 PDSSYLSGAN LNLSCHSASN PSPQYSWRIN GIPQHTQVL FIAKITPNMN GTYACFVSNL 660
 ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

Seq ID NO: 333 DNA sequence
 Nucleic Acid Accession #: NM_006952.1
 Coding sequence: 11..793

65 1 11 21 31 41 51
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 AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTTGC TTCCAGGGCC TGCTGATTTT 60
 TGGAAATGTG ATTATTGGTT GTTGGCGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120
 70 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACACAGATG ACATCTATGG 180
 GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCCGTGTCTG TTCTAGGCAT 240
 TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCAATC TGATGTTTAT 300
 AGTATATGCC TTTGAGTGG CATCTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
 75 ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAAACAA 420
 TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
 CAATTGCTGT GGCCTAAATG GTCCATCAGA CTGGCAAAA TACACATCTG CCTTCCGGAC 540
 TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
 AGAACTCTCT AACCTGGAGG CTGTGAACT AGGCGTGCCT GGTTTTATC ACAATCAGGG 660
 80 CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CTGGTTTGG 720
 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780
 AATTGAATAT TAAGAA

Seq ID NO: 334 Protein sequence
 Protein Accession #: NP_008883.1

1 11 21 31 41 51
 5 MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60
 IGIFVGICLF CLSVLGIIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL 120
 FLKQMLERYQ NNSPPNDDQ WKNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN 180
 DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAVFGFAI 240
 LCWTFWVLLG TMFYWSRIEY

10 Seq ID NO: 335 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120..473

15 1 11 21 31 41 51
 CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180
 AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCCTAT 240
 20 TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300
 CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
 TCCGGTGCAG CATGTTGAAT CCCCTTAACC GCTGCTTGAA AGATACTGAC TGCCACGGAA 420
 TCAAGAAAGT CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCCTCCAG TGAAGGGAGC 480
 25 CGGTCTCTGC TGCACTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
 TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCTCCCT ATTACAGATG CCCACGGCTG 600
 GAGCTGCCTC TCTCATCCAC TTCCAATAA A

30 Seq ID NO: 336 Protein sequence
 Protein Accession #: NP_002629.1

35 1 11 21 31 41 51
 MRASSFLIVV VFLLIAGTLVL EAAVTGVFVK GQDIVKGRVP FNGQDPVKGQ VSVKGQDKVK 60
 AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDTPCPG IKKCEGSGC MACFVPQ

Seq ID NO: 337 DNA sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

40 1 11 21 31 41 51
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCGCTGCG GGCAGCTGCT TCACCCCTCT 60
 CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGCGTCT CTCCTCCTTC TCCAGGTTTG 120
 45 CTGGCTGCAG TGCGCGGCTC CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
 CTGGAGGCGG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG 240
 CTGCCTTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
 TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
 TGAAAATGGC AAGGTTCCCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480
 50 AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540
 CTTGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCAATGG ACCGGGAGGA 600
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGGTGCTT CAGTGGAGGA 660
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAGGT 780
 55 GACAGCCAAG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
 CCATAGCCAA GAACCAAAGG ACCCACACGA CCTCATGTTT ACCATTACCC GGAGCACAGG 900
 CACCATCAGC GTCACTCTCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
 CATCCAGGCC ACAGACTAGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020
 60 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
 GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
 CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
 TACCATCACC ACCCACTCTG AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGGA 1260
 TTTTGAGGCC AAAAACCCAGC ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
 65 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
 ACCTGTGTTT GTCCCCACCCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
 GCCTGTGTGT GTCTACACTG CAGAAAGACC TGACAAGGAG AATCAAAAAGA TCAGCTACCG 1500
 CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
 70 TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTGTGAGG AACACATCT ATGAAGTCAT 1620
 GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
 ACTGATTGAT GTCAATGACC ATGGCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
 CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
 CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
 GGAAGGTGAC ACAGTGTGCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920
 75 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCCT 2040
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGTTGCTGC TTTTGTGGT 2100
 GAGAAAGAAG CGGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCGTGACAA 2160
 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
 80 GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGACG TGGCACCAAC 2280
 CATCATCCCG ACACCCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCACTT 2340
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCAAC GCCCGGCCCT ACGACACCTT 2400
 CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCGCGT TCCTGTAGCT CCTCACCTC 2460
 CTCGCGCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTCAA 2520
 GAAGCTGGCA GACATGTACG GTGCGGGGGA GGACGACTAG GCGGCTTGCC TGCAGGGCTG 2580

GGGACCAAAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTCAGCTGAG 2640
 GACTTCGGAG CTTGTGACGAG AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
 ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCCTCAG AGGCCAAGTT TCCAGAAGCC 2820
 TCTTACCTGC CGTAAATATG TCAACCTGT GTCCCTGGGCC TGGGCTGTCT GTGACTGACC 2880
 TACAGTGGAG TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
 TTTTTTAAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
 GCTGGGCCCA CTGGCCGTCC TGCATTCTG GTTCCAGAC CCAAATGCCT CCCATTCCGA 3060
 TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTGACC CCTTATTTT TATTTTCCCT 3120
 GTTGCGTTGC TATAGATGAA GGGTGGAGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
 TAAAGAAACT TTTCCAGAA AAAAA

Seq ID NO: 338 Protein sequence
 Protein Accession #: NP_001784.2

1 11 21 31 41 51
 | | | | |
 MGLPRGPLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
 KGFFPQRLNQ LKSNKORDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK 180
 YELFHGAHVE NGASVEDPMN ISIIITDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTYN GVVAYSISHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMGDGSGTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEM AVGHVEVRLT VTDLDAPNSP 360
 AWRAATYLMG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMPD DSQGVTAAGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTID 540
 VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPHTSPPQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFIPVL 660
 GAVLALLFL LVLALLVRKK RKIKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTII TPMPYRPRAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 339 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..672

1 11 21 31 41 51
 | | | | |
 ATGAGGCTCC AAAGACCCCG ACAGGCCCGG GCGGGTGGGA GGCAGCGGCC CCGGGGCGGG 60
 CGGGGCTCCC CCTACCGGCG AGACCCGGGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG 120
 AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG 180
 CTGCTCGCCT TGCTGCTGGT CGTGCCCTTA CCGCGGTGT GGACAGAGCG CAACCTGACT 240
 GCGAGACAAAC GAGATCCAGA GGACTCCCGC CGAACGAGCG AGGGTGACAA TAGAGTGTGG 300
 TGTCATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAAAATGG 360
 ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTC CACGTTTTTT CATGGTTGCG 420
 AAGCAGTGCT CCGCTGGTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
 CTCCTGGAAG AGCCCATGCC CTCTCTTTAC CTCAGTGTGT GTAAATTCG CTACTGCAAT 540
 TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGRAAT ATGCTGGGAG CATGGGTGAG 600
 AGCTGTGGTG GGCTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGCGCTC 660
 AGCCTGTCTT GA

Seq ID NO: 340 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MRLQRPRQAP AGRRRAPRGG RGSFYRPDPG RGARRLRRFQ KGGEGAPRAD PPWAPLGTMA 60
 LLALLLVVAL PRVWTDANLT ARQRPEDSQ RTDEGDNRVW CHVCERENTF ECQNPRRCKW 120
 TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEEKRF LLEEMPFFFY LKCKIRYCN 180
 LGGPPINSSV FKEYAGSMGE SCGGLNLAIL LLLASIAAGL SLS

Seq ID NO: 341 DNA sequence
 Nucleic Acid Accession #: XM_035292.2
 Coding sequence: 53..1576

1 11 21 31 41 51
 | | | | |
 GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
 TGCAGGGCCC AAGCGGCGCG CGCTAGCGGC GCCGCGCGCC GAGGAGAAGG AAGAGGCGCG 120
 GGAGAAGATG CTGGCCGCCA AGAGCGCGGA CGGCTCGGCG CCGGCGAGCG AGGGCGAGGG 180
 CGTGACCTCG CAGCGGAACA TCACGCTGCT CAACGCGGTG GCCATCATCG TGGGGACCAT 240
 TATCGGCTCG GGCATCTTCG TGACGCCAC GGGCGTGCTC AAGGAGGCAG GCTCGCGGG 300
 GCTGGCGCTG GTGGTGTGGG CCGCGTGCGG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360
 CGCGGAGCTC GGCACCAACA TCTCAAATC GGGCGGCGAC TACGCTTACA TGCTGGAGGT 420
 CTACGGCTCG CTGCCCGCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGCGCTTC 480
 ATCGCAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAGCCGCG TCTTCCCCAC 540
 CTGCCCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600
 GGCCGTGAAC TGCTACAGCG TGAAGGCCGC CACCGGGTTC CAGGATGCCT TTGCCGCGCG 660
 CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACCTGATG TGGGGAACAT 780
 TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGGAAATFACT TGAATTTTGT 840
 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTCG GCCATCATCA TCTCCCTGCC 900
 CATCGTGACG CTGCTGTAGC TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCACCCGA 960
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020

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GTCCTGGATC ATCCCCGTCT TCGTGGGCCT GTCCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
GTTACATACC TCAGGCTCTT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
CTCCATGATC CACCCACAGC TCCTCACCCC CGTGGCGTCC CTCTGTGTCA CGTGTGTGAT 1200
GACGCTGCTC TAGCCTTCTT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TGGCTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
TGAGCTTGAG CGGCCCATCA AGGTGAACCT GGCCTCGCTT GTGTTCTTCA TCCTGGCCTG 1380
CCTCTTCTCT ATCGCCGTCT CTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
CATCATCCTC AGCGGGCTGC CCGTCTACTT CTTGCGGGTC TGGTGGAAAA ACAAGCCCAA 1500
GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560
CCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

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Seq ID NO: 342 Protein sequence
Protein Accession #: XP_035292.2

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20
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1      11      21      31      41      51
|      |      |      |      |      |
MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYABELGTI SKSGGDYAYM 120
LEVVGSLPAF LKWLIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCLV 180
LLTAVNCYSV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV 240
GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNLPALIII SLPIVTLVYV LTNLAYFTTL 300
STEMLSSEA VAVDFGNYHL GVMSWIIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360
SILSMIHPQL LTPVPSLVFT CVMTLLYAFS KDIFSVINFF SFFNWLCLVAL AIIIGMIWLRH 420
RKPELERPIK VNLAIPVFFI LACLELIAVS FWKTPVECGI GFTIILSGLP VYFFGVWVWKN 480
KPKWLLQGIF STTVLCQKLM QVVPQET

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Seq ID NO: 343 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

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35
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1      11      21      31      41      51
|      |      |      |      |      |
TAAAAAGCAA AAGAATTGCG GGCCGCGTCG ACACGGGCTT CCCCAGAAAC CTTCCCCGCT 60
TCTGGATATG AAATTCAAGC TGCTTGCTGA GTCCTATTGC CGGCTGCTGG GAGCCAGGAG 120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGCTCTGGGT CTTCATCTTC CGCGTGCTGG TGTACCTGGT GACGCGCGAG CGTGTGTGGA 300
GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGCTGTGT 360
TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420
CATGCCCTTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTTACCT GAACCCCGGC AAGAAGCGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATGCGCT 600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTCTGTG GTCAAGTGCC 660
ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 720
TTTTACCCCT CTTATGGTG GCCACAGCTG CCATCTGCAT CTGCTCAAC CTCGTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCTGGC AGCAAGGAAA GCTCAAGCCA 840
TGTGCACAGG TCATACCCCC CACGGTACCA CCTCTTCTTG CAAACAAGAC GACCTCCTTT 900
CGGGTGACCT CATCTTCTG GGTCTCAGCA GTCATCTCTC TCTCTTACCA GACCGCCCCC 960
GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCCTG GACTGGTCTG GCAGGTTGGG 1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCTAGTCC 1140
TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCTCCCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTTCTAGA ATGGAATAG TGAGGGCCAA TGC

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Seq ID NO: 344 Protein sequence
Protein Accession #: NP_005259.1

60
65

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1      11      21      31      41      51
|      |      |      |      |      |
MNWSIFEGLL SGVNYSTAF GRIWLSLVI FRVLVYLVA ERVWSDHDKD FDCNTRQPGC 60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP 120
GKKRGGWLWT YVCSLVFKAS VDI AFLYVFH SFYPKYLPP VVKCHADPCP NIVDCFISKP 180
SEKNIFTLFM VATAAICILL NLVELIYLV KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ 240
DDLSSGLDIF LGSDSHPPLL PDRPRDHVKK TIL

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Seq ID NO: 345 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

70
75
80

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1      11      21      31      41      51
|      |      |      |      |      |
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCCTCTCTC TCACCTCTCT 60
CGCCCTGCTG GCGCTCACCT CCGCGGTGCG CAAAAGAGAA GATAAGGTGA AGAAGGGCGG 120
CCCGGGGAGC GAGTGCCTGC AGTGGGCTGC GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GGGCCAGACC CAGCGCATCC GGTGCAGGGT 240
GCCCTGCAAC TGGAGAAGG AGTTTGGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG 300
TGCGTGTGAT GGGGGCACAG GCACCAAGT CCGCCAAGGC ACCCTGAAGA AGCGCGCTA 360
CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGACCCCTCA AGACCAAGC 420
AAAGGCCAAA GCCAAGAAA GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
GCCCTGTGTG TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540
CACCAGTGCC TCTGTCTGCG TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCTCTCTC 600
ACTCCCCAGC CCCACCCCTA AGTGCCCAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720
ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCCC CAATAAAGC TCTTCTTTT 780

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TAATAT

Seq ID NO: 346 Protein sequence
Protein Accession #: NP_002382.1

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1      11      21      31      41      51
|      |      |      |      |      |
MQHRGFLLLT LLALLALTSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DCGVGFREGT 60
CGAQTQRI RC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLLKKA RYNAQCQETI 120
RVTKPCTPKT KAKAKAKGK GKD

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Seq ID NO: 347 DNA sequence
Nucleic Acid Accession #: NM_006783.1
Coding sequence: 1..786

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACTCTC CACCAGCATC 60
GGGAAGGTGT GGATCAGAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTCCTCC GTGTCCACAC TCCGGCTGTG GGGCCTCCAG 240
CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTTCA GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAAAAAGC ACAAGGTTCT GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCTT TTACAATGGG 480
TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCTT TGTGACTGTC 540
TTTATTTCTA GGCCAAACAG GAAGACCGTG TTTACCATTT TTATGATTTC TCGCTCTGTG 600
ATTTGCATGC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTATAG 660
AGATCAAAGA GAGCACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA

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Seq ID NO: 348 Protein sequence
Protein Accession #: NP_006774.1

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1      11      21      31      41      51
|      |      |      |      |      |
MDWGTLLHTFI GGVNKHSTSI GKVWITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC 60
KNVCYDHFPP VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDFKDIED 120
IKKHVRIEGL SLWWTYTSSI FRIIFEAFAF MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC 180
FISRPEKTV FTIFMISASV ICMLLNVAEL CYLLLVKVCFR RSKRAQTQKN HPNHALKESK 240
QNMNELISD SQQNAITGFP S

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Seq ID NO: 349 DNA sequence
Nucleic Acid Accession #: NM_002571.1
Coding sequence: 99..587

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1      11      21      31      41      51
|      |      |      |      |      |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60
TCACCCCTGGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCCC CTCTGAGGGT CCACATCACC TCACTGTTGC 240
CCACCCCCGA GGACAACTTG GAGATCGTTC TGCACAGATG GGAGAACAAAC AGCTGTGTTG 300
AGAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCAACGA GGCACGCTG CTCGATACTG ACTACGACAA TTTCTGTGTT CTCTGCCTAC 420
AGGACACCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCTGGTGG 480
AGGACGATGA GATCATGCA GATTTCATCA GGGCTTTCAG GCCCTTGCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAA CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCCT 600
CCAGGAAGAC GAGACTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCCCC 660
TTTCAAAGAA TAACCACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCCT 720
TCCTGCTGCA CACTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G

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Seq ID NO: 350 Protein sequence
Protein Accession #: NP_002562.1

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1      11      21      31      41      51
|      |      |      |      |      |
MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPPT EDNLEIVLHR 60
WENNSCVEKK VLGEKTNPK KFKINYTVAN EATLLDTDYD NFLFLCLQDT TTPIQSMMCO 120
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMEEPF RF

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Seq ID NO: 351 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

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1      11      21      31      41      51
|      |      |      |      |      |
ACTTGCCTCT CGCCCTCCGG CCAAGCATGG GGCTTCCAG GCTGGTCTGC GCCTTCTTGC 60
TCGCGCCTCT CTGCTGCTGT CCTCGCTGCG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG 120
CGCCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240
TCATCTTCCG TGTCGCGCAG GGCAGGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC 300

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TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCCTGACTCA AGTCACCCCC CAAGACGAGC 360
GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCCAGGA GTACCGCATC CAGCTCCGCG 420
TCTACAAAGC TCCGGAGGAG CCAAACATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA 480
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCTAAG 540
TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCAAGT 600
CGTCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660
TGGTTAAAGA AGACAAAGAT GCCCAGTTT ACTGTGAGCT CAACTACCGG CTGCCCAGTG 720
GGAACCATCAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCGG ACAGAAAAAG 780
TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT 840
GTTTGGCTGA TGGCAACCTT CCACCACACT TCAGCATCAG CAAGCAGAAC CCCAGCACCA 900
GGGAGGCAGA GGAAGAGACA ACCAACGACA ACGGGGTCTT GGTGTGGAG CCTGCCCGGA 960
AGGAACACAG TGGGCGCTAT GAATGTCAGG CCTGGAATT GGACACCATG ATATCGCTGC 1020
TGAGTGAACC ACAGGAACCTA CTGGTGAAT ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG 1080
CCCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140
ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAGG GGGCCTGTGC 1200
TTCAGTTGCA TGACCTGAAA CGGGAGGCAG GAGGCGGCTA TCGTGCCTG GCGTCTGTGC 1260
CCAGCATACC CGGCCTGAA CGCACACAGC TGGTCAAGCT GGCCATTTT GGCCCCCTT 1320
GGATGGCATT CAAGGAGAGG AAGGTGTGGG TGAAAGAGAA TATGGTGTG AATCTGTCTT 1380
GTGAAGCGTC AGGACACCCC CGGCCACCA TCTCCTGGA CGTCAACGGC ACGGCAAGTG 1440
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Seq ID NO: 352 Protein sequence
Protein Accession #: NP_006491.1

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 Protein Accession #: NP_068604.1

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 45 PDGKDLLAH AFPPGPGTQG DAHFDDDELW SLKGVVVPT RFGNADGAAC HFPFIFEGRS 240
 YSACTTDGRS DGLPWCSTTA NYDITDRFGF CPSERLYTRD GNADGKPCQF PFIFQGQSYS 300
 ACTIDGRSDG YRWCAATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST 360
 CTSEGRGDGR LWCATTSNFD SDKKWGFCDP QGYSFLVAA HEFHALGLD HSSVPEALMY 420
 PMYRTEGPF LHKDDVNGIR HLYGRPEPE PRPPTTTTPQ PTAPPTVCP PTGPVHPSE 480
 50 PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFKDGKYW 540
 RFSEGRGSRP QGPFLIADKW PALPRKLDV FEEPLSKLKF FFSGRQVWVY TGASVLGPRR 600
 LDKLGLGADV AQVTGALRSR RGMMLLFSGR RLWRFVKAQ MVDPRSASEV DRMFPGVPLD 660
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55 Seq ID NO: 359 DNA sequence
 Nucleic Acid Accession #: NM_000213.1
 Coding sequence: 127..5385

60 1 11 21 31 41 51
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 70 GAGCTGGAGG TGTTTGAGCC ACTGGAGAGC CCGTGGACC TGTACATCCT CATGGACTTC 540
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 GTCTTGAGCC AGCTCACCAG CGACTACACT ATTGGATTG GCAAGTTTGT GGACAAAGTC 660
 AGCGTCCCGC AGACGGACAT GAGGCCTGAG AAGCTGAAGG AGCCCTGGCC CAACAGTGAC 720
 CCCCCTTCT CTTCAAGAA CGTCATCAGC CTGACAGAAG ATGTGGATGA GTTCCGGAAT 780
 75 AAAGTGCAGG GAGAGCGGAT CTCAGGCAAC CTGGATGCTC CTGAGGGCGG CTTGATGCC 840
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 TACAGGACAC AGGACTACCC GTCGGTGCCC ACCCTGGTGC GCCTGCTGCG CAAGCAACA 1080
 80 ATCATCCCCA TTTTGTCTGT CACCAACTAC TCCTATAGCT ACTACAGAA GCTTCACACC 1140
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 10 GGCCGCTGCC ACTGCCACCA GCAGTCGCTC TACACGGACA CCATCTGCGA GATCAACTAC 1980
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 TACTG

Seq ID NO: 360 Protein sequence
 Protein Accession #: NP_000204.1

75 1 11 21 31 41 51
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 80 MAGPRPSPWA RLLLAALISV SLSGTIANRC KKAPVKSCTE CVRVKDKCAY CTDEMFRDRR 60
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 PQTDMRPEKL KFPWNNSDPF SFSKNVISLT EDVDEFNRKL QGERISGNLD APEGGFDAIL 240
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 TQDYPSPVPTL VRLLAKHNI IPIFAVTNYSY SYYEKLHTYF PVSSLGVLQE DSSNIVELLE 360
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 FQCPRTSGLF CNDGRGRCSMG QCVCEPFGWTG PSCDCPLSNA TCIDSNNGGIC NGRGHCECCR 600
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 LLPLLLALLL LCWKYCACK ACALALLPCCN RGHMVGFKEG HYMLRENMA SDHLDTPLMR 780
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 RVDGDSFESR LTVPLGSEN PYKFKVQART TEGFGPEREG IITIESQDGG PFFQLGSRAG 1680
 LFQHPQLQSEY SSITTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHVTQEF VSRTLTTSGT 1740
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Seq ID NO: 361 DNA sequence
 Nucleic Acid Accession #: NM_013332.1
 Coding sequence: 1..63

1 11 21 31 41 51
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 GAGCCATCG CCTGGGACCT CCGTGGACCAG CAGAAGCCAA CTAGCCACA CAGAGCCAC 360
 CAAGGGCCTT CCAGACCATC CATCCAGAAG CATGTGATAA GACCTCCTTC CATACTGGCC 420
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 CACTTTGGGA GGCTGAGGTG GGTGGATCAC CTGAGGTCAG GAGTTCGAGA CCAGCCTCGC 660
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 GGCCTGTAAT CCGATCTCTT TGGGAGGCTG AGGCGGGAGA ATTGCTTGAA CCCGGGGACG 780
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 CATCTCAAAA AAAAAAAGAA AAGAAAAAGC CTGTTTAATG CACAGGTGTG AGTGGATTGC 900
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 TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTCAGCTGT TGGGAGATGG 1020
 TGATATTTTC AACCTACTT CCTAAACATC TGTCTGGGGT TCCTTTAGTC TTGAATGTCT 1080
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 CAGTTGAAGA GGTGTGTGG GTGGGCTGTT GGGAGTGAGG ATGGAGTGTI CAGTGCCCAT 1200
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Seq ID NO: 362 Protein sequence
 Protein Accession #: NP_037464.1

1 11 21 31 41 51
 MKHVLNLYLL GVVLTLISIF VRVMSLEGL LESPSPGTSW TTRSQLANTE PTKGLPDHPS 60
 RSM

Seq ID NO: 363 DNA sequence
 Nucleic Acid Accession #: NM_023915.1
 Coding sequence: 250..1326

1 11 21 31 41 51
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 CAAGAGAGTC ACAATTTCAG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCTTCAC 360
 AATGAATTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTTGT GGCAAGCATC 420
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480
 TTCTATCTCA AAAACATAGT GGTTCGAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540
 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600
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 GATCGCTATC TGAAGGTTGT CAAGCCATTT GGGGACTCTC GGATGTACAG CATAACCTTC 720
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 ATCCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAA ACTTAAAGT 840
 CCTTTGGGG TCAATAGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960

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 TGTAGGTCAT TTTCAAGAAG GCTGTTCAAA AAATCAAATA TCAGAACCAG GAGTGAAGGC 1260
 ATCAGATCAC TGCAAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACTGTAT 1320
 GTGTAGGCCT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAAATA AATGTTTCTT 1380
 TTCATTATCC TTAATAAAAA AA

Seq ID NO: 364 Protein sequence
 Protein Accession #: NP_076404

1 11 21 31 41 51
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 FYANMYTSIV FLGLISIDRY LKVVKPFQDS RMYSTPTKV LSVCVWVIMA VLSLPNIIIT 180
 NGQPTEDNIH DCSLKSPPLG VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRRKRK NQSIRVVAVV FFTCFLPYHL CRIPFTFSLH DRLDESAQK ILYYCKEITL 300
 FLSACNVCLD PIIFYPMCRS FSRRLFKKSN IRTSESIRS LQSVRRSEVR IYYDYTDV

Seq ID NO: 365 DNA sequence
 Nucleic Acid Accession #: NM_005365.1
 Coding sequence: 1..948

1 11 21 31 41 51
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 GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTGCGACC AGCTCAGCTG 300
 GAGTTCAFTG TCCAAGAAGC ACTGAAATG AAGGTGGCTG AGTTGGTTCA TTTCTGCTC 360
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 CTTGGCCTCT CGTGGGATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCCGCCCTC 600
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 TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAGG AGCAGATGTT CTACGGGGAG 720
 CCCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAAACT ACCTGGAGTA CCGGCAGGTG 780
 CCCGGCAGTG ATCCTGCGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840
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 CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

Seq ID NO: 366 Protein sequence
 Protein Accession #: NP_005356.1

1 11 21 31 41 51
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 HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKASEFMQVI FGTDVKEVDP AGHSYILVTA 180
 LGLSCDSMLG DGHSMFPAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMFYGE 240
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Seq ID NO: 367 DNA sequence
 Nucleic Acid Accession #: NM_014400
 Coding sequence: 86..1126

1 11 21 31 41 51
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 GATCTGGACT CAGGGCTGGC TGCTGTGCTG GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180
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 GAAGTGCAGC CCGGGCGTGG ACCTCTGCAC CGAGGCGGTG GGGGCGGTGG AGACCATCCA 300
 CGGACAATTC TCGTGTGCGA TGCGGGGTGG CGGTTCGGGA CTCGCCGCA AGAATGACCG 360
 CGGCCTGGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
 CTGCAACGCC AAGCTCAACC TCACCTCGCG GGCGCTCGAC CCGGCAGGTA ATGAGAGTGC 480
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 GGGTACATCG CCGCGGGTGG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
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 CCTCGAATC CCACCCCTTG TCCGGCTGCC CCCTCCAGAG CCCACGACTG TGGCTCAAC 840
 CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAACCCAT 900
 GCCAGCGCCA ACCAGTCAGA CTCGAGACA GGGAGTAGAA CACGAGGCTT CCGGGATGA 960
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 TCCTGCAAAA GGGGGGGCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
 ATTGGCAGCC CTCTGTGTGG CCGTGGCTGC TGGTGTCTTA CTGTGAGCTT CTCACCTGG 1140
 AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTCTGT 1200
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Seq ID NO: 368 Protein sequence
 Protein Accession #: NP_055215

1 11 21 31 41 51
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 SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVTLT 180
 AANVTVSLPV RGCVDQEFCT RDGVTPGPGT LSGSCCQGSR CNSDLRNKTY FSPRIPLPLVR 240
 LPPPEPTTVA STTSVTSTTS APVRPTSTTK PMPAPTSQTP RQGVHEHESR DEEPRLTGGA 300
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Seq ID NO: 369 DNA sequence
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 GTGCGGTACT GGATGCGCTT CAACGTGGAG CGGGCTTGCC AGTCCTACTT TGGCTGTGTG 840
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Seq ID NO: 370 Protein sequence
 Protein Accession #: NP_005320.1

1 11 21 31 41 51
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 STFSCIMQKW GKGREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
 VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQGFLE 300
 DWYHQKFLGS KCSFGDDRHL TNRVLSLGYR TKYARSKCL TETPTKYLWR LNQTRWSKS 360
 YFREWLNSL WFKHHLWMT YESVVTGFFP FFLIATVIQL FYRGRIWNIL LFLITVQLVG 420
 IIKATYACFL RGNAMIFMS LYSLLYMSSL LPAKIFAIAT INKSGWGTSG RKTIVVNF 480
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 KKPEQYSLAF AEV

Seq ID NO: 371 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 148-7095

1 11 21 31 41 51
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5	GGAAAAAGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
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	CAGTTGGAGT	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
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	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACCTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGTACAA	1500
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	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCTG	TTCTTAGATC	TCCACATATG	1800
	AACCTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAAACAGAATA	TGAGGAGGAG	1860
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	GAAGATTCAA	CTTATCAGG	TTCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAT	2100
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	TCCTTTTCTG	CAGGCCCATG	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CTTTTGCTTA	CTTCCCAACT	GAGGTAAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAACCG	2400
	GTATACAATG	GTGAGACACC	TCTTCAACCT	TCCTACAGTA	GTGAAGTCTT	TCCTCTAGTC	2460
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	CCTCTCAGCC	CTGAATCTAA	AGCATGGGCA	GTCTGACAAA	GTGATGAAGA	AAGTGGATCA	4800
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Seq ID NO: 372 Protein sequence:
 Protein Accession #: built from XP_031379

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Seq ID NO: 384 Protein sequence

Protein Accession #: NP_005679.1

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Nucleic Acid Accession #: NM_001327.1
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      GACGGGCGAT GCTGATGGCC CAGGAGGCCC TGGCATTCTT GATGGCCCG GGGGCAATGC 180
10     TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCCCAGGGCG CAGGGGCAGC 240
      AAGGGCCTCG GGGCCGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGGCG CGGCTTCAGG 300
      GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGGAG AGCCCGCTGC TTGAGTTCTA 360
      CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
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15     CATACTGACT ATCCGACTGA CTGCTGCAGA CCACGCCCAA CTGCAGCTCT CCATCAGCTC 540
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      GGCTCAGCTT CCCTCAGGGT AGAGGCGCTA AGCCAGCCCT GGCGCCCCCT CCTAGGTCAT 660
      GCCTCTCTCC TTAGGGAATG GTCCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
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Seq ID NO: 386 Protein sequence
Protein Accession #: NP_001318.1

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Seq ID NO: 387 DNA sequence
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      GTGTTTTTGG CTCAAGCTCC CTCAGGGCAG AGGCCTAAG CCCAGCCTGG CGCCCTTCC 480
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Seq ID NO: 388 Protein sequence
Protein Accession #: Eos sequence

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Seq ID NO: 389 DNA sequence
Nucleic Acid Accession #: NM_005562.1
Coding sequence: 90..3671

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Seq ID NO: 390 Protein sequence
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	PEGCTQPCFY	GHSASCRSSA	EYSVHKITST	FHQDVGWKA	VQRNGSPAKL	QWSQRHQDV	240
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	MPLGKTLPCG	LTKYTFRLN	EHPNSNWSQ	LSYFEYRRL	RNLTLALRIR	TYGEYSTGYI	360
	DNVTILISAR	VSGAPAPWVE	QCICPVGYKG	QFCQDCASGY	KRDSARLGGF	GTICPCNCQG	420
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	CNNCPFGVTG	ARCELCADGY	FGDPFGEHGP	VRPCQPCQCN	NNVDPASAGN	CDRLTGRCLK	540
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Nucleic Acid Accession #: AF101051.1

Coding sequence: 221.856

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Seq ID NO: 394 Protein sequence
Protein Accession #: NP_006171.1

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	CATCACCGTC	ATCCCTAAGT	TCAGACCTGG	ACCACGGTGG	TGTGCGGTTC	AAGGCCAGGT	240
	GGATGAAAG	ACTTTTCTTC	ACTATGACTG	TGGCAACAAG	ACAGTCAAC	CTGTCACTCC	300
	CTTGGGAAG	AACTAAATG	TCACAACGGC	CTGGAAGCA	CAGAACCAG	TACTGAGAGA	360
30	GGTGGTGGAC	ATACTTACAG	AGCAACTGCG	TGACATTCAG	CTGGAGAATT	ACACACCCAA	420
	GGAAACCCCTC	ACCTTCGAGG	CCAGGATGTC	TTGTGAGCAG	AAAGCTGAAG	GACACAGCAG	480
	TGGATCTTGG	CAGTTCTTCA	TCGATGGGCA	GATCTTCTCT	CTCTTTGACT	CAGAGAAGAG	540
	AATGTGGACA	ACGGTTCATC	CTGGAGCCAG	AAAGATGAAA	GAAAAGTGGG	AGAATGACAA	600
	GGTGTGGCC	ATGTCTCTCC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
35	CTTCTTGATG	GGCATGGACA	GCACCCCTGA	GCCAAAGTGA	GGAGCACCAC	TCGCCATGTC	720
	CTCAGGCACA	ACCCAATCA	GGGCCACAGC	CACCACCCCTC	ATCCTTTGCT	GCCTCCTCAT	780
	CATCCTCCCC	TGCTTCAATC	TCCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTTA	840
	AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
	CCAGCTGCC	ACGACCTACG	GTGTATGTCC	AGTGGCCCTC	AGCAGATCAT	GATGACATCA	960
40	TGGACCCAAT	AGCTCATCA	CTGCCCTTGT	TCCTTTTGCC	AACAAATTTA	CCAGCAGTTA	1020
	TACCTAACAT	ATTATGCAAT	TTTCTCTTGG	TGCTACCTGA	TGGAATTCCT	GCACTTAAAG	1080
	TTCTGGCTGA	CTAAACAAGA	TATATCATTT	TCTTTCTTCT	CTTTTGTGTT	GGAAAATCAA	1140
	GTACTTCTTT	GAATGTATGAT	CTCTTCTTGG	CAAAATGATAT	TGTCACTAAA	ATAATCACGT	1200
	TAGACTTCAG	ACCTCTGGGG	ATTCTTTCCG	TGTCCTGAAA	GAGAATTTT	AAATTATTTA	1260
45	ATAAGAAAAA	ATTATATATTA	ATGATTGTTT	CCTTAGTAA	TTTATTGTTT	TGTACTGATA	1320
	TTTAAATAAA	GAGTTCTATT	TCCCAAAAAA	AAAAAATAAA	AA		

Seq ID NO: 398 Protein sequence
Protein Accession #: BAB61048.1

	1	11	21	31	41	51	
	MAAAATKIL	LCLPLLLLLS	GWSRAGRADP	HSLEYDITVI	PKFRPGPRWC	AVQGVVDEKT	60
	FLHYDCGNKT	VTPVSPGLKK	LNVTAWKAQ	NPVLREVVDI	LTEQLRDIQL	ENYTPKEPLT	120
55	LQARMSCEQK	AEHSSSGSQ	FSFDGQIFLL	FDSEKRMWTT	VHPGARKMKE	KWENDKVVM	180
	SFHYFSMGDC	IGWLEDFLMG	MDSTLEPSAG	APLAMSSGTT	QLRATATTLLI	LCCLLIILPC	240
	FILPGI						

Seq ID NO: 399 DNA sequence
Nucleic Acid Accession #: NM_001898.1
Coding sequence: 57..482

	1	11	21	31	41	51	
	GGCTCTCACC	CTCCTCTCCT	GCAGCTCCAG	CTTGTGCTC	TGCCTCTGAG	GAGACCATGG	60
65	CCCAGTATCT	GAGTACCCCTG	CTGCTCCTGC	TGGCCACCCCT	AGCTGTGGCC	CTGGCCTGGA	120
	GCCCAAGGA	GGAGGATAGG	ATAATCCCGG	GTGGCATCTA	TAAACGAGAC	CTCAATGATG	180
	AGTGGGTACA	GCGTGCCTCT	CACCTCGCCA	TCAGCGAGTA	TAAACAAGGC	ACCAAAGATG	240
	ACTACTACAG	ACGTCCGCTG	CGGGTACTAA	GAGCCAGGCA	ACAGACCGTT	GGGGGGGTGA	300
70	ATTACTTCTT	CGACGTAGAG	GTGGGCGGCA	CCATATGTAC	CAAGTCCCAG	CCCAACTTGG	360
	ACACCTGTGC	CTTCCATGAA	CAGCCAGAAC	TGCAGAAGAA	ACAGTTGTGC	TCTTTGCGAG	420
	TCTACGAAGT	TCCTTGGGAG	AACAGAAGGT	CCCTGGTGAA	ATCCAGGTGT	CAAGAATCCT	480
	AGGGATCTGT	GCCAGGCCAT	TCGCACCAGC	CACCACCCAC	TCCCACCCCT	TGTAGTGCTC	540
	CCACCCCTGG	ACTGGTGGCC	CCACCCCTGC	GGGAGGCTC	CCCATTGTGC	TGCGCCCAAG	600
75	GACAGACAGA	GAAGGCTGCA	GGAGTCTCTT	GTGTCTCAGC	AGGGGCTCT	GCCCTCCCTC	660
	CTTCTTCTT	GCTTCTAATA	GCCCTGGTAC	ATGGTACACA	CCCCCCCACC	TCCTGCAATT	720
	AAACAGTAGC	ATCGCC					

Seq ID NO: 400 Protein sequence
Protein Accession #: NP_001889.1

	1	11	21	31	41	51	
	MAQYLSTLLL	LLATLAVALA	WSPKEEDRII	PGGIYNADLN	DEWVQRALHF	AISEYNKATK	60
80	DDYYRRPLRV	LRARQQTVGG	VNYFFDVEVG	RTICTKSQPN	LDTCAPHEQP	ELQKKQLCSF	120

EIYEVWPWENR RSLVKSRQCE S

Seq ID NO: 401 DNA sequence

Nucleic Acid Accession #: NM_003976.2

Coding sequence: 299..961

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1      11      21      31      41      51
|      |      |      |      |      |
CTCTGAGCTT CTCTGAGCCT TGTTTGCTCA TCTGGAATAA GGGGATTAAA CCATTACCT 60
CATGGAGTTG TGAAGAATA GCTGCAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG 120
CTACTTCTGC TGGGTGTAGT CTAGCTGTGT AGGCCCTCTG TTCTCACTCT GGAGAACTG 180
GGGTGGCAGG CCGGTCCCCC ACAAAAGATA ACTCATCTCT TAATTGCAA GCTGCCTCAA 240
CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCTGGTGT TGATAGAGAT 300
GGAACTTGGG CTTGAGAGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GCGGCGAGCC 360
TGCCCTGTGG CCCACCTGG CCGCTCTGGC TCTGCTGAGC AGCGTCGAG AGGCCTCCCT 420
GGGCTCCGCG CCCCAGAGCC CTGCCCCCG CGAAGGCCCC CCGCTGTGCC TGGCGTCCCC 480
CGCCGCGCAC CTGCGGGGG GACGCACGGC CCGCTGGTGC AGTGAAGAG CCCGCGGCC 540
GCGGCGCAG CTTTCTCGGC CCGCGCCCC GCGGCTGCA CCCCCTCTG CTCTTCCCG 600
CGGGGGCCGC GCGGCGCGG CTGGGGGCC GGGCAGCCGC GCTCGGCGAG CCGGGGCGCG 660
GGGTGCGCG CTGCGCTCGC AGCTGGTGCC GGTGCGCGG CTGCGCCTGG GCCACCGCTC 720
CGACGAGCTG GTGCGTTTCC GCTTCTGAG CCGCTCCTGC CGCCGCGCGC GCTCTCCACA 780
CGACCTCAGC CTGGCCAGCC TACTGGGCGC CCGGGCCCTG CGACCGCCCC CGGGCTCCCG 840
GCCCGTCAGC CAGCCCTGCT GCCGACCAC GCGCTACGAA GCGGTCTCCT TCATGGACGT 900
CAACAGCACC TGGAGAACCG TGGACGCGCT CTCCGCCACC GCCTGCGGCT GCCTGGGCTG 960
AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCCTGGGAC 1020
CTTCCGCGAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCT CAAAGCTGAG 1080
AGGCCCTTAC CCGTGGGTGA TGGATATCAT CCCCAGAACG GTGAAGGGAC AACTGACTAG 1140
CAGCCCCAGA GCCCTCACC TGCGGATCCC AGCCTAAAAG ACACCAGAGA CCTCAGCTAT 1200
GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CAGGCGCTCG AACCTGGGAC 1260
CCCTCTCTCG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCGGCCAGG CCCTGTAGGG 1320
ACAGCATTTG AAGGACACAT ATTGCAGTTG CTGGTTGAA AGTGCTGTG CTGGAAGTGG 1380
CCTGTACTCA CTCATGGGAG CTGGCCCC

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Seq ID NO: 402 Protein sequence

Protein Accession #: NP_003967.1

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1      11      21      31      41      51
|      |      |      |      |      |
MELGLGLLST LSHCPWRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
PAGHLPGGRT ARWCSGRRAR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
RGCRRLSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGLG

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Seq ID NO: 403 DNA sequence

Nucleic Acid Accession #: NM_057091.1

Coding sequence: 783..1445

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1      11      21      31      41      51
|      |      |      |      |      |
ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60
GGACCCCCAA ATCTGCACGT ACCAGCAGTC AGCCGCCCCA CGCAGGGACC GGCTTACCCC 120
TCGCTCCCCG CCTCACTCA CTCTTCTCCG CCCTCGGCC GGCCTCCAG CTCTCTACTT 180
CGCGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCTCTC CACCGCTCGA GTTCTCTACT 240
CTCCATATCC GAGGGGGCCC TCCAGCATC TACCCCTCT CCAACCTCGG GGGACCTAGC 300
CAAGCTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAAGGTGGGG 360
CGGGGCGAGG GCGCTCCAG CCCCACCCCG GGATCTGGTG ACCTGCGGCG TGGAAATTGA 420
CACCGGACGG CTGCGCGCGC GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGCCCC 480
CAGACAAGGC CCGGGGGCTC CGCCAGCAGC AGGTCCCTCG GGGCCAGGCC CTCGCTGCCA 540
CCCGGGCCTG GAGCCCCACA CCGAGGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
TAAAGAGGCG ACTGCCAGT GTACAGTCTT GGGCATGCGC TGTTTAGCT TCGGGGGAGA 660
GCCCAGCACT GGTCCCCGGA AAGGTGCCTA GAAGAACAAG GTGCAGGACC CCGTGCTGCC 720
TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGCCTCTCTG GTGTTGATAG 780
AGATGGAACT TGGACTTGGA GGCTCTCCA CGCTGTCCA CTGCCCCTGG CTTAGGCGGC 840
AGCCTGCCTG GTGGCCACC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT 900
CCCTGGGCTC CGCGCCCGC AGCCCTGCC CCGCGAAGG CCCCCCGCT GTCTGGCGT 960
CCCCCGCCG CCACCTGCCG GGGGACGCA CGGCCCGCTG GTGCACTGGA AGAGCCCGGC 1020
GGCCCGCCG GCAGCTTCT CCGCCCGCG CCCCAGGCC TGCACCCCA TCTGCTTTC 1080
CCCGCGGGG CCGCGCGCG CCGGCTGGGG GCCCAGGAG CCGCGCTCG GCAGCGGGGG 1140
CGCGGGGCTG CCGCTGCGC TCGCAGCTGG TGCCGGTGG CCGCTCGGC CTGGGCCACC 1200
GCTCCGACGA GCTGGTGGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCG CCGCGCTCTC 1260
CACACGACCT CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CCGTGGACCG CCCCAGGCT 1320
CCCGGCCCTG CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
ACGTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCCG CACCGCTGC GGTGCTGG 1440
GCTGAGGGCT CGCTCCAGGG CTTTGACAG TGGACCTTA CCGGTGGCTC TTCTGCTG 1500
GGACCTCCCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC 1560
TGAGAGGCC CTACGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACCTGA 1620
CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAAGACACCA GAGACCTCAG 1680
CTATGGAGCC CTTCGAGACC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG 1740
GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT 1800
AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTCTTGGT TGAAAGTGCC TGTGCTGGAA 1860
CTGGCCTGTA CTCATCATG GGAGCTGGCC CC

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Seq ID NO: 404 Protein sequence

Protein Accession #: NP_003967.1

5
1 11 21 31 41 51
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
PAGHLPGGRT ARWCGRARR PPPQSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
RGCLRLSQLV PVRALGLGHR SDELVRFRFC SGSCRARSAP HDLSLASLLG AGALRPPPGS 180
RPVSPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

10 Seq ID NO: 405 DNA sequence
Nucleic Acid Accession #: NM_057160.1
Coding sequence: 1..714

15
1 11 21 31 41 51
ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCAAGGCC 60
CACCTGGGTG CCCTCTTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
TGGCCCAACC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCG CAGAGGCCTC CCTGGGCTCC 180
GGCCCCCGCA GCCCTGCCCC CCGCGAAGGC CCCCAGCCTG TCCTGGCGTC CCCCAGCGGC 240
20 CACCTGCCCG GGGGACGCAC GGCCCGCTGG TGCAGTGGAA GAGCCCGCGC GCCCGCGCGC 300
CAGCCTTCTC GGCCCGCGCC CCGCGCGCCT GCACCCCAT CTGCTCTTCC CCGCGGGGCG 360
CGCGCGGCGC GGGCTGGGGG CCGGGGACAG CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
CGCCTGCGCT CGCAGCTGGT GCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCGACGAG 480
CTGGTGCGTT TCCGCTTCTG CAGCGGCTCC TGCCGCGCGC CGCGCTCTCC ACAAGACCTC 540
25 AGCCTGGCCA GCCTACTGGG CGCCGGGGCC CTGCGACCGC CCCCAGGCTC CCGGCCCTGC 600
AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
ACCTGGAGAA CCGTGGAACG CCTCTCCGCC ACCGCTCGCG GCTGCTGGG CTGAGGGCTC 720
GCTCCAGGGC TTTCAGACTT GGACCTTAC CGGTGGCTCT TCCTGCCTGG GACCCCTCCG 780
30 CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGCCCC 840
TACCGGTGGG TGATGGATAT CATCCCGGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC 900
AGAGCCCTCA CCTGCGGAT CCCAGCCTAA AAGACACCA AGACCTCAGC TATGGAGCCC 960
TTGGAACCCA CTCTCAGAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020
CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCGCGCC AGGCCCTGTA GGGACAGCAT 1080
35 TTGAAGGACA CATATTGCA TTGCTTGGT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC 1140
TCACTCATGG GAGCTGGCCC C

Seq ID NO: 406 Protein sequence
Protein Accession #: NP_476501.1

40
1 11 21 31 41 51
MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSSVAEASLGS 60
APRSPAPREG PPPVLASPAH HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120
45 RAARAGGPGS RARAAGARGC RLRSQVLPVR ALGLGHRSD LVRFRFCSGS CRRARSPhDL 180
SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

Seq ID NO: 407 DNA sequence
Nucleic Acid Accession #: NM_057090.1
Coding sequence: 29..715

50
1 11 21 31 41 51
CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTTGA CTGGAGGCC TCTCCAGCT 60
55 GTCCCACTGC CCCTGGCCTA GGCGGCAGGC TCCACTTGGT CTCCTCCGCG AGCCTGCCCT 120
GTGGCCCAACC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCCTGGGCTC 180
CGCGCCCGCG AGCCTTGCCC CCGCGAAGG CCCCAGCCTG GTCTGGCGT CCCCAGCGGC 240
CCACTGCGCG GGGGACGCA CGGCCGCTG GTGCACTGGA AGAGCCCGGC GGGCCGCGCC 300
GCAGCCTTCT CGGCCCGCGC CCGCGCGGCC TGCACCCCA TCTGCTCTTC CCGCGGGGG 360
60 CCGCGCGCGC CGGGCTGGGG GCGCGGGCAG CCGCGCTCGG GCAGCGGGGG CCGGGGCTG 420
CCGCTGCGC TCGCAGCTGG TCGCGTGGC CGCGCTCGGC CTGGGCCACC GCTCCGACGA 480
GCTGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGCGCTCTC CACACGACCT 540
CAGCCTGGCC AGCCTACTGG GCGCGGGGC CCTGCGACCG CCCCAGGCT CCGGCCCTG 600
CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACCTCAACAG 660
CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGGCT 720
65 CGCTCCAGGG CTTTGACAGC TGGACCTTA CCGGTGGCTC TTCTGCTG TGAGCCCTCC 780
GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGCC 840
CTACCGGTGG GTGATGGATA TCATCCCGCA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900
CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
70 CTTGCGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG GGACCCCTCC 1020
TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCGCGC CAGGCCCTGT AGGGACAGCA 1080
TTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCCT TGTGCTGGA TGGCCTGTGTA 1140
CTCACTCATG GGAGCTGGCC C

Seq ID NO: 408 Protein sequence
Protein Accession #: NP_476431.1

75
1 11 21 31 41 51
80 MELGLGGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
GPPPVLASPA GHLPGGRTAR WSCGRARRPP PQPSRPAPP PAPPSPALPRG GRAARAGGPG 120
SRARAAGARG CLRLSQLVPV RALGLGHRSD ELVRFRFCSG SCRARSPhD LSLASLLGAG 180
ALRPPPGSRP VSQPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG

Seq ID NO: 409 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1746

5	1	11	21	31	41	51	
	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
	GCCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCCAGGT	GGAGTGCACC	120
	GGGGCACGCA	TTGTGGCGGT	GCCCAACCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
10	CTAACACGCG	ACATCACTGA	ACTCAATGAG	TCCCCGTTCC	TCAATATCTC	AGCCCTCATC	240
	GCCCTGAGGA	TTGAGAAGAA	TGAGCTGTGC	CGCATCACGC	CTGGGGCCTT	CCGAAACCTG	300
	GGCTCGCTGC	GCTATCTCAG	CCTCGCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCCCTC	360
	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAAGT	GTTCAGATC	420
	CAGCCGGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCAC	480
15	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540
	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCCCTCCGGC	TGTATGAGAA	CAGGCTCACG	GATATCCCCA	TGGGCACITT	TGATGGGCTT	660
	GTTAACTGCG	AGGAACCTGC	TCTACAGCAG	AACCAGATTG	GACTGCTCTC	CCCTGGTCTC	720
	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCACAT	CTCCAGCTG	780
20	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
	TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTCTGATT	TGAGCCGCAA	TCAGATCAGC	TTCATCTCCC	CGGGTGCTT	CAACGGGCTA	1020
	ATCGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
25	TTCCGCATGT	TGGCCAACTT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CTCAGGAATA	TCCTCGCCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCCAG	1200
	CTGGAGAACT	TGCCCCCTCG	CATCTTCGAT	CACCTGGGGA	AACTGTGTGA	GCTGCGGCTG	1260
	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCTGTCTC	1320
	AACCAAGCCTA	GGTTAGGGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCCAGC	CAATGTCCGA	1380
30	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTGTGCTTTC	CAAGCGTCCA	TGTCCCTGAG	1440
	GTGCCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCCGTCTCTT	CTACCACTGA	GCTAACCAAG	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTGAGTCTA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCCAGAG	CGGGCTGGCC	1620
	ATTGCGGCCA	TTGTAAATGG	CATTGTGCCC	CTGGCCTGCT	CCCTGGCTGC	CTGCGTGGCC	1680
35	TGTTGTCTGCT	GCAAGAAAGAG	GAGCCAAAGCT	GTCTGTATGC	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAATGATGG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTCTGTGCC	1860
	CTAGATAAAG	GTGTGCTTAC	CTCTTCCTGA	CTTGCCCTGAT	TCTCCCGTAG	AGAAGCAGGT	1920
	CGTGCCGGAC	CTTCTTACAA	TCAGGAAGAT	AGATCCAAC	GGCCATGGCA	AAAGCCCTGG	1980
40	GGATTTCGCA	TTTATACCCC	TGGGCTTCCT	TCGAGAGGGC	TCTTCTCCCA	AACTCTCCCC	2040
	ACCTGTCTCT	CAAGAACAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTC	2100
	AGTTAGTCCA	CAGCTGTCTC	ACTTCGTGGG	AAATAGTTCT	CGCTGAGATA	GCCCCCTCTG	2160
	CCTAAGTATT	ATGTAAGTTG	ATTTCCCTTC	TTTTGTCTCT	CTTGTTTGTG	CTATGGCTTG	2220
	ACCCAGCATG	TCCCTCTAAA	TGAAAGTTCT	CCCCTTGATT	TTCTGCTCCT	GAAGGCAGGG	2280
45	TGAGTTCTCT	CCTCAAAGAA	GACTTCAAAC	CATTTAAGTG	GTTCCTTAAG	AGCCGTCAAT	2340
	CAGCTGTGTT	TTGGGGATGC	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTCTG	2400
	AGACAGAAGA	GCCCTCATCA	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAGAAACAA	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAAACTGCA	AACTTTGCTT	2520
	TGAAAAGTTT	AGCCCTTTAA	GGAAATGAAAT	CATGTAGAAAT	TTTGGAATTC	TAAAAACATT	2580
50	AAAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCTGGGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTTTGTTTTA	AAATTTTAA	TGAAGCATG	TGAAGTGATC	STGCAGAAAA	2700
	GTGGGAACAT	GATAGTGTTT	GGCTTGGTGG	ATTTTCACAA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCCAAG	2820
	GGAGATGGGG	GCTTCTGTAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGCA	GCCAGGACGG	2880
55	TCCCCCACA	GTCAGCCTGT	GCAAGGCCCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATT	TATTATATCT	GGAGACCTTG	3000
	AGAGACCCCT	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGCAG	CCACACCCCT	TTCCCTGCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCC	3120
	TCCGCTGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTTAAATT	TTCATTCTTC	3180
60	ACTTAGGGGA	AGTGAATTCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAAAC	AAGTGTAAAC	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAT	TCTCCATCAA	CATCAAGTCT	AGCTGGCAGC	3300
	TGAACCTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACACTGG	3360
	GTCTGGGGGG	TCCCTGGAGC	TCCTCTGCG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
	TCCAGGGTTA	TTCTCTCTCT	CGAGTCACAG	TCACACGAAT	ACCTGCCTTC	TCTGGCTTTC	3480
65	CTGCTATACA	CATATTACAA	TGGCGTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGTCTTT	3540
	CTCTGGACAA	CTGGCCAGT	TTACAGTGAA	ATGGAGAATT	TCAGGTCTCC	ACGTCTGCCC	3600
	AGGAAAGAAC	TTCACTGAC	TCCACGGGGA	TCTGGAAATC	CACGACCAAT	CCCGATCGGC	3660
	TCTTATAGC	TCCCCGCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
	TCCGCTCTTA	TTAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAAATC	TACCACCAAT	3780
70	CCCGATCGGC	TCTTATTAGC	TCCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGC	TGCTGACCA	TTTCTCTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC	3900
	TGTTTGCAAA	CACCTAGTGCA	CTTTGTAGCT	TTTCAACCTC	TGTCCAGGGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAGAGTC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAAG	GCAATTTCCAC	4020
	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAACA	GGAAGTGAGC	4080
75	CCAGAGCATG	GCACATGAGC	ATCACCCGCT	GATGGTGGCC	TGCTGTGCCT	GGTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTCGCCAC	AGACCTGTCT	4200
	GGTGCTCTCT	TGAGTGGCCT	CCAGATGTCT	TTGTGCATAG	GCACAGTGG	GCCAGGGCTG	4260
	GAGGGAGGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCTTTA	4320
	GGTATTCTCT	CGAGTAGCCA	TGACATTGGA	GCACCTTCCT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCTCTCAGT	GACACCAACC	AGGAGCAACC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
80	GCCTCCTTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGG	GTCTCCTTTC	CAACAGGATG	ATGCATTTGC	TCAATTTCTA	4620
	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTTCAGTTT	4680

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GGTGTTCAAT AGGCTGGGAG TTTTATTAT CTCTTCAAC TTTGTACAAG AGCTCATGGC 4980
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Seq ID NO: 410 Protein sequence
Protein Accession #: BAB84587.1

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FQGLDSLESLL LSSNQQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFF HLVLTKLNL 180
GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQO NQIGLLSPGL 240
FHNHNLQRL YLSNHHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRLEWL 300
YDNHISLPD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLGDNV 360
FRMLANLQNI SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENLEPLGIFD HLGKLCBLRL 420
YDNWRCDSD ILPLRNWLLL NQPRLGTDIV PVCFSFANVR GQSLIIINVN VAVPSVHVPE 480
VPSYETPWPY PDTSPYDPT SVSSTELTS PVEDYDILT IQVTDDRSMV GMTQAQSGLA 540
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Seq ID NO: 411 DNA sequence
Nucleic Acid Accession #: XM_098151
Coding sequence: 1..447

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CTATTTTAA AAGAGTCTTA CTGTGCACAG ATACTCTTCA AGCAGCTGGAC GTGGATTCTC 240
TTCTAGCCCC TCAGCACCCC TGCGGTAGGA GTGCCGCCCT TACCCACTTG TGATGGGGTA 300
CAGAGGCACT TGCTCTCTG CATGGTGTTC AATAGGCTGG GAGTTTTATT TATCTCTTCA 360
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Seq ID NO: 412 Protein sequence
Protein Accession #: XP_098151

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Seq ID NO: 413 DNA sequence
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Coding sequence: 77..1372

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TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAAA 240
GAAATTCGGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
TCACCTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA 360
CTCTGCCACT GTCCTTCAGC AAACGTACCA TGCCACAGA TCTGATGCTC TTCAGCTGGG 420
CCTGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCTT GGTGCTATGT 480
GCAGGTGGCG CTAAAGCCGC TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA 540
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CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG 720
CCCTTGCTGG GTGATCAGCG CCACACACTG CTTCAATTGAT TACCCAAAAGA AGGAGGACTA 780
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GGTGGAAAAC CTCATCTCAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA 900
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CACTGGCTTT GGAAAAGAGA ATTCATCCGA CTATCTCTAT CCGGAGCAGC TGAAAATGAC 1080

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CACCACCAGG GTGAACGACA ATAGCTTTAC CCTCACGGAT AGGCCCTGGT GCTGGCTGCC 1560
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ATCCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTGCACACT TGTGTGTGG 1920
GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTCTCTT 1980
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ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT 2160
ATCCCTTCTT TTTAGCCTAG TTTATCCAA CTCTACTGGG TGGGTGAGG ACCACTCCTT 2220
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Seq ID NO: 414 Protein sequence
Protein Accession #: NP_002649.1

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YCRNPDPNRRR PWCVYQVGLK PLVQEVMVHD CADGKKFPSSP PEELKFQCGQ KTLRPRFKII 180
GGEFTTIENQ PFFAAIYRRH RGGSVTVYCG GSLISPCWVI SATHCFIDYP KKEDYIVYLG 240
RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHNDIALLK IRSKEGRCAQ PSRTIQTICL 300
PSMYNDPQFG TSCEITGPGK ENSTDYLYPE QLKMTVVKLI SHRECQPHY YGSEVTTKML 360
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Seq ID NO: 415 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

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GAGCATCAA CAAAGGTCCT AAAGAAAAGA CATACTAAAG AAAAAGTTCT AAGGCGCGCC 600
AAGAGAAGAT GGGCTCCAAT TCCTTGTTGG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660
CTTTTCTTCT AACAGGTTCA ATCTGACACG GCCCAAACT ATACCATA TAATTCCATA 720
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Seq ID NO: 416 Protein sequence
 Protein Accession #: NP_077740.1

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 KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PPFLLQVQV SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLFFYVER DTGNLYCTRP VDREQYESFE IIAFATPDG YTPELPLPLI IKIEDENDNY 240
 PIFTEETYTF TIFENCVRGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFSMHPT 300
 TVGIVTTSSQ LDRELIDKYQ LKIKVQMDMG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KTNIEGVLV 420
 KPLNLYEEKQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDEPT RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540
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Seq ID NO: 417 DNA sequence
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 15 AGTACACAAA TTTTCAAT TTTACATATT TTAAATTAC TTATCTCTA TCCAAGGAGG 3180
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 TTTATAGTGC AATAAATGT AATTAATTCA AGTCCTTATT ATAGACTATT TGAAGCACAA 3300
 CCTAATGGAA AATTGTAGAG ACCTTGCTTT AACATTATCT CCAGTTAATT AAGTGTTCAT 3360
 GTGGTGGCTT GAAACTGTTG TTTTCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT 3420
 20 ATTATTTTAT TCTGTGAATG TGACCTTTTC ACTGTGCAAA GGGAGATTTC TAGCCAGGCA 3480
 TTGACTATTA CAATTCATT

Seq ID NO: 418 Protein sequence
 Protein Accession #: NP_004940.1

25 1 11 21 31 41 51
 MEAARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLHVP SKLDAEKLVG RVNLKECFTA 60
 ANLIHSSDDP FQLEDGDSVY TTNITLLSSE KRSFTILLSN TENQEKKKIF VFLEHQTKVL 120
 30 KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PPLFLQVQV SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPLEPLPLI IKIEDENDNY 240
 PIFTEETYTF TIFENCRVGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPLFSMHPT 300
 TGVITTTSSQ LDRELIDKYQ LKIKVQMDMG QYFGLQTTST CIINIDVDND HLPTFTRTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KINEGVLCVV 420
 35 KPLNYEEKQO MILQIGVUNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540
 KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDPD 600
 EPIHGPPDF SLESTSEVQ RMWRLKAIND TAARLSYQND PPFSGYVVI TVDRDLGMSS 660
 VTSLDVLTCD CITENDCTHR VDPRIIGGGV QLGKWAIIAI LLGIALLFICI LFTLVCGASG 720
 40 TSKQPKVIPD DLAQNLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780
 QETIEMVKGK HQTSESCRGA GHHHTLDSR GGHTEVDNCR YTYSEWHSFT QPRLGEESIR 840
 GHTLIKN

Seq ID NO: 419 DNA sequence
 Nucleic Acid Accession #: NM_002722.1
 Coding sequence: 14..301

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 50 ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCACGTA TGCAGCTGAT CTCCGTAGAT 180
 ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAAGACA CAAAGAGGAC ACGCTGGCCT 240
 TCTCGGAGTG GGGGTCCCG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGGACTTAT 300
 55 AATGCCACCT TCTGCTCTCT ACGACTCCAT GAGCAGCGCC AGCCCCAGTC TCCCCTCTGC 360
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Seq ID NO: 420 Protein sequence
 Protein Accession #: NP_002713.1

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 65 TRPRYKGRHK EDTLAFSEWG SPHAAPREL SPLDL

Seq ID NO: 421 DNA sequence
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 Coding sequence: 46..718

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 75 CTATCAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTTG CCACTCAGAA 180
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 CGAGGGCTGG GGGCCGGAGG AGCCGCTCCC CTACTCCCGG GCTTTCGGAG AGGGTGCCTC 300
 CGCGCGGCGG CGCTGCTGCA GGAACGGCGG TACCTGCGTG CTGGGCGAGT TCTGCGTGTG 360
 CCCGGCCAC TTACACGGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC 420
 80 CCTGGAGCAC GAGCGCTGGA CCCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGGC 480
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 CCACGCTCAC GGGCCGAGCG CCGGGGGCGC GCCCAGCCTG CTACTCTTGC TGCCTTGCCTC 600
 ACTCTGCAC CGCTCTCTGC GCCCGGATGC GCCCGGCGAC CCTCGGTCCC TGGTCCCTTC 660
 CGTCTCCAG CGGAGCGGCG GCCCTGCGG AAGGCCGGA CTTGGGCATC GCCTTTAATT 720
 TTCTATGTTG TAAATAATAG ATGTGTTTAG TTTACCGTAA GCTGAAGCAC TGGGTGAATA 780

TTTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840
AAAAAA

Seq ID NO: 422 Protein sequence
Protein Accession #: NP_115934.1

1 11 21 31 41 51
| | | | |
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VTGSAEGWGP EEPLPYSAF GEGASARPRC CRNGGTCVLG SFCVCPAFT GRYCEHDQRR 120
SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL 180
LLPCALLHRL LRPDAPAPHR SLVPSVLQRE RRPCGRPLG HRL

Seq ID NO: 423 DNA sequence
Nucleic Acid Accession #: NM_006533.1
Coding sequence: 72..467

1 11 21 31 41 51
| | | | |
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CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT 120
TCTCCGGACC TGGTGTCAGG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180
CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240
CCGACTGCCG ATTCCTGACC ATTCACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300
AGGGCCGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360
CTGCTCGCCT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAGACC CTGAAACCTG 420
GCAAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAAGTACGT CAGCCTACCG 480
CTGGCCCTGC CGTTTCCCCT CTTTGGGTTT ATGCAAATAC AATCAGCCCA GTGCAAAC

Seq ID NO: 424 Protein sequence
Protein Accession #: NP_006524.1

1 11 21 31 41 51
| | | | |
MARSLVCLGV IILLSAFSGP GVRGGMPKPL ADRKLCADQE CSHPISTMAVA LDYMAPDCR 60
FLTIRHQVQV YVFSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD 120
VKTDKWDYFC Q

Seq ID NO: 425 DNA sequence
Nucleic Acid Accession #: NM_080870.1
Coding sequence: 3..710

1 11 21 31 41 51
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AGAAAAACAC AAGAACCCCA GAAAAGCCTA CGCTATACTC AGAGAAGACC ATATGCACCA 120
AAGGGA AAAA CACACCACTG CCAGAAAAGC CTACAGAAAA CCTGGGGAAC ACCACACTGA 180
CCACTGAGAC CATAAAAGCC CCAGTAAAGT CCACAGAAAA CCCAGAAAAA ACAGCAGCAG 240
TCACAAAGAC TATAAAACCT TCAGTCAAGG TCACAGGAGA CAAATCTCTC ACTACTACCT 300
CTTCTCATCT AAATAAAACT GAAATTACTC ATCAGGTGCC CACTGGTCTT TTCACCTCA 360
TTACATCTAG AACGAAGCTG AGTTCTATCA CATCAGAAAG CACAGGAAAC GAGAGCCATC 420
CATACCTCAA TAAAGATGGC TCACAGAAAG GTATCCACGC TGGACAGATG GGAGAGAATG 480
ATTCAATCCC TGCATGGGCC ATAGTTATTG TGGTCCTGGT GGTCTGTGATT CTCCTCTCTG 540
TGTTCTCTGG CCTGATCTTC TTGGTCTCCT ATATGATGCG GACACGCCGC ACTACTAACC 600
AGAACACCCA GTACAATGAT GCAGAGGATG AGGGTGGCCC CAATTCTTAC CCGGTCTACC 660
TGATGGAGCA GCAGAATCTT GGCATGGGCC AGATCCCTTC CCCACGGTGA TCTTGGAGTA 720
GGCGCCACG CCTGCTCTCT CCATGCTCTG CCCCTTTCTT GGATGAGGAA CCGGACTCAC 780
AATTCTATT TCCGGGACTA CAGGAAGGGC AGAGAATACT GACGGTTACC AGTATTAACC 840
CTTCATCTGT TCTTGAAACT GGTGGGGGAA TGAGGTGATA AGCAAGGAGG GTGTAAGTTT 900
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TGAGTCTTAA AGGAAGGACA GGAGCCTTAT AGGCAATGCC CCAGACTGAC TTGTGAGTGG 1080
GGTTTATGGG GAAAGGGAGG GACTGAGGGC AGAGTCTCTG GGTTCAGGA CAGCATTATG 1140
TTATTTCAT TCACTATTAC TTAAGAGTTT GTGTGTAAC AGGCTCATCT CTGAGTTCTC 1200
AGGACCCTTG CCCCCACCCC CATTTTTTTA ATGAAAAAAA AAAACAAAAA AACCGATCC 1260
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CCAGAAAGAA TCATAAATAT CTCTCATCTA CATGGTTGCT TCCTCTCTCT CCCAAATCCC 1380
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GACCTTCCCT GATTGGTGTC TCAGCATTTA TTTTCTGTG TCTTCCACCA AAAGCCAGCT 1560
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ATGTT

Seq ID NO: 426 Protein sequence
Protein Accession #: NP_543146.1

1 11 21 31 41 51
| | | | |
MTQVTEKSTE HPEKTTSTTE KTRTPPEKPT LYSEKTICTK GKNTVPVEPK TENLGNITLI 60
TETIKAPVKS TENEKTAAY TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI 120
TSRTKLSSIT SEATGNESHP YLNKDGSKQG IHAGQMGENG SFPAAVIVIV VLVAVILLV 180

FLGLIFLVSY MMRTTRTLTQ NTQYNDAEDE GGPNSYPVYL MEQQNLGMGQ IPSPR

Seq ID NO: 427 DNA sequence
Nucleic Acid Accession #: XM_069480.1
Coding sequence: 1..4383

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1 11 21 31 41 51
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GCAATTGTCA GCCTAATGTA CGGTATCAAG AAGGCCGTGCC AGTTCGGAG GGAGATGAGT 180
CTGGGGTGTG GCTGTGGCTC TGTGACCCTT TACAGCAGCC ACCATGAGGG GGAGGCTGCC 240
AGCCAGCGCT ACTCTTGTC AATGAAAGCT TCTTGGGGGG CAGGTGCTAC TACATTCCAA 300
GAATATCAGA AAATGAGGA ACTCTCAACA TCCGATCACA TATTTCCCTT CACTCCAGGC 360
CTTGTATTATA GTATCCCTTT TGATCACAAT GTTCTGCATT CAGGACAAAG ACCTCCAGAG 420
CTCCCTAAAT CTACAGAAAT CCATGAGCAA AAACGCCACT GCAACACCAC ACGCCATTCT 480
AAGCCAACCTG ACAAGCCTAC AGGCAATCC AAAACTATAG ACCACAAAAG CTCTACAGAT 540
AATCATGAGG CTCTCCACAT TTCTGAAGAA AACTCCAGCA ACCAAGGGA AGACCCAATG 600
ATCCGGAACC AGCGCTCTGT TGATCCTGCT GACTCCACTA CCACACATA AGAATCCGCT 660
GGAAAAAACA ATATAACGCC AGCACCACAG AGCAAAATAA ACTGTCTGTA GTCCACAACA 720
GGCAATCAAT CGGTAAACAAG AAAATCAGAT AAAACTGGAA GACCTTTGGA AAAGTCCATG 780
AGTACTTTGG ATAAGACAAG TACCAGCTCA CATAAGACTA CAACTTCTTT CCACAACCTA 840
GGCAATTACAG AGACCAAGCA AAAAAGCACA TCTTTTCCAG AAAAAATCAC AGCAGCCTCA 900
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TCAGCCAATG AGCTCACACA ATCTCTAGCA GAGCCTACAG AACATGGAGG AAGGACAGCC 1080
AATGAGAAAC ACACACCATC CCCAGCAGAG CCTACAGAAA ATAGAGAAAG GACAGCCAAT 1140
GAGAACAACA CACTATCCCC AGCAGAGCCT ACAGAAAATA GAGAAAGGAC AGCCAATGAG 1200
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ACCACACTAT TCCCAGCAGA GCCTACAGAA CATGGAGAAA GGACAGCCAA TGAGAACACC 1320
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TCATCCTCAG CAGAGCCTAC AGAACACGGA GAAAGGACCC CACTGGCCAA TGAGAACACC 1800
ACACCATCCC CAGCAGAGCC TACAGAAAAT AGAGAAAGGA CAGCCAATGA GAAGACCACA 1860
CCATCCCCAG CAGAGCCTAC AGAAAAATAGA GAAACAACAG CCAATGAGAA GACCACACCA 1920
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AACGAGAGCC ATCCATACCT CAATAAAGAT GGCTCACAGA AAGGTATCCA CGCTGGACAG 4140
ATGGGAGAGA ATGATTCAAT CCCTGCATGG GCCATAGTTA TTGTGGTCTT GGTGGCTGTG 4200
ATTCTCTCTC TGGTGTTCCT TGGCCTGATC TTTCTGTGCT CCTATATGAT GCGGACACGC 4260
CGCACACTAA CCCAGAACAC CCAGTACAAT GATGCAGAGG ATGAGGGTGG CCCCATTCC 4320
TACCCGGTCT ACCTGATGGA GCAGCAGAA CTGCGCATGG GCCAGATCCC TTCCCCACGG 4380

TGA

Seq ID NO: 428 Protein sequence
Protein Accession #: XP_069480.1

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LVYSIPFDHI VLHSGQRPPE LPKSTEIHEQ KRHCNTRHS KPTDKPTGNS KTIDHKSSTD 180
NHEAPPTSEE NSSNQGDPM IRNQRSVDPA DSTTHKESA GKKHITPAK SKINCRKSTT 240
10    GKSTVTRKSD KTRGRPLEKSM STLDKTSTSS HKTTTSFHNS GNSQTKQKST SFPEKITAAS 300
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      NENNTSPSPAE PTENRERTAN ENTTLSPAEP TENRERTANE NTAPFPAGPT ENREMTANEN 420
      TTLFPAEPT EHGERTANENT TPSPAEPTEH GERTANENTT PSPAEPTEHG ERTPFANDKT 480
      TSSSAESTEH GERTPLANEN TTPSPAEPTE NRERTANENT TSPAPAGPTEN RETTANEKTT 540
15    LSPVEPTENR ETTANEKTTT SPAEPTENGQ RTPFANEKTT SSSAEPTHEG ERTPLANENT 600
      TPSPAEPTE RERTANEKTT PSPAEPTEH DRTPLANEKT TPLAEPTEEN GQRTPFANEK 660
      TTSSSAEPT EHEERTPLANE NTTPSPAEPTE ENRERTANEN TTPSPAEPTE NREMTANEK 720
      TLFPAEPTEN RERTANEKTT SSPAEPTEH QRTPFANEKT TSSPAEPTEH GERTPLANEN 780
      TTLSPAEPTE NRERTANEKT TFPFAEPTEN RERTANENTT PSPAQPTENG DRTPLANEKT 840
20    TPLAEPTEEN GKRTPFANEK TTSSSAEPT HAERTPLANE NTSSPAEPT ENRERTANEK 900
      TTQFPAEPT NRESTANEKT TFPFAEPTEN REWTANENTT LSPAEPTEHE EMTPLANEKT 960
      TPLAEPTEEN GERTPFTEK TTPSSAEPT EHGERTPLANE ITTPSRAEPT EHGERIANEK 1020
      ATPSPAEPTE HGETTVNEDT TPSSAEPTEN GERTPLANEN TTSPTESTE HGERTANEKT 1080
      TPSPAEPTEH GERTPSANEK TTPSPAEPTE HEEMTPSANE NTTPSPVKPT EHGEKTTLAN 1140
25    EKITLSPGEP TEHGAKTTSA NEKITPSLAK PTEHGERTTS PNDKITSSAA ESTEHRDRAT 1200
      SANVITPAPA EPIKHAKTIT LAHEKMTQVT EKSTHEPEKT TSTTEKTRT PEKPTLYSEK 1260
      TICTKGKNTV VPEKPTENLG NTTLTETETIK APVKSTENPE KTAAVTKTIK PSVKVTGDKS 1320
      LTTTSSHLNK TEVTHQVPTG SFTLITSRTK LSSITSEATG NESHYPYLNKD GSQKGIHAGQ 1380
30    MGENDSFPAP AIVIVLVAV ILLLVFLGLI FLVSYMMRTR RTLTQNTQYN DAEDEGGPNS 1440
      YPVYLMQEQN LGMGQIPSPR

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Seq ID NO: 429 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..10674

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      GGGGCCCCCG GGAGTATCCC CGCGCCGCCC GCTCCTGGCG ACGAAGCGGC GGGGAGCAGA 180
      GTGGAGCGCG TGCGCCAGGC GTTCCGCGCA CGCGTGCGGC TGCTGCGGGA GCTCAGCGAG 240
      CGCTCGGAGC TTGTCTCTCT GGTGGATGAT TCGTCCAGCG TGGGCGAAGT CAACTTCCGC 300
      AGCGAGCTCA TGTTCGTCGG CAAGCTGCTG TCCGACTTCC CCGTGGTGCC CACGGCCACG 360
      CGCGTGCCCA TCGTGACCTT CTGTCCTCAAG AACTACGTGG TGCCGCGCGT CGATTACATC 420
45    TCCACCCGCC GCGCGCGCCA GCACAAGTGC GCGCTGCTCC TCCAAGAGAT CCCTGCCATC 480
      TCCTACCGAG GTGGCGGCAC CTACACCAAG GCGCCTTCC AGCAAGCCGC GCAAAATCTT 540
      CTTTCATGCTA GAGAAATCTC AACAAAGTT GTATTCTCA TCACTGATGG ATATTCCAAT 600
      GGGGGAGACC CTAGACCAAT TGCAGCGTCA CTGCGAGATT CAGGAGTGA GATCTTCACT 660
      TTTGGCATAT GGCAGGGGAA CATTCGAGAG CTGAATGACA TGGCTTCCAC CCCAAAGGAG 720
50    GAGCACTGTT ACCTGCTACA CAGTTTGAAG GAATTTGAGG CTTTAGCTCG CCGGGCATTG 780
      CATGAAGATC TACCTCTGAG GAGTTTATT CAAGATGATA TGGTCCACTG CTCATATCTT 840
      TGTGATGAAG GCAAGGACTG CTGTGACCGA ATGGGAAGCT GCAAATGTGG GACACACACA 900
      GGCATTTTGG AGTGCATCTG TGAAGGGGG TATTACGGGA AAGGTCTGCA GTATGAATGC 960
      ACAGCTTGCC CATCGGGGAC ATACAAACCT GAAGGCTCAC CAGGAGGAAT CAGCAGTTGC 1020
55    ATTCCATGTC CTGATGAAAA TCACACCTCT CCACCTGGAA GCACATCCCC TGAAGACTGT 1080
      GTCTGCAGAG AGGGATACAG GGCATCTGGC CAGACCTGTG AACTTGTCCA CTGCCCTGCC 1140
      CTGAAGCCTC CCGAAATATG TTACTTTATC CAAACACTT GCAACAACCA CTTCAATGCA 1200
      GCCTGTGGGG TCCGATGTCA CCCTGGATT GATCTTGTGG GAAGCAGCAT CATCTTATGT 1260
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60    CTCCGCCAGC CGAAACATGG CCACATCAGC TGTCTACAA GGGAAATGTT ATATAAGACA 1380
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65    ATGCTGAGAT GTACCACTTC TGGAAATATG AATGTCGGAG TTCAGGCAGC TGTGTGTAAA 1680
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      GCTATCGTAT ACACGGCAAC TGACCTATCC GGCAACCAAG CCAGCTGCAT TTTCCATATC 1920
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 A A T T A C G C C T A T C C T T T T G A T T G C A A T A T T A T C T G G T C A T T G G T G C A A T T T C A T A G A C C 1740
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 10 A T T G T A T A A T G T G A T T T T T T T A G A A T A G G G G A A C C T T A T T A T T G T G T T A A C T G A 2100
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 A G A T T A C A G G T G T G A G C C C A C C G T G C C C G C C C A T T C T A A G G G T T T C T T T G A A G A C A G G T 3960
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 A A T T A A A A T C A C T A T A T C T C

Seq ID NO: 434 Protein sequence
 Protein Accession #: NP_009162.1

55 1 11 21 31 41 51
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 L D S Q F A S I E T I T T I Q D L F P K V M K K M R V P I T L G C L L V L F L L G L V C V T Q A G I Y W V H L I D H F 480
 C A G W G I L I A A I L E L V G I I W I Y G N R F I E D T E M M I G A K R W I F W L W R A C W F V I T P I L L I A I 540
 F I W S L V Q F H R P N Y G A I P Y P D W G V A L G W C M I V F C I I W I P I M A I I K I I Q A K G N I F Q R L I S C C 600
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70 Seq ID NO: 435 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 51..1085

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 T C A T A A G A T C A G A T C T T G T G A A T G A A G A A G C A A C C G G A C A G T T C C A T G T A T A C C C G G A G C 480
 T G C C C A A G C C C T C C A T C T C C A G C A C A A C T C C A A C C C C G T G A G G A C A A G A T G C T G T G G 540

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Seq ID NO: 436 Protein sequence
 Protein Accession #: AAA59907.1

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 TLQVIKSDLV NEBATQQPHV YPELPKPSIS SNNSNPVEDK DAVAFTEPE VQNTTYLWVW 180
 NGQSLPVSPP LQLSNGNMTL TLLSVKRNDG GSYECEIQNP ASANRSDPVT LNVLYGPDVP 240
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Seq ID NO: 438 Protein sequence
 Protein Accession #: AAA59908.1

1 11 21 31 41 51
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Seq ID NO: 439 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 2370..2501

1 11 21 31 41 51
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 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCTTGACAGA TTGCATGTCC CCTGGAAGGA GGTCCCTGCTC ACAGCCTCAC 120
 TTCTAAACCTT CTGGAACCCA CCCACCATG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
 ATGTCGCAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAAGCTCA ACAGAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCCGACA GTTCCATGTA TACCCGGAGC 480
 TGCCCAAGCC CTCATCTTCC AGCAACCACT CCAACCCCGT GGAGGACAA GATGCTGTGG 540
 CCTTCACCTG TGAACCTGAG GTTCAGAACCA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
 GCCTCCCGGT CAGTCCCGAG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA 660
 GCGTCAAAAG GAACGATGCA GGTCTCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGCAAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTCCCC 780
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCAC GCAGCCTCTA 840
 ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
 TATAGCAGCC CTGGTGATT TTCGATATT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140
 GAATCTTCT AGCTCCTCCA ATCCCATT TATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
 CTCGTCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAATC AATGAAAATT TAAAGGGAAA 1260
 ACCCTCAGG CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAAC 1320
 GCAACCATG CTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
 AACAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTTGTCCT TGCTTATGCC 1440
 TGCTCTTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAGAAG TAGCTTCAGA 1500
 GGGTAACCTTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAAAAG 1560
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTT 1620
 AAATGTACAG TGGTCCCTTT CAGAGTTGGA CTCTAGACT CACCTGTTCT CACTCCCTGT 1680
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAAACAT GGCTAATAC AATGGGTATC 1800
 GCTGAGACTA AGTGTAGTAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860
 CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
 CTCTTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAATTTAAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTCT TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400
 TGTTCCTTGG TTCCAATTG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
 CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

Seq ID NO: 440 Protein sequence
 Protein Accession #: AAA59909.1

1 11 21 31 41 51
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 MLTNVFISVV LFPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

Seq ID NO: 441 DNA sequence
 Nucleic Acid Accession #: NM_002381.2
 Coding sequence: 64..1524

1 11 21 31 41 51

	1	11	21	31	41	51	
	AAATCCGAGC	CTCGCGTGGG	CTCCTGGCCC	CCGACGGACA	CCACCAGGCC	CACGGAGCCC	60
	ACCATGCCGC	GCCCGGCCCC	CGCGCGCCGC	CTCCCGGGAC	TCCTCCTGCT	GCTCTGGCCG	120
5	CTGCTGCTGC	TGCCCTCCGC	CGCCCCCGAC	CCCGTGGCCC	GCCCGGGCTT	CCGGAGGCTG	180
	GAGACCCGAG	GTCCCGGGGG	CAGCCCTGGA	CGCCGCCCTT	CTCCTGCGGC	TCCGACGCGC	240
	GCGCCCGCTT	CCGGGACCAG	CGAGCCTGGC	CGCGCCCGCG	GTGCAGGTGT	TTGCAAGAGC	300
	AGACCCCTGG	ACCTGGTGT	TATCATTGAT	AGTTCTCGTA	GCGTACGGCC	CCTGGAATTC	360
	ACCAAAGTGA	AAACTTTTGT	CTCCCGGATA	ATCGACACTC	TGGACATTGG	GCCAGCCGAC	420
10	ACGCGGGTGG	CAGTGGTGAA	CTATGCTAGC	ACTGTGAAGA	TCGAGTTCCA	ACTCCAGGCC	480
	TACACAGATA	AGCAGTCCCT	GAAGCAGGCT	GTGGGTGAA	TCACACCCCT	GTCAACAGGC	540
	ACCATGTGAG	GCCTAGCCAT	CCAGACAGCA	ATGACAGGAA	CCTTCACAGT	GGAGGCAGGG	600
	GCTCGAGAGC	CCTCTTCTAA	CATCCCTAAG	GTGGCCATCA	TTGTTACAGA	TGGGAGGCC	660
	CAGGACCAGG	TGAATGAAGT	GGCGGCTCGG	GCCCAAGCAT	CTGGTATTGA	GCTCTATGCT	720
15	GTGGGCGTGG	ACCGGGCAGA	CATGGCGTCC	CTCAAGATGA	TGGCCAGTGA	GCCCTAGAG	780
	GAGCATGTGT	TCTACGTGGA	GACCTATGGG	GTCAATTGAGA	AACTTTCCTC	TAGATTCCAG	840
	GAAACCTTCT	GTGCGCTGGA	CCCCGTGTGT	CTTGGAACAC	ACCAAGTCCA	GCACGTCTGC	900
	ATCAGTGATG	GGGAAGGCAA	GCACCACTGT	GAGTGTAGCC	AAGGATACAC	CTTGAATGCC	960
	GACAAGAAAA	CGTGTTCAGC	TCTTGATAGG	TGTGCTCTTA	ACACCCACGG	ATGTGAGCAC	1020
20	ATCTGTGTGA	ATGACAGAGA	TGGCTCTTAT	CATTGTGAGT	GCTATGAAGG	TTATACCTTG	1080
	AATGAAGACA	GGAAACTTGG	TTCAGCTCAA	GATAAATGTG	CTTTGGGTAC	CCATGGGTGT	1140
	CAGCACATTT	GTGTGAATGA	CAGAACAGGG	TCCCATCATT	GTGAATGCTA	TGAGGGCTAC	1200
	ACTCTGAATG	CAGATAAAAA	AACATGTTCA	GTCCGTGACA	AGTGTGCCCT	AGGCTCTCAT	1260
	GGTTGCCAGC	ACATTGTGTG	GAGTGATGGG	GCCGCATCCT	ACCACTGTGA	TTGCTATCCT	1320
25	GGCTACACCT	TAAATGAGGA	CAAGAAAAACA	TGTTCAAGCA	CTGAGGAAGC	ACGAAGACTT	1380
	GTTTCCACTG	AAGATGCTTG	TGGATGTGAA	GCTACACTGG	CATTCCAGGA	CAAGGTGAGC	1440
	TCGTATCTTC	AAAGACTGAA	CACTAAACTT	GATGACATTT	TGGAGAAGTT	GAAAAATAAT	1500
	GAATATGGAC	AAATACATCG	TTAAATTGCT	CCAATTTCTC	ACCTGAAAAA	GTGACAGCTG	1560
30	TGGTGTACTT	AATACATGCG	CATTCTTTTG	CACACCTGTT	ATTGCCAATG	TTCTGCTATA	1620
	TAATTTGCCA	TTATCTGTAT	TAATGCTTGA	ATATTACTGG	ATAAATTTGA	TGAAGATCTT	1680
	CTGCAGAAAT	AGCATGATT	TTCCAAGGAA	ATACATATGC	AGATACTTAT	TAAGAGCAAA	1740
	CTTTAGTGTC	TCTAAGTTAT	GACTGTGAAA	TGATTGGTAG	GAAATAGAAT	GAAAAGTTTA	1800
	GTGTTTCTTT	ATCTACTAAT	TGAGCCATTT	AATTTTAAAA	TGTTTATATT	AGATAACCAT	1860
35	ATTCACAATG	GAAACTTTAG	GCTAGTTTTC	TTTTGATAGT	ATTTATAATA	TAAATCAATC	1920
	TTATTACTGA	GAGTGCAAA	TGTACAAGGT	ATTTACACAT	ACAACCTCAT	ATAACTGAGA	1980
	TGAATGTAAT	TTGAACTGT	TTAACACTTT	TTGTTTTTTG	CTTATTTTGT	TGGAGTATTA	2040
	TTGAAGATGT	GATCAATAGA	TTGTAATACA	CATATCTAAA	AATAGTTAAC	ACAGATCAAG	2100
	TGAACATTAC	ATTGCCATTT	TTAATTCATT	CTGGTCTTTG	AAAGAAATGT	ACTACTAAAG	2160
40	AGCACTAGTT	GTGAATTTAG	GGTGTAAAC	TTTTTACCAA	GTACAAAAAT	CCCAAAATTC	2220
	CTTTATTATT	TTGCTTCAGG	ATCCAAGTGA	CAAAGTTATA	TATTTATATA	ATTGCTATAA	2280
	ATCGACAAAA	TCTAATGTTG	TCTTTTTAAT	GTTAGTGATC	CACCTGCCCT	AGCCTCCCAA	2340
	AGTGCTGGGA	TTACAGGCTT	GAAAGTCTAA	CTTTTTTTTA	CTTATATATT	TGATACATAT	2400
	AATTCTTTTG	GCTTTGAAAC	TTGCAACTTT	GAGAACAAAA	CAGTCCCTTA	AATTTTGCAC	2460
	TGCTCAATTC	TGTTTTTCGT	TTGCATTGTC	TTTAATATAA	TAAAGTTTAT	TACCTTTACA	2520
45	TATTATCATG	TCTATTTTGG	ATGACTCATC	AATTTTGCT	ATTAAAGATA	TTTCTTTAAA	2580
	TTAAAAAAA	AAAAAAA					

Seq ID NO: 442 Protein sequence
Protein Accession #: NP_002372.1

	1	11	21	31	41	51	
	MPRPAPARRL	PGLLLLLLWPL	LLLPSAAPDP	VARPGFRRLE	TRGPGGSPGR	RPSAPAPDGA	60
	PASGTSEPR	ARGAGVCKSR	PLDLVFIIDS	SRSVRPLEFT	KVKTFVSRIL	DTLDIGPADT	120
55	RVAVVNYAST	VKIEFQLQAY	TDKQSLKQAV	GRITPLSTGT	MSGLAIQTAM	DEAFTEVAGA	180
	REPSSNIPKV	AIIVTDGRPQ	DQVNEVAARA	QASGIELYAV	GVDRADMASL	KMMASEPLEE	240
	HVFYVETYG	IEKLSSRFQE	TFCALDPCVL	GTHQCQHVCI	SDGEGKIHCE	CSQYTYLNAD	300
	KKTCALDR	ALNTHGCEHI	CVNDRSGSYH	CECYEGYTLN	EDRKTCSAQD	KCALGTHGCQ	360
	HICVNDRTGS	HHCECYEGYT	LNADKKTCVS	RDKCALGSHG	CQHICVSDGA	ASYHCDCYFG	420
60	YTLNEDKKTC	SATEBARRLV	STEDACGCEA	TLAFQDKVSS	YLQRLNTKLD	DILEKLKINE	480
	YQIHR						

Seq ID NO: 443 DNA sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

	1	11	21	31	41	51	
	GCGGCGGGCG	CAGACAGCGG	CGGGCGCAGG	ACGTGCACTA	TGGCTCGGGG	CTCGCTGCGC	60
	CGGTGCTGCG	GGCTCCTCGT	GCTGGGGCTC	TGGCTGGCGT	TGCTGCGCTC	CGTGGCCGGG	120
70	GAGCAAGCGC	CAGGCACCGC	CCCTTGTCTC	CGCGGCAGCT	CCTGGAGCGC	GGACCTGGAC	180
	AAGTGCAATG	ACTGCGCGTC	TTGCAGGGCG	CGACCGCACA	GCGACTTCTG	CCTGGGCTGC	240
	GCTGCAGCAC	CTCTGCGCCC	CTTCCGGCTG	CTTTGGCCCA	TCCTTGGGGG	CGCTCTGAGC	300
	CTGACCTTCG	TGCTGGGGCT	GCTTCTGTGC	TTTTTGGTCT	GGAGACGATG	CCGACGAGGA	360
	GAGAAGTTCA	CCACCCCATC	AGAGGAGACC	GGCGGAGAGG	GCTGCCACGC	TGTGGCGCTG	420
75	ATCCAGTGAC	AATGTGCCCC	CTGCCAGCCG	GGGCTCGCCC	ACTCATCATT	CATTATCCCA	480
	TTCTAGAGCC	AGTCTCTGCC	TCCAGACGCG	GGCGGGAGCC	AAGCTCCTCC	AACCACAAGG	540
	GGGGTGGGGG	GCGGTGAATC	ACCTCTGAGG	CCTGGGCCCA	GGGTTCAGGG	GAACCTTCCA	600
	AGGTGTCTGG	TTGCCCTGCC	TCTGGCTCCA	GAACAGAAAG	GGAGCCTCAC	GCTGGCTCAC	660
80	ACAAAACAGC	TGACACTGAC	TAAGGAACTG	CAGCATTTGC	ACAGGGGAGG	GGGTGCGCCT	720
	CCTTCTCTAG	GACCTGGGGG	CCAGGCTGAC	TTGGGGGGCA	GACTTGACAC	TAGGCCCCAC	780
	TCACCTCAGAT	GTCTCTGAAAT	TCCACCAGCG	GGGTCAACCT	GGGGGGTTAG	GGACCTATTT	840
	TTAACACTAG	GGGCTGGCCC	ACTAGGAGGG	CTGGCCCTAA	GATACAGACC	CCCCAACTC	900
	CCCAAGCGG	GGAGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAATTTATT	960

AATAAAAGAA TCTTTAACTT TAAAAA AAAA

Seq ID NO: 444 Protein sequence
Protein Accession #: NP_057723.1

1	11	21	31	41	51	
MARGSLRRLL	RLVLGLWL	LLRSVAGEQA	PGTAPCSRGS	SWSADLDKCM	DCASCRARPH	60
SDFCLGCAAA	PPAPFRLLWP	ILGALSILTF	VLGLLSGFLV	WRRCRREKF	TTPIETGGE	120
GCPAVALIQ						

Seq ID NO: 445 DNA sequence
Nucleic Acid Accession #: AF322916.1
Coding sequence: 50..4300

1	11	21	31	41	51	
GCACTCCGCA	GCCTTTAAGG	TTCGCGCGGG	GGCCAGGCAA	GAGTTAGCCA	TGAAGAGCCT	60
CAAGTCCCGC	CTGAGGAGGC	AGGACGTGCC	CGGCCCGCG	TCGTCTGGCG	CCGCCCGCGC	120
CAGCGCGCAT	GCAGCAGATT	GGAATAAATA	TGATGACCGA	TTGATGAAAG	CAGCAGAAAG	180
GGGGGATGTA	GAAAAAGTGA	CCTCAATCCT	TGCTAAAAAG	GGGGTCAATC	CAGGCAAACT	240
AGATGTGGAA	GGCAGATCTG	TCTTCCATGT	TGTGACCTCA	AAGGGGAATC	TTGAGTGTTC	300
GAATGCCATC	CTTATACATG	GAGTTGATAT	TACAACCACT	GACACTGCAG	GGAGAAATGC	360
TCTTCACTCG	GCTGCTAAGT	ATGGACATGC	ATTGTGCCCTA	CAAAAACCTTC	TACAGTACAA	420
TTGTCCCACT	GAGCATGCAG	ACCTGACGGG	AAGAACTGCA	CTTCAAAAAA	AAGCAATGGC	480
AGATTGTCTT	TCTAGCATAC	AGCTGCTTTG	TGACCATGGG	GCCTCTGTGA	ATGCCAAAGA	540
TGTAAGAGGG	CGGACACCA	TTGTCTGGC	TACTCAGATG	AGTAGGCCAA	CAATATGTCA	600
ACTGCTGATA	GATGAGGAG	CGGATGTTAA	TTCCAGAGAC	AAACAAAACA	GAAGTGCCTT	660
CATGCTAGGT	TGCGAATATG	GTTGCAGAGA	TGCAGTAGAA	GTCTTAATTA	AAAAATGGTG	720
TGATATAAGC	TTGTCTGGATG	CGCTTGGCCA	TGATAGTTCT	TACTATGCAA	GAATTTGGTGA	780
CAATCTGGAC	ATTCTAACCT	TGTTGAAGAC	TGCATCGGAA	AATACCAACA	AAGGGAGAGA	840
ACTTTGGAAG	AAAGGACCAT	CTTTGCAACA	GCGAAATTTG	ACACACATGC	AAGATGAAAT	900
AAATGTGAAG	TCACATCAGA	GGGAGCATCA	AAATATTTCAG	GATTTGGAGA	TTGAAAATGA	960
AGATTGTAAA	GAGAGGTTGA	GAAAAATTCA	GCAAGAACAA	AGAATACTTT	TGGATAAAGT	1020
CAATGGTTTA	CAGTTACAGC	TGAATGAGGA	AGTTATGGTT	GCTGATGATC	TGGAAGCGGA	1080
GAGAGAAAAG	CTGAAGTCCC	TTTTGGCAGC	TAAAGAAAAG	CAACATGAAG	AAAGCTTAAG	1140
GACTATTGAG	GCTCTGAAAA	ATAGATTTAA	ATATTTTGAG	AGTGATCATT	TAGGATCAGG	1200
AGTCATTTC	AGTAACCGAA	AAGAAGATAT	GCTTCTTAAA	CAAGGTCAGA	TGTATATGGC	1260
AGACTCACAG	TGTACTTCCC	CAGGTATACC	AGCCCATATG	CAAGCAGATG	CTATGTTAAG	1320
ACCTCTGGAA	CTATCTTTAC	CCAGTCAAA	GTCATACTCT	GAAAATGAAA	TTTTAAAGAA	1380
AGAGTTAGAA	GCAATGCGAA	CTTTCTGTGA	GTCAGCAAAA	CAAGACCGAC	TGAAGCTCCA	1440
AAATGAACAT	GCACACAAAG	TGGCAGAAAT	CAAGCTTTTA	GCATTAGAA	GTGAAAGGGT	1500
CAAGGAGGAT	TCAGATGAAC	AGATAAAGCA	ATTAGAAGAT	GCATTAAAA	ATGTGCAGAA	1560
GAGGATGTAT	GAGTCAAGAG	GTAAGTTTAA	ACAAATGCAG	ACCCATTTTC	TTGCCCTTAA	1620
AGAACACTTA	ACAAGTGAAG	CAGCCTCAGG	GAATCACAGA	CTAACCGAGG	AACTGAAGGA	1680
TCAGTTGAAA	GACTTGAAAG	TAAAATATGA	AGGTGCTTCA	GCAGAGTGG	GGAAATTAAG	1740
AAACCAATC	AAACAAATG	AGATGATAGT	AGAAGAGTTT	AAGAGGGATG	AAGGCAAGCT	1800
GATAGAAGAA	AATAAGCGAT	TACAGAAGGA	ACTTAGTATG	TGTGAATGG	AGCGAGAGAA	1860
GAAAGGAAGA	AAGGTCACAG	AGATGGAAGG	CCAGGCCAAA	GAATTTGTCAG	CGAAGTTGGC	1920
CCTTTCCATT	CCAGCTGAAA	AATTTGAAAA	CATGAAGAGC	TCATTATCAA	ATGAAGTGAA	1980
TGAGAAAGCA	AAAAAATTAG	TAGAAATGGA	AAGAGAACAT	GAAAAATCAC	TTAGTGAAAT	2040
TAGACAGTTA	TAGAGAGAAC	TTGAGAAATG	TAAGGCCAAG	CTTGCTCAGC	ACGTCAAAAC	2100
AGAGGAACAT	GAACAGGTTA	AGAGCAGATT	AGAACAGAAA	TCAGGAGAAC	TTGGGAAGAA	2160
GATCACTGAG	TTAACAATTG	AAAATCAGAC	ACTACAAAAG	GAAATTGAAA	AAGTTTATTT	2220
GGATAATAAG	CTCCTCAAGG	AGCAAGCACA	TAACCTAACA	ATTGAAATGA	AAAATCATT	2280
TGTTCCCTTA	AAAGTAAAGT	AAGACATGAA	AAAGTCACAT	GATGCAATTA	TTGATGATCT	2340
TAATAGAAAG	CTTTTAGATG	TAACACAAA	ATATACAGAA	AAGAAGTTGG	AAATGGAGAA	2400
ATTGCTACTG	GAAATAGTGA	GCTTAAGTAA	GGATGTAAGC	CGCCTAGAAA	CTGTGTTTGT	2460
ACCTCCTGAG	AAACATGAAA	AAGAGATAAT	AGCTCTGAAA	TCCAATATTG	TTGAACCTTA	2520
GAAACAGCTG	TCTGAACTTA	AGAAAAATG	TGGTGAAGAC	CAGGAGAAAA	TACACGCTCT	2580
CACATCTGAA	AACACTAACT	TGAAGAAGAT	GATGAGTAAT	CAGTATGTGC	CAGTTAAAC	2640
CCATGAAGAG	GTTAAATATG	CACGTAATGA	CACGTTAGCC	AAAACATA	GAGAAATATT	2700
AGATGTGAAG	AAAAAATTG	AAGATATAAA	TCAGGAATTT	GTAATAATAA	AAGATAAGAA	2760
TGAAATATTA	AAAAGAAACC	TGGAAACAC	TCAGAACCAA	ATAAAGCTG	AGTACATCAG	2820
CCTGGCAGAG	CACGAGGCAA	AGATGAGCTC	GCTAAGTCAG	AGCATGAGAA	AGGTGCAGGA	2880
TAGTAATGCT	GAAATCTTGG	CCAACTACAG	AAAAGGCCAA	GAAGAGATTG	TGACACTGCA	2940
TGCCGAAATT	AAAGCCGAGA	AGAAGGAGCT	CGACACAATA	CAAGATGCA	TTAAGGTAAA	3000
ATATGCCCCA	ATTGTGAGCT	TTGAGGAGTG	CGAGAGAAAA	TTTAAAGCAA	CAGAGAAAGA	3060
ACTAAAGAC	CAGTTATCAG	AGCAGACACA	AAAGTATAGT	GTCAGTGAAG	AAGAAGTCAA	3120
GAAAAACAAG	CAAGAGAATG	ACAAGTTAAA	GAAGGAGATT	TTTACCCTTC	AGAAAGATT	3180
GAGAGATAAG	ACAGTTCTCA	TTGAGAAGTC	TCATGAAATG	GAAAGAGCAT	TAAGCAGAAA	3240
ACAGACGAG	CTAACAACAC	AGTTAAAGAA	CTTGTCACAG	AAATACACGG	AAGTAAAGAA	3300
TGTGAAGAG	AAGCTAGTAG	AAGAAATGTC	CAACACAGCT	TCTGAGATAC	TTGCAGTGCA	3360
AAATCTTTTG	CAAAAAACAC	ATGTTCCATT	GGAACAGGTT	GAGGCTCTGA	AAAAATCTCT	3420
TAATGGCACA	ATTGAAATC	TAAAGGAAGA	ACTGAAGAGT	ATGCAAGAGT	GTTACGAGAA	3480
AGAGCAGCAG	ACAGTGACCA	AACTGCATCA	ATTGTTGGAG	AATCAAAAGA	ACTCTTCTGT	3540
ACCCTCGGCA	GAGCATTTGC	AGATTAAAGA	AGCATTTGAG	AAAGAAGTTG	GAATCATAAA	3600
AGCCAGCTTG	AGAGAAAAGG	AAGAAGAAAG	CCAAAACAAA	ATGGAAGAAG	TCTCCAAACT	3660
TCAGTCGAG	GTTTCAGATG	CTAAACAAAG	ATTAACAAA	TTAGAGACTA	GAGAGGTAGT	3720
TGACTTGCT	AAATATAAAG	CAACAAAAG	TGATTGGAG	ACACAGATTT	CTAGCTTAAA	3780
TGAAAAATTG	GCCATCTGTA	ATAGAAAGTA	TGAGGAAGTA	TGTGAGGAAG	TTTTGCATGC	3840
CAAAAGAAG	GAAATATCTG	CAAAAGATGA	GAAGGAATTA	CTGCATTTCA	GCATTGAGCA	3900
AGAAATTAAG	GATCAGAAGG	AACGATGTGA	TAAGTCCTTA	ACAACATCA	CAGAGTTACA	3960
AAGAAGAATA	CAAGAATCTG	CTAAACAAAT	AGAAGCAAAA	GATAATAAGA	TAACCTGAAT	4020

GCTTAATGAT GTGGAAAGAT TAAACAGGC ACTCAATGGC CTTTCCCAAC TCACCTACAC 4080
 AAGTGGGAAC CCCACCAAGA GGCAGAGCCA GCTGATTGAC ACTCTGCAGC ACCAAGTGAA 4140
 ATCTCTGGAG CAACAGCTGG CCGATGCTGA CAGACAGCAC CAAGAAGTAA TTGCAATTTA 4200
 TCGGACACAC CTTCTTAGTG CTGCACAGGG TCACATGGAT GAAGATGTTT AGGAGGCTCT 4260
 GCTCCAGATC ATACAAATGC GGCAGGGGCT TGTGTGCTAG CCGTTAGCAC TGACTGCCAG 4320
 TATCTGTTTT ATCTTGCTGG TGCTGAACAT TCTTTGTGCA ACTCCATGGT CTTTCTGGGC 4380
 CTTACTGTGC TGGTATAATT AAAATAAAAT ATATTTTGTG CTGGGTGT

Seq ID NO: 446 Protein sequence

Protein Accession #: AAG49577.1

1 11 21 31 41 51
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 MKSLKSRLRR QDVPGPASSG AAAASAHAA WNKYDDRLMK AAERGDVEKV TSILAKKGVN 60
 PGKLDVBRGS VFHVVTSGKN LECLNAILIH GVDITTSDDTA GRNALHLAAK YGHALCLQKL 120
 LQYNCPTEHA DLQGRALQK KAMADCPSSI QLLCDHGASV NAKDVKGRTPLVLATQMSRP 180
 TICQLLIDRG ADVNSRDQKN RTALMLGCEY GCRDAVEVLI KNGADISLLD ALGHDSSYYA 240
 RIGDNLIDLT LLKTASENTN KGRELWKKGP SLQQRNLTHM QDEVNVKSHQ REHQNIQDLE 300
 IENEDLKERL RKIQQEQIRIL LDKVNGQLQL LNEEVMVADD LESEREKLKS LLAKEKQHE 360
 ESLRTIEALK NRFKYFESDH LSGSGSHFSNR KEDMLLKQGG MYMADSQCTS PGIPAHMQSR 420
 SMRLPLELSL PSQTSYSENE ILKKELEAMR TFCESAKQDR LKLQNLALHK VAECKALALE 480
 CERVKEDSDE QIKQLEDALK DVQKRMYESE GKVKQMTHF LALKEHLTSE AASGNHRLTE 540
 ELKDQLKDLK VKYEGASAEV GKLRNQIKQN EMIVBEFKRD EGKLIENKR LQKELSMCEM 600
 EREKKGRKVT EMEGQAKELS AKLALSIPAE KFENMKSSLS NEVNEKAKKL VEMEREHEKS 660
 LSIRQLKRE LENVKAKLAQ HVKPEEHEQV KSRLEQKSSE LGKKITELTL KNQTLQKEIE 720
 KVLIDNKLK EQAHNLTIEM KNHYVPLKVS EDMKKSHDAI IDDLNRKLLD VTQKYTEKKL 780
 EMEKLLLEND SLKSDVSRLE TVFVPPKEKE KEIIALKSNI VELKKQLSEL KKKCGEDQEK 840
 IHALTSENTN LKMMNSQYV FVKTHEEVKM TLNDTLAKTN RELLDVKKKF EDINQEPVKI 900
 KDNNEILKRN LENTQNIKA EYISLAHEHA KMSSLSQSMR KVQDSNAEIL ANYRKQGEIE 960
 VTLLHAETKAQ KKLBDITQEC IKVKYAPIVS FEBCERKFKA TEKELKDQLS EQTKYKYSVE 1020
 BEVKNKQEN DKLKEIFTEL QKDLRDKTVL IEKSHEMERA LSRKTDELNK QLKDLQSKYT 1080
 EVKNVKEKLV EENAKQTSEI LAVQNLLQKQ HVPLEQVEAL KKSLLNGTIEN LKEELKSMQR 1140
 CYEKEQQTVT KLHQLLENQK NSSVPLAEHL QIKEAFEKEV GIIKASLREK EESQNKME 1200
 VSKLQSEVQN TKQALKKLET REVVDLSKYK ATKSDLETQI SSLNEKLANL NRKYEVEVCEE 1260
 VLHAKKEIS AKDEKELLHF SIEQEIKDQK ERCDKSLTTI TELQRRIQES AKQIEAKDNK 1320
 ITELNDVER LKQALNGLSQ LTYTSGNPTK RQSLIDTLQ HQVKSLEQQL ADADRQHQEV 1380
 IAIYRTHLLS AAQGHMDEDV QEALLQIIQM RQGLVC

Seq ID NO: 447 DNA sequence

Nucleic Acid Accession #: NM_003020.1

Coding sequence: 29..664

1 11 21 31 41 51
 | | | | |
 CGCTCCTCGG GCTGCCCTC GGTGACAAT GGTCTCCAGG ATGGTCTCTA CCATGCTATC 60
 TGGCCTACTG TTTTGGCTGG CATCTGGATG GACTCCAGCA TTTGCTTACA GCCCCCGGAC 120
 CCCTGACCGG GTCCTCAGAG CAGATATCCA GAGGCTGCTT CATGGTGTTA TGGAGCAATT 180
 GGGCATTGCC AGGCCCGGAG TGGAAATATCC AGCTCACCAG GCCATGAATC TTGTGGGCCC 240
 CCAGAGCATT GAAGGTGGAG CTCATGAAGG ACTTCAGCAT TTGGGTCCTT TTGGCAACAT 300
 CCCCAACATC GTGGCAGAGT TGACTGGAGA CAACATTCCCT AAGGACTTTA GTGAGGATCA 360
 GGGGTACCCA GACCTCCAA ATCCTGTGCC TGTGGGAAAA ACAGATGATG GATGCTTAGA 420
 AAACACCCCT GACACTGCAG AGTTCAGTCG AGAGTTCAG TTGCACCAG ATCTCTTTGA 480
 TCCGGAACAT GACTATCCAG GCTTGGGCAA GTGGAACAAG AAACCTCCTT ACGAGAAGAT 540
 GAAGGGAGGA GAGAGACGAA AGCGGAGGAG TGTCAATCCA TATCTACAAG GACAGAGACT 600
 GGATAATGTT GTTGCAAAGA AGTCTGTCCC CCATTTTTCA GATGAGGATA AGGATCCAGA 660
 GTAAAGAGAA GATGCTAGAC GAAACCCAC ATTACCTGTT AGGCCTCAGC ATGCTTATG 720
 TGCACGTGTA AATGGAGTCC CTGTGAATGA CAGCATGTTT CTTACATAGA TAATTATGGA 780
 TACAAAGCAG CTGTATGTAG ATAGTGTATT GTCTTCACAC CGATGATTC GCTTTTGTG 840
 AAATTAGAA AAGAGCTTTT TTGTTCTTG GGTTTTTAAA ATGTGAATCT GCAATGATCA 900
 TAAAAATTAA AATGTGAATG TCAACAATAA AAAGCAAGAC TATGAAAGGC TCAGATTTCT 960
 TGCAGTTTAA AATGGTGTCT GAGGTGTGAC TATTTTGGCC AAGTCTGTAG AAAGCTGTCA 1020
 TTTGATTTTG ATTATGTAGT TCATCCAGCC CTGGGCGATT GTTATACACC AGTAAAGAAG 1080
 GCTGTACTCA AGAGGAGGAG CTGACACATT TCACTTGGCT GCGTCTTAAT AAACATGAAT 1140
 GCAAGCATTG GC

Seq ID NO: 448 Protein sequence

Protein Accession #: NP_003011.1

1 11 21 31 41 51
 | | | | |
 MYSRMVSTML SGLLFWLASS WTPAFAYSPP TPDRVSEADI QRLHGVMEQ LGIARPRVEY 60
 PAHQAMNLVG PQSIEGGAHE GLQHLGPFNG IPNIVAELETG DNIPKDFSED QGYPDPPNFC 120
 PVGKTDDGCL ENTPDTAEFS REFQLHQHLE DPEHDYPGLG KWNKKLLYEK MKGGERRKRR 180
 SVNPLYQQQR LDNVVAKKSV PHFSDEKDP E

Seq ID NO: 449 DNA sequence

Nucleic Acid Accession #: NM_003816.1

Coding sequence: 79..2538

1 11 21 31 41 51
 | | | | |
 CGGCAGGGTT GGAATATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60
 CCTGCCGAAT CGGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCTCGGGGAC CCTTCGTGTC 120
 CGGTGGTTGC TGTGTCTTGG CTTGGTGGGC CCAGTCCTCG GTGCGCGCGC GCCAGGCTTC 180

	CAACAGACCT	CACATCTTTC	TTCTTATGAA	ATTATAACTC	CTTGGAGATT	AACTAGAGAA	240
	AGAAGAGAAG	CCCCTAGGCC	CTATTCAAAA	CAAGTATCTT	ATGTTATTCA	GGCTGAAGGA	300
	AAAGAGCATA	TTATTTCACCT	GGAAAGGAAC	AAAGACCTTT	TGCCTGAAGA	TTTTGTGGTT	360
5	TATACTTACA	ACAAGGAAGG	GACTTTAATC	ACTGACCATC	CCAATATACA	GAATCATTTG	420
	CATTATCGGG	GCTATGTGGA	GGGAGTTTAT	AATTCATCCA	TTGCTCTTAG	CGACTGTTTT	480
	GGACTCAGAG	GATTGCTGCA	TTTAGAGAAT	CGCAGTTATG	GGATTGAACC	CCTGCAGAAC	540
	AGCTCTCATT	TTGAGCACAT	CATTTATCGA	ATGGATGATG	TCTACAAAGA	GCCTCTGAAA	600
	TGTGGAGTTT	CCAACAAGGA	TATAGAGAAA	GAAACTGCAA	AGGATGAAGA	GGAAGAGCCT	660
10	CCCAGCATGA	CTCAGCTACT	TCGAAGAAGA	AGAGCTGTCT	TGCCACAGAC	CCGGTATGTG	720
	GAGCTGTTCA	TTGTCTGTA	CAAGGAAAGG	TATGACATGA	TGGGAAGAAA	TCAGACTGCT	780
	GTGAGAGAAG	AGATGATTCT	CCTGGCAAAC	TACTTGGATA	GTATGTATAT	TATGTTAAAT	840
	ATTCGAATTG	TGCTAGTTGG	ACTGGAGATT	TGGACCAATG	GAAACCTGAT	CAACATAGTT	900
	GGGGGTGCTG	GTGATGTGCT	GGGGAACCTC	GTGCAGTGGC	GGGAAAAGTT	TCTTATCACA	960
15	CGTCGGAGAC	ATGACAGTGC	ACAGCTAGTT	CTAAGAAAAG	TTTTTGGTGG	AACGTCAGGA	1020
	ATGGCATTGG	TGGGAACAGT	GTGTTCAAGG	AGCCACGACG	GCGGGATTAA	TGTGTTTGGG	1080
	CAATCATCTG	TGGAGACATT	TGCTTCCATT	GTGCTCATG	AATTGGGTCA	TAATCTTGGA	1140
	ATGAATCACG	ATGATGGGAG	AGATTGTTCC	TGTGGAGCAA	AGAGCTGCAT	CATGAATTCA	1200
	GGAGCATCGG	GTTCCAGAAA	CTTTAGCAGT	TGCAGTGCAG	AGGACTTTGA	GAAGTTAACT	1260
20	TTAAATAAAG	GAGGAAACTG	CCTTCTTAAT	ATTCCAAAGC	CTGATGAAGC	CTATAGTGCT	1320
	CCCTCCTGTG	GTAATAAGTT	GGTGGACGCT	GGGGAAGAGT	GTGACTGTGG	TACTCCAAAG	1380
	GAATGTGAAT	TGGACCTTGG	CTGCGAAGGA	AGTACCTGTA	AGCTTAAATC	ATTTGCTGAG	1440
	TGTGCATATG	GTGACTGTTG	TAAAGACTGT	CGGTTCCCTC	CAGGAGGTAC	TTTATGCCGA	1500
	GGAAAAACCA	GTGAGTGTGA	TGTTCCAGAG	TACTGCAATG	GTTCTTCTCA	GTTCTGTGAG	1560
25	CCAGATGTTT	TTATTTCAGAA	TGGATATCCT	TGCCAGAATA	ACAAAGCCTA	TTGCTACAAAC	1620
	GGCATGTGCC	AGTATTATGA	TGCTCAATGT	CAAGTCATCT	TTGGCTCAAA	AGCCCAAGGCT	1680
	GGCCCAAAAG	ATTGTTTCAT	TGAAGTGAAT	TCTAAGGTG	ACAGATTTGG	CAATTGTGGT	1740
	TTCTCTGGCA	ATGAATACAA	GAAAGTGTGCC	ACTGGGAATG	CTTTGTGTGG	AAAGCTTCAG	1800
	TGTGAGAAAT	TACAAGAGAT	ACCTGTATTT	GGAATTTGTG	CTGCTATTAT	TCAAACGCCT	1860
30	AGTCGAGGCA	CCAATGTTG	GGGTGTGGAT	TTCCAGCTAG	GATCAGATGT	TCCAGATCCT	1920
	GGGATGGTTA	ACGAAGGCAC	AAAATGTGGT	GCTGGAAAAG	TCTGTAGAAA	CTTCCAGTGT	1980
	GTAGATGCTT	CTGTTCTGAA	TTATGACTGT	GATGTTTCAG	AAAAGTGTCA	TGGACATGGG	2040
	GTATGTAATA	GCAATAAGAA	TTGTCACTGT	GAAAATGGCT	GGGCTCCCC	AAATTGTGAG	2100
	ACTAAGAGAT	ACGGAGGAAG	TGTGGACAGT	GGACCTACAT	ACAATGAAAT	GAATACTGCA	2160
35	TTGAGGGACG	GACTTCTGGT	CTTCTTCTTC	CTAATTGTTT	CCCTTATTGT	CTGTGCTATT	2220
	TTTATCTTCA	TCAAGAGGGA	TCAACTGTGG	AGAAGCTACT	TCAGAAGAA	GAGATCACAA	2280
	ACATATGAGT	CAGATGGCAA	AAATCAAGCA	AACCTTCTTA	GACAGCCGGG	GAGTGTTCCT	2340
	CGACATGTTT	CTCCAGTGGC	ACCTCCACGA	GAAGTTCCTA	TATATGCAAA	CAGATTGCA	2400
	GTACCAACCT	ATGCAGCCAA	GCAACCTCAG	CAGTTCCTAT	CAAGGCCACC	TCCACCACAA	2460
40	CCGAAAGTAT	CACTCTGAGG	AACTTAATT	CCTGCCCGTC	CTGCTCCTGC	ACCTCCTTTA	2520
	TATAGTTCCC	TCACTTGATT	TTTTTAACCT	TCTTTTGGCA	AATGTCCTCA	GGGAAGTGAG	2580
	CTAATACTTT	TTTTTTTCT	TGATGTTTTT	TTGAAAAGCC	TTTCTGTTGC	AACTATGAAT	2640
	GAAAACAAA	CACCACAAA	CAGACTTCAC	TAACACAGAA	AAACAGAAAC	TGAGTGTGAG	2700
	AGTTGTGAAA	TACAAGGAAA	TGCAGTAAAG	CCAGGGAATT	TACAATAACA	TTTCCGTTTC	2760
45	CATCATTGAA	TAAGTCTTAT	TCAGTCATCG	GTGAGGTTAA	TGCACATAAT	ATGGATTTTT	2820
	TGAACATGTT	ATTGCAAGTA	TTCTCAAATT	AACGTATTGG	GTGTAAGATT	TTTGTGCTTA	2880
	AGTGTTTAAG	TGTTATTTCT	AATTTTCTAC	CTTAGTTATC	ATTAATGTAG	TTCTCTATTG	2940
	AACATGTGAT	AACTAATAC	CTGTGAAAAC	TGACTAATCA	GCTGCCAATA	ATATCTAATA	3000
	TTTTTCATCA	TGCACGAATT	AATAATCATC	ATACTCTAGA	ATCTTGTCTG	TCACCTACTA	3060
50	CATGAATAAG	CAAAATATTGT	CTTCAAAAGA	ATGCACAAGA	ACCACAATTA	AGATGTCATA	3120
	TTATTTTGAA	AGTACAAAAT	ATACTAAAAG	AGTGTGTGTG	TATTCACGCA	GTTACTCGCT	3180
	TCCATTTTAA	TGACCTTTCA	ACTATAGGTA	ATAACTCTTA	GAGAAATTAA	TTTAATATTA	3240
	GAATTTCTAT	TATGAATCAT	GTGAAAGCAT	GACATTGCTT	CACAATAGCA	CTATTTTAAA	3300
	TAAATTATAA	GCTTTAAGGT	ACGAAGTATT	TAATAGATCT	AATCAATAAT	GTTGATTCAT	3360
55	GGCTATAATA	AAGCAGGAGC	AATATAAAAA	TCTTCAATCA	ATTGAACCTT	TACAAAACCA	3420
	CTTGAGAAAT	TCATGAGCAC	TTTAAATCT	GAACTTTCAA	AGCTTGTCTAT	TAAATCATT	3480
	AGAATGTTTA	CATTACTACT	GGTGTGCTGG	GTGATGTAAA	ATATTAGACA	CTAATATTTT	3540
	CATAGAAAT	AGGCTGGAGA	AAGAAGGAAG	AAATGGTTTT	CTTAAATACC	TACAAAAAAG	3600
	TTACTGTGGT	ATCTATGAGT	TATCATCTTA	GCTGTGTTAA	AAATGAATTT	TTACTATGGC	3660
60	AGATATGGTA	TGGATCGTAA	AATTTTAAGC	ACTAAAAATT	TTTTCATAAC	CTTTCATAAT	3720
	AAAGTTTAAT	AATAGGTTTA	TTAACTGAAT	TTCAATTAGT	TTTTAAAAAGT	GTTTTTGGTT	3780
	TGTGTATATA	TACATATACA	AATACAACAT	TTACAATAAA	TAAATACTCT	GAAATTCCTA	3840
	AAAAAATAAA	AAAAAATAAA	AAAAA				

Seq ID NO: 450 Protein sequence
Protein Accession #: NP_003807.1

	1	11	21	31	41	51	
70	MSGARFSPG	TLRVRLLLL	GLVGPVLGAA	RPGFQQTSHL	SSYEIITPWR	LTRERREAPR	60
	PYSKQVSVYI	QAEQKEHIIH	LERNKDLLPE	DFVVYTYNKE	GTLLTDHPNI	QNHCHYRGYV	120
	EGVHNSIAL	SDCFGLRLGL	HLENASYGIE	PLQNSHFEH	IIRMDDVYK	EPLKCGVSNK	180
	DIEKETAKDE	EEPPSMTQL	LRRRAVLPO	TRYVELFIVV	DKERYDMMGR	NQTAVREEMI	240
	LLANYLDSMY	IMLNIRIVLV	GLEIWTNGNL	INIVGGAGDV	LGNFVQWREK	FLITRRRHDS	300
	AQLVLKKEFG	GTAGMAFVGT	VCSRSHAGGI	NVFGQITVET	FASIVAHELK	HNLGMNHDDG	360
75	RDCSCGAKSC	IMNSGASGR	NFSSCSAEDF	EKLTLNKGKN	CLLNIPKPE	AYSAPSCGNK	420
	LVDAGEECD	GTPKECELD	CCEGSTCKLK	SFAECAYGDC	CKDCRFLPGG	TLCRGKTSEC	480
	DVPEYCNSS	QFCQPDVFIQ	NGYPQNNKA	YCYNGMCQYY	DAQCQVIFGS	KAKAAPKDCF	540
	IEVNSKGRDF	GNCGFSNGEY	KKCATGNALC	GKLQCEVQVE	IPVFGIVPAI	IQTSPRGTKC	600
	WGVDFQLGSD	VDPDGMVNEG	TKCGAGKICR	NFQCVDAVSL	NYDCDVQKKK	HGHGVCNSNK	660
80	NCHCENGWAP	PNCETKGYGG	SVDSGPTYNE	MNTALRDGLV	VFFFLIVPLI	VCAIFIFIKR	720
	DQLWRSYFRK	KRSQTYESDG	KNQANPSRQP	GSVPRHVSPL	TPPREVPIYA	NRFVAVPTYAA	780
	KQPQQFPSPR	PPQPKVSSQ	GNLIPARPAP	APPLYSSLT			

Seq ID NO: 451 DNA sequence
Nucleic Acid Accession #: NM_016650.1
Coding sequence: 196..789

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      GGTTC AATA TATGC AGATG TCTCG ATATA GGAAT GAAAT TACGT CTTTG GAACA ACTTA 60
      AATAAGTCAA ATATACTTGG AGCTTTAAAA ATTAAGGA GAGAGATTG AGCACCTTTT 120
10     CTGCTGCCAT GACAACCATG CAAGGAATGG AACAGGCCAT GCCAGGGTTG GCCTGGTGTG 180
      CCCCAGCTGG GAAACATGGC TGTCAATACAT TCACATCTGT GGAAAGGATT GCAAGAGAAG 240
      TTCTTGAAGG GAGAACCCAA AGTCCTTGGG GTTGTGCAGA TTCTGACTGC CCTGATGAGC 300
      CTTAGCATGG GAATAACAAT GATGTGTATG GCATCTAATA CTTATGGAAG TAACCCATT 360
      TCCGTGCATA TCGGGTACAC AATTTGGGGG TCAGTAATGT TTATTATTTC AGGATCCTTG 420
      TCAATTGCAG CAGGAATTAG AACTACAAAA GGCCTGGTCC GAGGTAGTCT AGGAATGAAT 480
15     ATCACCAGCT CTGTACTGGC TGCATCAGGG ATCTTAATCA ACACATTAG CTGCGCTTT 540
      TATTCATTCC ATCACCCTTA CTGTAACATC TATGGCAACT CAAATAATTG TCATGGGACT 600
      ATGTCCATCT TAATGGGTCT GGATGGCATG GTGCTCCTCT TAAGTGTGCT GGAATTTCTGC 660
      ATTGCTGTGT CCTCTCTGCG CTTTGGATGT AAAGTGTCTCT GTTGTAACCC TGTTGGGGTT 720
      GTGTTAATTC TGCATCACA TTCTCACATG GCAGAAACAG CATCTCCAC ACCACTTAAT 780
20     GAGGTTGAG GCCAACAAAA GATCAACAGA CAAATGCTCC AGAAATCTAT GCTGACTGTG 840
      ACACAAGAGC CTCACATGAG AAATTACCAG TATCCAACTT CGATACTGAT AGACGTGTTG 900
      ATATTATTAT TATATGTAAT CCAATTATGA ACTGTGTGTG TATAGAGAGA TAATAAATTC 960
      AAAATTATGT TCTCATTTTT TTCCCTGGAA CTCAATAACT CACTTCACTG GCTCTTTATC 1020
      GAGAGTACTA GGAGTTAAAT TAATAAATAA TGCATTTAAT GAGGCCACAG GAAAAA

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Seq ID NO: 452 Protein sequence
Protein Accession #: NP_057734.1

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      MAVIHSHLWK GLQEKFLKGE PKVLGVVQIL TALMSLSMGI TMMCMASNTY GSNPISVHIG 60
      YTIWGSVMFI ISGSLSLAAG IRTTKGLVRG SLGMNITSSV LAASGILINT FSLAFYSFHH 120
      PYCNYYGNSN NCHGTMSILM GLDGMVLLLS VLEFCIAVSL SAFGCKVLCC TPGGVVLILP 180
      SHSHMAETAS PTPLENEV

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Seq ID NO: 453 DNA sequence
Nucleic Acid Accession #: NM_002091.1
Coding sequence: 56..503

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40     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTCTCTGCT CTTCCAGGCC TCTCCGGCGC GCTCCAAGGG CTTCCCGTCG GGACCATGCG 60
      CGGCAGTGAG CTCCCGCTGG TCCTGCTGGC GCTGGTCTCT TGCTTAGCGC CCCGGGGGCG 120
      AGCGGTCCCG CTGCTCTGCG GCGGAGGGAC CGTGTGACC AAGATGTACC CGCGCGGCAA 180
45     CCAGTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTCTGTGTTT 240
      TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
      GAATTTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCAACCCAA 360
      GGCCTGGGCG AATCAGCAGC CTTCTGTTGG TACAGAGGAT AGCAGCAACT TCAAAGATGT 420
      AGGTTCAAAA GCGAAAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
50     CCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
      TAAGAGACTG AGTCTGCAAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTGTGCA 600
      AAATATTTGA CTATTCTGTA TCTTTTATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
      CTTCTGTTT AAACCTGTGTT GCTGTGAACA ATTGTGAAA AGAGTCTTCC AATTAATGCT 720
      TTTTATATC TAGGCTACCT GTTGGTTAGA TTCAAGGCCC CGAGCTGTGA CCATTACAA 780
      TAAAGCTTA AACACAT

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Seq ID NO: 454 Protein sequence
Protein Accession #: NP_002082.1

```

60     1      11      21      31      41      51
      |      |      |      |      |      |
      MRGSELPLVL LALVLCLAPR GRAVPLPAGG GTVLTMYPR GNHWAVGHLM GKSTGESS 60
      VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQPS WDSSESSNFK 120
      DVGSKGVGR LSAPGSQREG RNPQLNQ

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Seq ID NO: 455 DNA sequence
Nucleic Acid Accession #: NM_016522.1
Coding sequence: 265..1299

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70     1      11      21      31      41      51
      |      |      |      |      |      |
      GCGGAAGCAG CGAGGAGGGA GCCCCCTTTG GCCGTCTCC GTGGAACCGG TTTTCCGAGG 60
      CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGCGC 120
      TTTTCTCTC CCCGCGCTC CCGTCTCGCG CGGGTTCACC GCTCAGTCCC CGCGCTCGCT 180
75     CCGCACCCCA CCCACTTCTT GTGCTCGCCC GGGGGGCGTG TGCCGTGCGG CTGCGGAGT 240
      TCGGGGAAGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACCTGTTCTT GCCCTGGAAG 300
      TGCCCTCGTG TCGTCTCTCT CAGGCTGCTG TTCCTGTAC CCACAGGAGT GCCCGTGC 360
      AGCGGAGATG CCACTTCCC CAAAGCTATG GACAACGTGA CGGTCCGCA GGGGAGAGC 420
      GCCACCTCA GGTGCACTAT TGACAACCGG GTCACCCGGG TGGCTGGCT AAACCGCAGC 480
80     ACCATCTCT ATGCTGGGAA TGACAAGTGG TGCCTGGATC CTCGCTGGT CCTTCTGAGC 540
      AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
      TACACCTGCT CGGTGCAGAC AGACAACCAC CCAAGACCT CTAGGGTCCA CCTCATTTG 660
      CAAGTATCT CCAAATTTGT AGAGATTCTT TCAGATATCT CCATTATGA AGGGAACAAT 720
      ATTAGCTCTA CTGCAATAG AACTGGTAGA CCAGAGCCTA CGGTACTTGG GAGACATC 780

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TCTCCCAAAG CGGTTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC 840
 CGGGAACAGT CAGGGGACTA CGAGTGCAGT GCCTCCAATG ACGTGGCCGC GCCCGTGGTA 900
 CGGAGAGTAA AGGTCAACCGT GAACTATCCA CCATACATTT CAGAAGCCAA GGGTACAGGT 960
 GTCCCGCTGG GACAAAGGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
 TTCCAGTGGT ACAAGAGATGA CAAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080
 AACAGACCTT TCCTCTCAAA ACTCATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140
 TACACTTGGC TGGCCTCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTGGT 1200
 CCAGGCGCCG TCAGCGAGGT GAGCAACGGC ACGTCGAGGA GGGCAGGCTG CGTCTGGCTG 1260
 CTGCCCTCTC TGGCTCTGCA CCTGCTCTCT AAATTTTGAT GTGAGTGCCA CTCCCCACC 1320
 CGGGAAGAGC TGGCCGCCACC ACCACCACA ACACAACAGC AATGGCAACA CCGACAGCAA 1380
 CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTGTA 1440
 GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTTT AAAAAAGAAA TTGAAAATTG 1500
 CCTTGAGAT ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560
 CCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CACGTGGAAC ATTCTGGAGC TGGCCATCCC 1680
 AAATTCATC AGTCCCTAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740
 CCGGCCCAAG CGTGGCGCTG CCGGCACCTT GGTAGACTGT GCCACCACGG CGTGTGTTGT 1800
 GAAACGTGAA ATAAAAAGAG CAAAAAATA AAAAAAATA

Seq ID NO: 456 Protein sequence
 Protein Accession #: NP_057606.1

1 11 21 31 41 51
 | | | | |
 MGVCGLFLFP WKCLVVVSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60
 NRVTRVAWLN RSTILYAGND KWCLDPRVVL LSNTQTQYSI EIQNVVDVDE GPYTCVQTD 120
 NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTCTAT GRPEPTVWR HISEPKAVGFV 180
 SEDEYLEIQG ITRQSGDYE CSASNDVAAP VVRVKVTVN YPPYISEAKG TGVPGVKQGT 240
 LQCBASAVPS AEFQWYKDDK RLIEGKKGVK VENRPFLLSKL IFFNVSEHDY GNYTCVASNK 300
 LGHTNASIML FGPAVSEVS NGTSRRAGCV WLLPLLVLHL LLKF

Seq ID NO: 457 DNA sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 203..1045

1 11 21 31 41 51
 | | | | |
 GATTGTCTCT GCCAGCAGCT GTCGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC 60
 ACAGAATACG CGCTCCCTTC CTCCCTCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC 120
 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180
 CCTCATTCGG GGCAGTCCGA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240
 ACTTCGAGTT CTCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAGAAGT 300
 GGAAATCTCT TCAGGCCTTT CCACTAACCC TGAAAAAGAT ATATTGTGGT TGCGGGAAAA 360
 TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420
 GGCCAGCAAC TACGTAGATC TGATCAGAGA ACAGGCCGAT ATCGCATTGA CCCGGGGAGC 480
 TGAGGTGAAG GGCCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGGTGGATCG 540
 CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGACCTGA 600
 GGCGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660
 CAAAGACGCA GTCAGTGTCT GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCCTGGT 720
 CACCCCGGCT GGGAAAGTCT ATGAGTGTCA AGCTCAACAA ACCATTTTAC TGGCCTCTAG 780
 TGATCGCAG AAGACGGTCA CCATGATCCT GTCTGCGGTC CACATCCAAC CTTTGTGACAT 840
 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
 GGAAGAAACC TTGCCCTTGA TTTTGGGGCT CATCTTGGGC CTCGTCATCA TGGTAACACT 960
 CGCGATTTAC CACGTCCACC ACAAAATGAC TGCCAAACCA GTGCAGATCC CTCGGGACAG 1020
 ATCCAGTAT AAGCATATGG GCTAGAGGCC GTTAGGCAGG CACCCCTTAT TCCTGCTCCC 1080
 CCAACTGGAT CAGGTAGAAC AACAAAGCA CTTTTCATC TTGTACACGA GATACACCAA 1140
 CATAGCTACA ATCAACAGG CCTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
 AACCACGGA AGGGGGAGAG TCTTTCGGAT TTGTAGGGT AAATGGCAAT TATTCTCTCC 1260
 ATGCTGGGGA GGAGGGGAGG AGGGTCTCAG ACAGCTTTCG TGCTCATGTT GGCTTGGCTT 1320
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGCCCCCAA AGTTTAGGGA 1380
 TTGAAACAT GCTTCTTTGA GGAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGCCT 1440
 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAAAC 1500
 TCATGCTCCC TGCAGCAAGA CCCTGAAAG TGATTATGCT TTCTGGCTGG CATTCTGCAT 1560
 GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620
 AAAACGACTA ATGTAACATAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC 1680
 GGGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAAATA AAACACACTA 1740
 TTCTCTGGC

Seq ID NO: 458 Protein sequence
 Protein Accession #: NP_036393.1

1 11 21 31 41 51
 | | | | |
 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60
 EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEBVKRCG HSQSELQVFW VDRAYALKML 120
 FVKESHNMMSK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHHLS ALVTPAGKSY 180
 ECQAQQTISL ASSDPQKTVT MILSAVHIQF FDIISDFVFS EEHKCPVDER EQLEETLPLI 240
 LGLILGLVIM VTLAIYVHH KMTANQVQIP RDRSQYKHM

Seq ID NO: 459 DNA sequence
 Nucleic Acid Accession #: NM_001169.1
 Coding sequence: 85..870

1 11 21 31 41 51

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10
15
20
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	TAGGAGATAA		GAGTATCTTG		CACAGCAGGT		GCAGGTTTCC		CAGCAGCTCA		GGCAAGAGTC	60
	CGATGTTTGT		GCCATCTGAT		CCTGATGTCT		GGAGAGATAG		CCATGTGTGA		GCCTGAATTT	120
	GGCAATGACA		AGGCCAGGGA		GCCGAGCGTG		GGTGCGAGGT		GGCGAGTGTC		CTGGTACGAA	180
	CGGTTTGTGC		AGCCATGTCT		GGTCGAACTG		CTGGGCTCTG		CTCTCTTCAT		CTTCATCGGG	240
	TGCTGTGCGG		TCATTGAGAA		TGGGACGGAC		ACTGGGCTGC		TGCAGCCGGC		CCTGGCCAC	300
	GGGCTGGGCT		TGGGGCTCGT		GATTGCCACG		CTGGGGAATA		TCAGTGGTGG		ACACTTCAAC	360
	CCTGCGGTGT		CCCTGGCAGC		CATGCTGATC		GGAGGCCTCA		ACCTGGTGAT		GCTCCTCCCG	420
	TACTGGGTCT		CACAGCTGCT		CGGGGGGATG		CTCGGGGCTG		CCTTGGCCAA		GGTGGTGAGT	480
	CCTGAGGAGA		GGTTCGGAA		TGCATCTGGG		GCGGCCTTTG		TGACAGTCCA		GGAGCAGGGG	540
	CAGGTGGCAG		GGGCGTTGGT		GGCAGAGATC		ATCCTGACGA		CGCTGCTGGC		CCTGGCTGTA	600
	TGCATGGGTG		CCATCAATGA		GAAGACAAAG		GGCCCTCTGG		CCCCGTTCTC		CATCGGCTTT	660
	GCCGTACCGG		TGGATATCCT		GGCTGGGGGC		CCTGTGTCTG		GAGGCTGCAT		GAATCCCGCC	720
	CGTGCTTTTG		GACCTGCGGT		GGTGGCCAAC		CACTGGAACT		TCCACTGGAT		CTACTGGCTG	780
	GGCCCACTCC		TGGCTGGCCT		GCTTGTGTGA		CTGCTCATT		GGTGCTTCAT		TGGAGATGGG	840
	AAGACCCGCG		TCATCTGAA		GGCTCGGTGA		GCAGAGCTCG		TGGGATTCCT		GCTGCTCCAG	900
	GTGTCTCTAG		CTCAGCTGTC		CCAGCTGAG		GACAGGGGAG		TTCTGCTCAT		TCCTGCCAGG	960
	GCAGAGGCCC		AGAGGAGCGA		CCCCCTGCTT		CCACTGCTTG		GGCCTGCTTT		CTCAGATAGA	1020
	CTGACTGCTG		AGGAGGCTCT		AGGTTCTTGG		AATTCCTTTG		TGCTCATCAG		AGACCCAGC	1080
	CTGGGGAACA		CGCTGCCCGC		ACTGCCCAGA		GAGCAGTGCA		AACACCACAA		CACGAGCGTG	1140
	TTTCTTGAGA		GGAATGTCCC		CGAGTTGGAC		AAGGAGGCTG		TTTCTGCACA		TCAGTCTATT	1200
	TCCCGCACCC		CATTCTTTCG		TTGATTGCTT		TGTTGGGGGC		CTGGCCACTT		CCTTGCTTCT	1260
	CAAGCTGACA		ATTCTCACTT		TGCAATAAAT		AGTCCAGTGT		TTCTTTCAT			

Seq ID NO: 460 Protein sequence
Protein Accession #: NP_001160.1

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35

	1		11		21		31		41		51	
	MSGHIAMCEP		EPGNDKAREP		SVGGRWRVSW		YERFVQPCLV		ELLGSALFIF		IGCLSVIENG	60
	TDTGLLQPAL		AHGLALGLVI		ATLGNISGGH		FNPVSLAAM		LIGGLNLVLM		LPYVWSQLLG	120
	GMLGAALAKV		VSPEERFWNA		SGAAFVTQVE		QGQVAGALVA		EIIILTLLAL		AVCMGAINKE	180
	TKGPLAPFSI		GFAVTVDLIA		GGPVSGGCMN		PARAFGPAVV		ANHWNFWIY		WLGPLLAGLL	240
	VGLLIRCFIG		DGKTRLILKA		R							

Seq ID NO: 461 DNA sequence
Nucleic Acid Accession #: NM_003226.1
Coding sequence: 2..226

45
50

	1		11		21		31		41		51	
	GATGCTGGGG		CTGGTCTTGG		CCTTGCTGTC		CTCCAGCTCT		GCTGAGGAGT		ACGTGGGCCT	60
	GTCTGCAAAAC		CAGTGTGCCG		TGCCGGCCAA		GGACAGGGTG		GACTGCGGCT		ACCCCATATG	120
	CACCCCAAG		GAGTGCAACA		ACCGGGGCTG		CTGCTTTGAC		TCCAGGATCC		CTGGAGTGCC	180
	TTGGTGTTC		AAGCCCCTGA		CTAGGAAGAC		AGAATGCACC		TTCTGAGGCA		CCTCCAGCTG	240
	CCCCTGGGAT		GCAGGCTGAG		CACCTTTGCC		CGGCTGTGAT		TGCTGCCAGG		CACTGTTTCAT	300
	CTCAGTTTTT		CTGTCCCTTT		GCTCCCGGCA		AGCTTTCTGC		TGAAAGTTCA		TATCTGGAGC	360
	CTGATGTCTT		AACGAATAAA		GGTCCCATGC		TCCACCCG					

Seq ID NO: 462 Protein sequence
Protein Accession #: NP_003217.1

55
60

	1		11		21		31		41		51	
	MLGLVLALLS		SSSAEEYVGL		SANQCAVPAK		DRVDCGYPHV		TPKECNRRGC		CFDSRIPGVP	60
	WCFKPLTRKT		ECTF									

Seq ID NO: 463 DNA sequence
Nucleic Acid Accession #: NM_002993.1
Coding sequence: 64..408

65
70
75
80

	1		11		21		31		41		51	
	GGCACGAGCC		AGTCTCCGCG		CCTCCACCCA		GCTCAGGAAC		CCGCGAACCC		TCTCTTGACC	60
	ACTATGAGCC		TCCCGTCCAG		CGCGCGCGCC		CGTGTCCCGG		GTCCCTTCGGG		CTCCTTGTGC	120
	GCGCTGCTCG		CGCTGCTGCT		CCTGCTGACG		CCGCGGGGCG		CCCTCGCCAG		CGCTGGTCCT	180
	GTCTCTGCTG		TGCTGACAGA		GCTGCGTTGC		ACTTGTTTAC		GCGTTACGCT		GAGAGTAAAC	240
	CCCAAAACGA		TTGGTAAACT		GCAGGTGTTT		CCCGCAGGCC		CGCAGTGCTC		CAAGGTGGAA	300
	GTGGTAGCCT		CCCTGAAGAA		CGGGAAGCAA		GTTTGTCTGG		ACCCGGAAGC		CCCTTTTCTA	360
	AAGAAAGTCA		TCCAGAAAAT		TTTGGACAGT		GGAAACAAGA		AAAACGTAGT		AACAAAAAAG	420
	ACCATGCATC		ATAAAAATTG		CCAGTCTTCA		GCGGAGCAGT		TTTCTGGAGA		TCCCTGGACC	480
	CAGTAAGAAT		AAGAAGGAAG		GGTTGGTTTT		TTTCCATTTT		CTACATGGAT		TCCTTACTTT	540
	GAAAGAGTGT		GGGGAAGGCC		TACGCTTCTC		CCTGAAGTTT		ACAGCTCAGC		TAATGAAGTA	600
	CTAATATAGT		ATTTCCACTA		TTTACTGTTA		TTTTACCTGA		TAAGTTATTG		AACCCTTTGG	660
	CAATTGACCA		TATTTGTAGC		AAAGAATCAC		TGGTTATTAG		TCTTTCAATG		AATATTGAAT	720
	TGAAGATAAC		TATTTGATTT		CTATCATACA		TTCTTTAAAG		TCTTACCGAA		AAGGCTGTGG	780
	ATTTCTGATG		GAAATAATGT		TTTATTAGTG		TGCTGTTGAG		GGAGGTATCC		TGTTGTTCTT	840
	ACTCACTCTT		CTCATAAAT		AGGAAATATT		TTAGTTCTGT		TTTCTTGGGG		AATATGTTAC	900
	TCTTTACCCCT		AGGATGCTAT		TTAAGTTGTA		CTGTATTAGA		ACACTGGGTG		TGTCATACCG	960
	TTATCTGTGC		AGAATATATT		TCCTTATTCA		GAATTTCTAA		AAATTTAAGT		TCGTAAAGGG	1020
	CTAATATATT		CTCTTCCTAT		GGTTTATGAT		GTTTGTATGC		TTCTTAGTAT		GGCATAATGT	1080
	CATGATTTAC		TCATTAAACT		TTGATTTTGT		ATGCTATTTT		TTCACTATAG		GATGACTATA	1140

ATTCTGGTCA CTAAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC 1200
 TGATTGTCTAA TTTACATAGA AATGTATTCT CTGGTTT TAAATAAAAG CAAAATTAAC 1260
 AATGATCTGT GCTCTGCAAA GTTTTGAAA TATATTGAA CAATTGGAAT ATAAATTCAT 1320
 CATTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
 TTTAAAGGTT TIGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
 AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCATT 1500
 TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAAAAAA AAAAAA

Seq ID NO: 464 Protein sequence
 Protein Accession #: NP_002984.1

1 11 21 31 41 51
 MSLPSSRAAR VPGPSGLCA LLALLLLTLP PGPLASAGPV SAVLTELRCR CLRVTLRVNP 60
 KTIQKLVFP AGPQCSKVEV VASLKNKGQV CLDPEAPFLK KVIQKILDSG NKKV

Seq ID NO: 465 DNA sequence
 Nucleic Acid Accession #: NM_002038.2
 Coding sequence: 108..500

1 11 21 31 41 51
 GAACCGTTTA CTCGCTGCTG TGCCCATCTA TCAGCAGGCT CCGGGCTGAA GATTGCTTCT 60
 CTTCTCTCCT CCAAGGTCTA GTGACGGAGC CCGCGCGCGG CGCCACCATG CGGCAGAAGG 120
 CGGTATCGCT TTTCTTGTGC TACCTGCTGC TCTTCACTTG CAGTGGGGTG GAGGCAGGTA 180
 AGAAAAAGTG CTCGGAGAGC TCGGACAGCG GCTCCGGGTT CTGGAAGGCC CTGACCTTCA 240
 TGGCCGTCCG AGGAGGACTC GCAGTCGCCG GGCTGCCCGC GCTGGGCTTC ACCGCGCCCG 300
 GCATCGCGCG CAACTCGGTT GCTGCCCTCG TGATGAGCTG GTCTGCGATC CTGAATGGGG 360
 CGCGCGTGCC CGCCGGGGGG CTAGTGGCCA CGCTGCAGAG CCTCGGGGCT GGTGGCAGCA 420
 GCCTCGTCAT AGGTAATATT GGTGCCCTGA TGGGCTACGC CACCCACAAG TATCTCGATA 480
 GTGAGGAGGA TGAGGAGTAG CCAGCAGCTC CCAGAACCCT TTCTTCCTTC TTGGCCTAAC 540
 TCTTCCAGTT AGGATCTAGA ACTTGGCTTT TTTTTTTTTT TTTTTTTTTT TTTGAGATGG 600
 GTTCTCACTA TATTGTCCAG GCTAGAGTGC AGTGGCTATT CACAGATGCG AACATAGTAC 660
 ACTGCAGGCT CCAACTCCTA GCCTCAAGTG ATCCTCCTGT CTCAACCTCC CAAGTAGGAT 720
 TACAAGCATG CGCCGACGAT GCCCAGAATC CAGAACCTTG TCTATCACTC TCCCCAACAA 780
 CCTAGATGTG AAAACAGAAT AAACCTTACC CAGAAAA

Seq ID NO: 466 Protein sequence
 Protein Accession #: NP_002029.3

1 11 21 31 41 51
 MRQKAVSLFL CYLLLFCTSG VEAGKKKCE SSDSGSGFWK ALTFMAVGGG LAVAGLPALG 60
 FTGAGIAANS VAASLMSWSA ILNGGGVPAG GLVATLQSLG AGGSSVVIGN IGALMGYATH 120
 KYLDSEEDDE

Seq ID NO: 467 DNA sequence
 Nucleic Acid Accession #: NM_003469.2
 Coding sequence: 92..1945

1 11 21 31 41 51
 GAAACGCCCC GAGAAGCTCG CCCGGAGAAC GGGGAGGAAT ATGCTGTGGA GTCCTCTGTC 60
 CATATAAACA AAAAGAGGAA ATCTTTCAAA CATGGCTGAA GCAAAGACCC ACTGGCTTGG 120
 AGCAGCCCTG TCTCTTATCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180
 TCAGAGAAAC CAGCTGTCTC AGAAAGAACC AGACCTCAGG TTGGAAGATG TCCAAAAGTT 240
 TCCCAGTCTT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACCAAGCTCA 300
 TAAGGAAGAA AGCAGCCAGG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA 360
 AAAAGAAAT GGCATGAAA GCCACTTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG 420
 GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAT GAGCCTCAGT CTGCACCAA 480
 AGAAAATAAG CCCTATGCCT TGAATTCAGA AAAGAACTTT CCAATGGACA TGAGTGATGA 540
 TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCCTATGTA 600
 TGAAGAGAA TCCAGGGATA ACCCTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660
 TACTCCTCAA AGCCTTGCTA CATTGGAATC TGCTTTCCAA GAGCTGGGGA AACTGACAGG 720
 ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACTTTATA CGGATGATGA 780
 AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTCGGGG GAGAAGACTG 840
 GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAAGA 900
 GAATATAGGA AAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT 960
 CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT 1020
 AATTGCTTAT TTGAAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080
 AATGGGGAA AGGGCCACCA GGCTTTTGA GAAACCTCTT GATTCTCAGT CTATTATCA 1140
 GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCAGAA GACTTAATTG AGATGCTCAA 1200
 AACTGGGGAG AAGCCGAATG GATCAGTGGA ACCGGAGCGG GAGCTTGACC TTCTGTTGA 1260
 CCTAGATGAC ATCTCAGAGG CTGACTTAGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT 1320
 CTCAGAGAGT GGTACCTTA AAACACTGG TCGTGTGGG ACTGAGGCC TACCAGACGG 1380
 GCTCAGTGTG GAGGATATTT TAAATCTTTT AGGGATGGAG AGTGCAGCAA ATCAGAAAAA 1440
 GTCGTATTTT CCAATCCAT ATAACAGGA GAAAGTTCTG CCAAGGCTCC CTTATGGTGC 1500
 TGGAGATCT AGATCGAACC AGCTTCCCAA AGCTGCCTGG ATTCCACATG TTGAAAACAG 1560
 ACAGATGGCA TATGAAAACC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG 1620
 GATGCTAGTT AAATACCTG AGATCATTA TTAACCAA GTGAAGCGAG TTCTGGTCA 1680
 AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAAT GAGCAGGCCA TCAAGAGCA 1740
 TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGGTTCCC 1800
 TGTGGGGCCC CCGAAGAAAT ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860
 AATGAAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGGAAGGG AGCATATTGC 1920

TAAGAGAGCA ATGGAAAATA TGTAAGCTGC TTTCATTAAT TACCCTACTT TCATTCTCTC 1980
 CACCCCAAGC AATATCCCAAC ATTTCTCTTC AGTGTGTGA CTTCTATCCT GTTAACACTG 2040
 TAATATCTTT AATGATGTA CAGGCAGATG AAACCAGGTC ACTGGGGAGT CTGCTTCATT 2100
 TCCTCTGAGC TGTATCTGTG TGTATGGATA TGTGTAAATG TTATGACTCC TTGATAAAAA 2160
 ATTTATTATG TCCATTATTC AAGAAAGATA TCTATGACTG TGTTAATAG TATATCTAAT 2220
 GGCTGTGGCA TTGTGTATGC TCACATATGA TAAAAAAGTG TCCTATAATT CTATTGAAAG 2280
 TTTTAAATAT TTATTGAATT ATTTTGTTCAC TGTCTGTAGC GTTTTGTGGA GTACTGGACC 2340
 AAAAAAATAA AGCATTATAA ATATA

Seq ID NO: 468 Protein sequence
 Protein Accession #: NP_003460.1

1 11 21 31 41 51
 MAEAKTHWLG AALSLIPLIF LISGAEAAAF QRNQLLQKEP DLRLNVQKF PSEPMIRALE 60
 YIENLRQQAQ KEESPDPNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ 120
 AENEPQSAFK ENKPYALNSE KNFPMDSDD YETQQWPERK LKHMQFPMPY EENSRLNPFK 180
 RTNEIVEEQY TPQSLATLES VFQELGKLTG PNNQKRERMD EQKLYTDEE DDIYKANNIA 240
 YEDVVGGEDW NPVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSQQLGI QEEDLRKESK 300
 DQLSDDVSKV IAYLRLRVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRLNLI 360
 PPDLEIEMLK TGEKPNGSVE PERELDLFVD LDDISEADLD HPDLFQNRML SKSGYPKTPG 420
 RAGTEALPDG LSVEDILNLL GMESAANQKT SYFPNPYNQE KVLPRLPYGA GRSRSNQLPK 480
 AAWIHPVENR QMAYENLNDK DQELGEYLAR MLVKYPEIIN SNQVKRPVPG GSSEDDLQEE 540
 EQIEQAIEKH LNQSSSQETD KLAPVSKRFP VGPPKNDITP NRQYWEDELL MKVLEYLNQE 600
 KAEKGREHIA KRAMENM

Seq ID NO: 469 DNA sequence
 Nucleic Acid Accession #: NM_006398.1
 Coding sequence: 19..516

1 11 21 31 41 51
 GGCCCTTGT CTGCAGAGAT GGCTCCCAAT GCTTCTCTGC TCTGTGTGCA TGTCCGTTCC 60
 GAGGAATGGG ATTTAATGAC CTTTGATGCC AACCCATATG ACAGCGTGAA AAAAAATCAA 120
 GAACATGTCC GGTCTAAGAC CAAGGTTCCT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180
 AAGATCTTAA AGCCACGGAG AAGCCTCTCA TCTTATGGCA TTGACAAAGA GAAGACCATC 240
 CACCTTACCC TGAAGTGGT GAAGCCAGT GATGAGGAGC TGCCCTTGT TCTTGTGGAG 300
 TCAGGTGATG AGGCAAGAG GCACCTCTCT CAGGTGCGAA GGTCACGCTC AGTGGCACAA 360
 GTGAAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC 420
 AATGGAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGGCATCAG AAAGGGCAAC 480
 TTACTCTTCC TGGCATCTTA TTGTATTGGA GGGTGACCAC CCTGGGGATG GGGTGTGGC 540
 AGGGGTCAA AAGCTTATTT CTTTAACTCT CTACTCAAC GAACACATCT TCTGATGATT 600
 TCCCAAATAT AATGAGAATG AGATGAGTAG AGTAAGATTT GGGTGGGATG GGTAGGATGA 660
 AGTATATTGC CCAACTCTAT GTTCTTTTGA TTCTAACACA ATTAATTAAG TGACATGATT 720
 TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCAAAATAG AGCATTC

Seq ID NO: 470 Protein sequence
 Protein Accession #: NP_006389.1

1 11 21 31 41 51
 MAPNASCLCV HVRSEEWDLN TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR 60
 RSLSSYGIDK ERTIHLTLKV VKPSDEELPL FLVESGDEAK RHLLQVRRSS SVAQVKAMIE 120
 TKTGIIPETQ IVTCNGKRLE DGRMMADYGI RKGNNLFLAS YCIGG

Seq ID NO: 471 DNA sequence
 Nucleic Acid Accession #: XM_094741.1
 Coding sequence: 1..948

1 11 21 31 41 51
 ATGAAGGCCA ACTACAGCGC AGAGGAGCGC TTTCTCTGTC TGGGTTTCTC CGACTGGCCT 60
 TCCCTGCAGC CGGTCTCTTT CGCCCTTGTC CTCTCTGTGCT ACCTCCTGAC CTTGACGGGC 120
 AACTCGGCGC TGGTGTCTGCT GCGGTGCGC GACCCGCGCC TGCACACGCC CATGTACTAC 180
 TTCCTCTGCC ACCTGGCCTT GGTAGACGCG GGCCTTCTCA CTAGCGTGGT GCCGCGCTG 240
 CTGGCCAACC TGCGCGGACC AGCGCTCTGG CTGCGCGGCA GCCACTGCAC GGCCAGCTG 300
 TGCGCATCGC TGGTCTCTGG TTCGCGCGAA TCGCTCTCTC TGGCGGTGAT GGTCTCTGAC 360
 CGCGCGCGCG CAGTGTGCGC CCGCTGCGC TATGCGGGGC TCGTCTCCCC GCGCCTATGT 420
 CGCACGCTGG CCAGCGCCTC CTGGCTAAGC GGCCTCACCA ACTCGGTGTC GCAAAACCGC 480
 CTCCTGGCTG AGCGGCGGCT GTGCGCGCCC CGCTCTGTGG ACCACTTCAT CTGTGAGCTG 540
 CCGCGTTGTC TCAAGCTGGC CTGCGGAGGC GACGGAGACA CTACCGAGAA CCAGATGTTC 600
 GCGCGCCGCG TGGTCTCTCT GCTGCTGCGG TTTGCGGTCA TCCTGGCCTC CTACGGTGCC 660
 GTGGCCCGAG CTGTCTGTTC CATGCGGTTT AGCGGAGGCC GGAGGAGGCC GGTGGGCACG 720
 TGTGGGTCCC ACCTGACAGC CGTCTGCTGT TTCTACGGCT CGGCCATCTA CACCTACCTG 780
 CAGCCCGCGC AGCGCTACAA CCAGGCACGG GGCAAGTTCT TATCGCTCTT CTACACCGTG 840
 GTCACACCTG CTCTCAACCC GCTCATCTAC ACCCTCAGGA ATAAGAAAGT GAAGGGGGCA 900
 GCGAGGAGGC TGCTGCGGAG TCTGGGGAGA GGCCAGGCTG GGCAGTGA

Seq ID NO: 472 Protein sequence
 Protein Accession #: XP_094741.1

1 11 21 31 41 51
 MKANYSABER FLLLGFSWDP SLQPVLFALV LLCYLLTLTG NSALVLLAVR DPLRLTPMY 60

FLCHLALVDA GFTTSVVPPL LANLRGPALW LPRSHCTAQL CASLALGSAE CVLLAVMALD 120
 RAAAVCRPLR YAGLVSPRLC RTLASASWLS GLTNSVAQTA LLAERPLCAP RLDDHFICEL 180
 PALLKLACGG DGTITTENQMF AARVVILLLP FAVILASYGA VARAVCCMRF SGGRRRAVGT 240
 CGSHLTAVCL FYGSAIYTYL QPAQRYNQAR GKFVSLFYTV VTPALNPLIY TLRNKKVKGA 300
 ARRLRLSLGR GQAGQ

Seq ID NO: 473 DNA sequence
 Nucleic Acid Accession #: NM_001062.1
 Coding sequence: 76..1380

1 11 21 31 41 51
 | | | | |
 GCTCTCATT CTTCTGCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG 60
 TACACTGTTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTTT 120
 TCTTTTATTC CAAGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180
 CTAAACCTC TGTGAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC 240
 AATGTTGTGT TGTCCCTCAA ACTTGTGGA ATCCAGATCC AAACCTGAT GCAAAAGATG 300
 ATCCAACAAA TCAAAATCAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACGCTG AGGAAAACCTT AATATATGAT 420
 TACCACCTGA CTGACAAGCT AGAAAATAAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480
 CACAATGGCA CTCCCCTGAC TAACACTACT CAGCTCAGCC TGGACGTTT GGCCTTGTGT 540
 CTGTTCAATG GGAACACTC AACCGCCGAA GTTGTCAACC ACTTCACTCC TGAATAATAA 600
 AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CCTGGCTCTG 660
 ACCTGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAAG CAGATGAAGG CAGTTTAAAG 720
 AACATCAGTA TTTATACAAA GTCACCTGTA GAAAAGATTC TGTCTGAGAA AAAAGAAAAAT 780
 GGTCTCATTT GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840
 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAAACTC TGAATACAGT GCTCAGCGAA 900
 ATTTCTCAAG GAGCACTTCA TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960
 GAAAAGACCT TCTTGGATAT TAACAAAGAC TCTTCTTGGC TCTCTGCTTC AGGTAACCTC 1020
 AATATCTCCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC 1080
 GTCATTTACT CTGTGAGAA CAATGAAACA TATTTACCCA ATGTCAGTGT GCTAAATGGT 1140
 TCTGTCTTCC TCACTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACAT ATTTGGTTTC 1200
 ACAAATGGAG AGCGCTCATG GGGGCCCTAT ATCACTGTGA TTCAGGGCCT ATGTGCCAAC 1260
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCACTGAG CCAAGGAGCT 1320
 GGTATGTTACG TTGTCGCGAA TGGAGAAAAC TTGGAGGTTT GCTGGAGCAA ATACTAATAA 1380
 GCCCAAACCT TCTCAGCTG CATAAAATCC ATTTGCAGTG GAGTTCATG TTTATTGTCC 1440
 TTATGCCTTC TTCTTCATTT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCTTCTC 1500
 TCTCTACATG TTAATAAAA GTTGTGAAA GATTAAC

Seq ID NO: 474 Protein sequence
 Protein Accession #: NP_001053.1

1 11 21 31 41 51
 | | | | |
 MRQSHQLPLV GLLLSFPIPS QLCEICEVSE ENYIRLKPILL NTMIQSNYNR GTSAVNVVLS 60
 LKLVGIQIQI LMQMKIQIQL YNVKSRSLSDV SSGELALIL ALGVCNRNAAE NLIYDYHLTD 120
 KLENKFQAEI EMQEAHNGTP LTNYYQLSLD VLALCLFNNG YSTAEEVNHF TPENKNYYFG 180
 SQFSVDTGAM AVLALTCVKK SLINGQIKAD EGSLLNISIY TKSLVEKILS EKKENGLIGN 240
 TFSTGEAMQA LFPVSSDYNE NDWNCQQTILN TVLTEISQGA FSNPNAAAQV LPALMGKTFL 300
 DINKDSSCVS ASGNCACCTG EPITVTPPDS QSYISVNYSV RINETYFTNV TVLNGSVFLS 360
 VMEKAQKMDN TIFGFTMEER SWGPYITTCQ GLCANNDRT YWELLSGGEF LSQAGASYVV 420
 RNGENLEVRW SKY

Seq ID NO: 475 DNA sequence
 Nucleic Acid Accession #: NM_004852.1
 Coding sequence: 89..1546

1 11 21 31 41 51
 | | | | |
 GCCCCGCCCC GCCCGGGGCC CTGATGGAAT GAATGAAGGC TGCCCTACACC GCCTATCGAT 60
 GCCTCACCAA AGACCTAGAA CGTGCGCCAT GAACCCGAG CTGACAATGG AAAGTCTGGG 120
 CACTTTGCAC GCGCGCGCGC GCGCGCGCAG TGGCGGGGGC GCGCGCGGGG GCGCGCGGGG 180
 CGGCGGCGGG GCGCGGGGCC ATGAGCAGGA GCTGCTGGCC AGCCCCAGCC CCCACCACGC 240
 GCGCGCGGGC CCGCGTGGCT CGCTGCGGGG CCCTCCGCGC CTCCAACCG CGCACCAGGA 300
 GCTGGGCAGC GCGGCAGCGC CGGCAGCGGC GCGCTCGGC TCGGCCATGG TCACCAGCAT 360
 GGCCTCGATC CTGGACGGCG GCGACTACCG GCCCGAGCTC TCCATCCCGC TGCACCACGC 420
 CATGAGCATG TCTCTGCACT CGTCTCCGCC TGGCATGGGC ATGAGCAACA CCTACACCAC 480
 GCTGACACCG CTCACGCCGC TGCCACCCAT CTCACCCGTG TCTGACAAAT TCCACCACCC 540
 TCACCCGCAC CACCATCCGC ACCACCACCA CCACCACCAC CACCAGCGCC TGTCGGCAA 600
 CGTCAGCGGC AGCTTCACCC TCATGCGCGA CGAGCGCGGG CTCCCGGCCA TGAACAACCT 660
 CTACAGTCCC TACAAGGAGA TGCCCGGCAT GAGCCAGAGC TGTCCCCGCT TGGCCGCCAC 720
 GCGCGTGGG AACGGGCTAG GCGGCCTCCA CAACGCGCAG CAGAGTCTGC CCAACTACGG 780
 TCCGCGGGC CAGCAAAA TGCTCAGCCC CAACTTCGAC GCGCACCACA CTGCCATGCT 840
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Seq ID NO: 476 Protein sequence
 Protein Accession #: NP_004843.1

1 11 21 31 41 51
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 DERGLPAMNN LYSYPKEMPG MSQSLSPALAA TPLGNLGLGL HNAQQSLPNY GPPGHDKMLS 240
 PNFDAAHTAM LTRGEQHLRS GLGTPPAAMM SHLNLHLHPG HTQSHGVLPA PSRERPPSSS 300
 SSSQVATSGQ LEEINTKEVA QRITAEKRY SIPQAIFAQR VLCSQGTLS DLLRNPKPWS 360
 KLKSGRETFR RMWKWLQEPF FORMSALRLA ACKRKEQEPN KDRNNSQKKS RLVFTDLQRR 420
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 TCTKA

Seq ID NO: 477 DNA sequence
 Nucleic Acid Accession #: NM_013271.1
 Coding sequence: 27..809

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 TGCTGCGAG CGCCTCTTTG CCACCTGAG CACTGCCCCG ATCCCGTGCA CCCTGGGACC 840
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Seq ID NO: 478 Protein sequence
 Protein Accession #: NP_037403.1

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 PALGLDDDPD APAQALARAL LRLRLDPAAL AAQLVPAPVP AAALRPRPVV YDDGAPGPD 180
 EEAGDETPDV DPELLRYLLG RILAGSADSE GVAAPRRLRR AADHDVGSSEL PPEGVLGALL 240
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Seq ID NO: 479 DNA sequence
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 681..2990

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 TCCCTCGAC CTGCGCGCG TACCCTCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
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 TGGCCGTGCA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCGGTGCC GAGCCGGGAG 480
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Seq ID NO: 480 Protein sequence

Protein Accession #: NP_002205

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GEVSIQLRPG AEANFMKVH PLKKYPVDLY YLVDVSASMH NNIEKLN SVG NDLSRKMAFF 180
SRDFRLGFGS YVDKTVSPYI SIHPERIHNQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA 240
VHRQKISGNI DTEGGEFDAM LQAAVCESHI GWRKEAKRL LVMTDQTSHL ALDSKLAGIV 300
VPNDGNCHLK NNVVVKSTTM EHPSLQQLSE KLIDNNINVI FAVQKGQFHW YKDLLPLLP 360
TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420
NVTSDNEVLF NVTVTMKKCD VTGKKNYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK 480
CVDETFLDSK CFQCDENKCH FDEDQFSSES CKSHKDQFVC SGRGVCVCGK CSCCHKIKLGK 540
VYGYKCEKDD FSCPYHHGNL CAGHGECEAG RCQCFSGWEG DRQCQPSAAA QHCNVNSKGQV 600
CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNL QAILDQCKTS 660
CALMEQQHYV DQTSCECFSS SYLRIFPIIF IVTFLIGLLK VLIIRQVILQ WNSNKKIKSS 720
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Seq ID NO: 481 DNA sequence

Nucleic Acid Accession #: NM_003318.1

Coding sequence: 1..2574

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AACCAGAGG ACTGTTGAG TTTGTTGCTC AAAGTAGAGA AAAACAGTGT TCCGCTAAGT 240
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GCTATTCAAG AGCCAGATGA TGCACGTGAC TACTTTCAAA TGGCCAGAGC AAATGCAAG 420
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 25 TCTCCTAATC CCATTTTGAA AGCTGCTAAA ACTTTATATG AACACTATAG TGGTGGTGAA 2520
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Seq ID NO: 482 Protein sequence
 Protein Accession #: NP_003309.1

30 1 11 21 31 41 51
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Seq ID NO: 483 DNA sequence
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Seq ID NO: 484 Protein sequence
 Protein Accession #: NP_003658.1

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QLCRKIKKKQ LGAQRKTSIQ DLRSIAGLTF LLGITWGFAP FAWGVPNVTF MYLFAIFNTL 840
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GKQHMFNKEE DSCNGKGRMA LRRTSKRGS LHFIEQM
  
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	GTGTCCAGCT	CTTCAAATTC	CTTACAGTCA	AGCAGTAACT	CCACTAACTC	CACCACACTG	2820
	CTAGTGAATA	ATGATTGCTC	AGTACACGCA	AGCGGGAATG	GAAATGCCTC	TACAGAGAGG	2880
	AATGGGGTCT	CTTTTAGTGT	TCAGAATGGA	GATGTGTGCC	TTTACGATTT	CCTGGGAAAA	2940
20	CAGCACATGT	TTAACGAGAA	GGAAGATTCC	TGCAATGGGA	AAGGCCGTAT	GGCTCTCAGA	3000
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Seq ID NO: 492 Protein sequence

Protein Accession #: Eos sequence

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	TLNCTFTIKL	NNTMNACAAI	AALERVKIRP	MEHCCCSVRI	PCPSSPEELG	KLQCDLQDPI	240
	VCLADHPRGP	PFSSSQSPV	VPRATVLSQV	PKATSFABPP	DYSPVTHNPV	SPIGEIQPLS	300
	PQPSAPIASS	PAIDMPPQSE	TISSPMPQTH	VSGTPPPVK	SFSSPTVSAP	ANVNNTSAPP	360
	VQTDIVNTSS	ISDLENQVLQ	MEKALSLGSL	EPNLAGEMIN	QVSRLLSHPP	DMLAPLAQRL	420
35	LKVVDDIGLQ	LNFNTTISL	TSPSLALAVI	RVNASSFNNT	TFVAQDPANL	QVSLETQAPE	480
	NSIGITITLPS	SLMNNLPAHD	MELASRVQFN	FFETPALFQD	PSLENLSLIS	YVSSSVANL	540
	TVRNLTNRVT	VTLKHINPSQ	DELTVRVFW	DLGRNGRGG	WSDNGCSVKD	RRLNETICTC	600
	SHLTSFGVLL	DLRSVSLVPA	QMMALTFTTY	IGCGLSSIFL	SVTLVTYIAF	EKIRRDYPSK	660
	ILIQLCALL	LLNLVFLDLS	WIALYKMQGL	CISVAVFLHY	FLLSVFTWMG	LEAFHMYLAL	720
40	VKVFNTYIRK	YILKFCIVGW	GVPVAVVTII	LTISPNDYGL	GSYGFKNPNS	PDDFCWINNN	780
	AVFYITVVG	YFVIFLLNVS	MFIVVLVQLC	RIKKKKQLGA	QRKTSIQDLR	SIAGLTFFLG	840
	ITWGAFFAW	PCNVNVTFFML	FAIFNTLQGF	FIFIFYCVAK	ENVRKQWRRY	LCCGKLRLAE	900
	NSDWSKTATN	GLKKQTVNQG	VSSSSNSLQS	SSNSTNSTTL	LNVNDCSVHA	SGNGNMASTER	960
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Nucleic Acid Accession #: NM_015507

Coding sequence: 241..1902

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55	GGGTCCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
	ATGCTCTGCT	CCTGGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
	GGGAACGCGG	CCAGTCAAG	GCATCACGGG	TTGTTAGCAT	CGGCACGTCA	GCCTGGGGTC	360
	TGTCACTATG	GAACATAACT	GGCTGCTGTC	TACGGCTGGA	GAAGAACACG	CAAGGGAGTC	420
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	TTAGAAATTAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCTT	2040

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 Protein Accession #: NP_056322

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Seq ID NO: 496 Protein sequence
Protein Accession #: NP_003497.1

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CAPPCPNMYF	KSDELEFAKS	FIGTVSIFCL	CATLFTFLTF	LIDVRRFRYP	ERPIIYYSVC	240
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VILTITWFLA	AGRKWSCEAI	EQKAVWFHAV	AWGTPGFLT	MLLALNKVEG	DNISGVCFVG	360
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LMTLIVGISA	VFWVGSKKTC	TEWAGFFKRN	RKRDPISER	RVLQESCEFF	LKHNSKVHKH	540
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CGCTGCGAAC	CCCCTGGAAC	CACCTGTACT	GTCTCCGGCT	GGGGCACTAC	CACGAGCCCA	480
GATGTGACCT	TTCCTCTTGA	CCTCATGTGC	GTGGATGTCA	AGCTCATCTC	CCCCCAGGAC	540
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CAAGGTCTGG	TGTCTCTGGG	AACCTTCCCT	TGCGGCCAAC	CCAATGACCC	AGGAGTCTAC	720
ACTCAAGTGT	GCAAGTTTCA	CAAGTGGATA	AATGACACCA	TGAAAAAGCA	TCGCTAACGC	780
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Seq ID NO: 498 Protein sequence
Protein Accession #: NP_005037

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QARLSSMVKK	VRLPSRCEPP	GTCTVSGWG	TTTSPDVTFP	SDLMCVDVKL	ISPQDCTKVY	180
KDLLENSMLC	AGIPDSKINA	CNGDSGGPLV	CRGTLQGLVS	WGTFPCGQPN	DPGVYTQVCK	240
FTKWINDTMK	KHR					

Seq ID NO: 499 DNA sequence
Nucleic Acid Accession #: NM_007196
Coding sequence: 182..962

60
65
70
75
80

1	11	21	31	41	51	
GTTCCAGAA	GCTCCCCAGG	CTCTAGTGCA	GGAGGAGAAG	GAGGAGGAGC	AGGAGGTGGA	60
GATTCCCACT	TAAAGGCTC	CAGAATCGTG	TACCAGGCAG	AGAACTGAAG	TACTGGGGCC	120
TCCTCCACTG	GGTCCGAATC	AGTAGGTGAC	CCCGCCCTG	GATTCTGGAA	GACCTCACCA	180
TGGGACGCCC	CCGACCTCGT	GCGGCCAAGA	CGTGGATGTT	CCTGCTCTTG	CTGGGGGAG	240
CCTGGGCAGG	ACACTCCAGG	GCACAGGAGG	ACAAGGTGCT	GGGGGGTCAT	GAGTGCCAAC	300
CCCATTCGCA	GCCTTGGCAG	GCGGCCCTGT	TCCAGGGCCA	GCAACTACTC	TGTGGCGGTG	360
TCCTTGTAGT	TGGCACTGG	GTCCTTACAG	CTGCCCCACTG	TAAAAAACCG	AAATACACAG	420
TACGCCCTGGG	AGACCACAGC	CTACAGAATA	AAGATGGCCC	AGAGCAAGAA	ATACCTGTGG	480
TTCACTCCAT	CCCACACCCC	TGCTACAACA	GCAGCGATGT	GGAGGACCAC	AACCATGATC	540
TGATGCTTCT	TCAACTGCGT	GACCAGGCAT	CCCTGGGGTC	CAAAGTGAAG	CCCATCAGCC	600
TGGCAGATCA	TTGCACCCAG	CCTGGCCAGA	AGTGCACCGT	CTCAGGCTGG	GGCACTGTCA	660
CCAGTCCCGG	AGAGAAATTT	CCTGACACTC	TCAACTGTGC	AGAAGTAAAA	ATCTTTCCCC	720
AGAAGAAGTG	TGAGGATGCT	TACCCGGGGC	AGATCACAGA	TGGCATGGTC	TGTGCAGGCA	780
GCAGCAAAGG	GGCTGACACG	TGCCAGGGCG	ATTCTGGAGG	CCCGCTGGTG	TGTGATGGTG	840
CACCTCAGGG	CATCACATCC	TGGGGCTCAG	ACCCTGTGG	GAGGTCCGAC	AAACCTGGCG	900
TCTATACCAA	GATCTGCCGC	TACCTGGACT	GGATCAAGAA	GATCATAGGC	AGCAAGGGCT	960
GATTCTAGGA	TAAGCACTAG	ATCTCCCTTA	ATAAACTCAC	AACTCTC		

Seq ID NO: 500 Protein sequence
Protein Accession #: NP_009127

1 11 21 31 41 51

5 MGRPRPRAAK TWMFLLLLGG AWAGHSRAQE DKVLGGHECQ PHSQPWQAAAL FQGQQLLCGG 60
 VLVGGNWWLT AAHCKKPKYT VRLGDHSLQN KDGPEQEIPV VQSIHPHCYN SSDVEDHNIH 120
 LMLQLLRDQA SLGSKVKPIS LADHCTQPGQ KCTVSGWGTV TSPRENFPDT LNCAEVKIFP 180
 QKKCEDAYPG QITDGMVCAG SSKGADTCQG DSGGPLVCDG ALQGITSWGS DPCGRSDKPG 240
 VYTNICRYLD WTKKIIGSKG

Seq ID NO: 501 DNA sequence
 Nucleic Acid Accession #: NM_006103
 Coding sequence: 29..406

15 1 11 21 31 41 51
 CACCTGCACC CCGCCCGGGC ATAGCACCAT GCCTGCTTGT CGCCTAGGCC CGCTAGCCGC 60
 CGCCCTCCTC CTCAGCCTGC TGCTGTTCGG CTCACCCCTA GTCTCAGGCA CAGGAGCAGA 120
 GAAGACTGGC GTGTGCCCGC AGCTCCAGGC TGACCAGAAC TGACGCAAG AGTGCGTCTC 180
 GGACAGCGAA TCGCCCGACA ACCTCAAGTG CTGCAGCGCG GGCTGTGCCA CCTTCTGCCT 240
 TCTCTGCCCA AATGATAAGG AGGGTTCCTG CCCCCAGGTG AACATTAACT TTCCCCAGCT 300
 CGGCCTCTGT CGGGACCAGT GCCAGGTGGA CAGCCAGTGT CCTGGCCAGA TGAATGCTG 360
 20 CGCAATGGC TGTGGGAAGG TGTCTGTGT CACTCCCAAT TTCTGAGTTC CAGCCACCAC 420
 CAGGCTGAGC AGTGAGGAGA GAAAGTTTCT GCCTGGCCCT GCATCTGTTT CCAGCCACC 480
 TGCCTCCCC TTTTTCGGGA CTCTGTATTC CCTCTGGGCG TGACCACAGC TTCTCCCTTT 540
 CCAACCAAT AAGTAACCA CTTTCAGCAA AAAAAAAAAA AAAA

25 Seq ID NO: 502 Protein sequence
 Protein Accession #: NP_006094

30 1 11 21 31 41 51
 MPACRLGFLA AALLLSLLLF GFTLVSGTGA EKTGVCPQLQ ADQNTQECV SDSECADNLK 60
 CCSAGCATFC LLCPNDKEGS CPQVNIINFPQ LGLCRDQCQV DSQCPGQMKC CRNGCGKVSC 120
 VTPNF

35 Seq ID NO: 503 DNA sequence
 Nucleic Acid Accession #: NM_002407
 Coding sequence: 65..352

40 1 11 21 31 41 51
 CCTCCACAGC AACTTCCTTG ATCCCTGCCA CGCAGGACTG AACACAGACA GCAGCCGCCT 60
 CGCCATGAAG CTGCTGATGG TCCTCATGCT GCGCGCCCTC CTCCTGCACT GCTATGCAGA 120
 TTCTGGCTGC AAATCCTGG AGGACATGGT TGAAAAGACC ATCAATTCCG ACATATCTAT 180
 ACCTGAATAC AAAGAGCTTC TTCAAGAGTT CATAGACAGT GATGCCGCTG CAGAGGCTAT 240
 45 GGGGAAATTC AAGCAGTGT TCCCTCAACA GTCACATAGA ACTCTGAAAA ACTTTGGACT 300
 GATGATGCAT ACAGTGTACG ACAGCATTGT GTGTAATATG AAGAGTAATT AACTTTACCC 360
 AAGGCGTTTG GCTCAGAGGG CTACAGACTA TGGCCAGAAC TCATCTGTGT ATTGCTAGAA 420
 ACCACTTTTC TTTCTGTGT TGTCTTTTA TGTGGAAACT GCTAGACAAC TGTGTAAGAC 480
 TCAAATTCAT TTCCATTCA ATAATAACT GCAAATC

50 Seq ID NO: 504 Protein sequence
 Protein Accession #: NP_002398

55 1 11 21 31 41 51
 MKLLMLMLA ALLLHCYADS GCKLLEDMEV KTINSDISIP EYKELLQEFI DSDAAAAMG 60
 KFKQCFLNQS HRTLKNFGLM MHTVYDSIWC NMKSN

60 Seq ID NO: 505 DNA sequence
 Nucleic Acid Accession #: NM_014791.1
 Coding sequence: 171..2126

65 1 11 21 31 41 51
 TTGGCGGGCG GAAGCGGCCA CAACCCGCGC ATCGAAAAGA TTCTTAGGAA CGCCGTACCA 60
 GCCGCGTCTC TCAGGACAGC AGGCCCTGT CTCTCTGTG GCGCGCGCTC AGCCGTGCCC 120
 TCCGCCCTC AGGTTCTTTT TCTAATCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180
 ATGATGAAT TCTCAAATAT TATGAATTAC ATGAAACTAT TGGACAGGT GGCTTTGCAA 240
 AGGTCAAAT TGCCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300
 70 AAAACACAT AGGGAGTGAT TTGCCCGGGA TCAAAACGGA GATTGAGGCC TTGAAGAACC 360
 TGAGACATCA GCATATATGT CAACTCTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA 420
 TGGTCTTGA GTACTGCCCT GGAGGAGAGC TGTTTGACTA TATAATTTC CAGGATCGCC 480
 TGTGAGAAGA GGAGACCCGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC 540
 ACAGCCAGGG CTATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC 600
 75 ATAAATTAAA GCTGATTGAC TTTGGTCTCT GTGCAAAACC CAAGGGTAAC AAGGATTACC 660
 ATCTACAGAC ATGCTGTGGG AGTCTGGCTT ATGCAGCACC TGAGTTAATA CAAGGCAAT 720
 CATATCTTG ATCAGAGGCA GATGTTTGA GCATGGGCAT ACTGTTATAT GTTCTTATGT 780
 GTGATTCTT ACCATTGAT GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG 840
 80 GAAAATATGA TGTTCCTCAAG TGGCTCTCTC CCAGTAGCAT TCTGCTTCTT CAACAAATGC 900
 TGCAGGTGGA CCCAAAGAAA CGGATTCTTA TGAATAATCT ATTGAACCAT CCCTGGATCA 960
 TGCAGATTA CAATATCTCT GTTGAGTGGC AAAGCAAGAA TCCTTTTATT CACCTCGATG 1020
 ATGATTGCGT AACAGAACT TCTGTACATC ACAGAAACAA CAGGCAACAA ATGGAGGATT 1080
 TAAATTCAT GTGGCAGTAT GATCACCTCA CGGCTACCTA TCTTCTGCTT CTAGCCAAGA 1140
 AGGCTCGGG AAAACAGTT CGTTTAAGGC TTTCTTCTT CTCTGTGGA CAAGCCAGTG 1200
 CTACCCCAT CACAGATATC AAGTCAATA ATTGGAGTCT GGAAGATGTG ACCGCAAGTG 1260

ATAAAAATTA TGTGGCGGGA TTAATAGACT ATGATTGGTG TGAAGATGAT TTATCAACAG 1320
 GTGCTGCTAC TCCCCGAACA TCACAGTTTA CCAAGTACTG GACAGAATCA AATGGGGTGG 1380
 AATCTAAATC ATTAACITCCA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAAG 1440
 AAAATGTATA TACTCCTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCTTGAGC 1500
 CAAAGACTCC AGTTAATAAG AACCAGCATA AGAGAGAAAT ACTCACTACG CCAAATCGTT 1560
 ACACTACACC CTCAAAGCT AGAAACCACT GCCTGAAAGA AACTCCAATT AAAATACCAG 1620
 TAAATTCAAC AGGAACAGAC AAGTTAATGA CAGGTGTCAT TAGCCCTGAG AGGCGGTGCC 1680
 GCTCAGTGGG ATTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAAA AGAAAGGGAG 1740
 CCAAAGTGTT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA 1800
 GCAAAAGGAA GGGTTCTGCC AGAGACGGGC CCAGAAGACT AAAGCTTCAC TATAATGTGA 1860
 CTACAACATG ATTAGTGAAT CCAGATCAAC TGTGTAATGA AATAATGTCT ATTCTTCCAA 1920
 AGAAGCATGT TGACTTTGTA CAAAAGGGTT ATACACTGAA GTGTCAAACA CAGTCAGATT 1980
 TTGGGAAAGT GACAATGCAA TTTGAATTAG AAGTGTGCCA GCTTCAAAAA CCGATGTGG 2040
 TGGGTATCAG GAGGCAGCGG CTTAAGGGCG ATGCCTGGGT TTACAAAAGA TTAGTGAAG 2100
 ACATCCTATC TAGCTGCAAG GTATAATTGA TGGATTCTTC CATCCTGCCG GATGAGTGTG 2160
 GGTGTGATAC AGCCTACATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCATTGGAA 2220
 CTACCAACTT GTTCTCTAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAACAACAA 2280
 GATATTATTT TGTGTATGAA TCTAAATCAA GCCCATCTGT CATTATGTTA CTGTCTTTTT 2340
 TAATCATGTG GTTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG 2400
 AATGTAAGCT CTTAACTATG TCTCTTTGTA ATGTGTAATT TCTTCTGAA ATAAACCAT 2460
 TTGTGAATAT

Seq ID NO: 506 Protein sequence
 Protein Accession #: NP_055606.1

1 11 21 31 41 51
 MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA 60
 LKNLRHQHIC QLYHVLETAN KIFMVLEYCP GGELEFDYIIS QDRLESEETR VVFRQIVSAV 120
 AYVHSQGYAH RDLKPENILF DEYHKLKID FGLCAKPKGN KDYHLQTCGG SLAYAAPELI 180
 QGKSYLGSEA DVWSMGILLY VLMCGFLPFD DDNMALYK KMRGKYDVPK WLSFSSILL 240
 QQMLQVDPKK RISMKNLLNH PWIMQDYNYP VEWQSKNPFH HLDDDCVTEL SVHHRNNRQT 300
 MEDLISLWQY DHLTATYLLL LAKKARGKPV RLRLSSFSCG QASATPFTDI KSNNWSLEDV 360
 TASDKNYVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTIPANKL 420
 KNKENVYTPK SAVKNBEEYFM FPEPKTPVKN NQHKREILT PNRYTTPSKA RNQCLKETPI 480
 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV 540
 LTRSKRKGS A RDGPRRLKLH YNVTTTRLVN PDQLLNEIMS ILPKKHVDFV QKGYTLKQQT 600
 QSDFGKVTMQ FELEVCQLQK PDVVGIRRRQ LKGDWVYKR LVEDILSSCK V

Seq ID NO: 507 DNA sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88..990

1 11 21 31 41 51
 GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
 AACGCCGACC AAGGAAACTC CACTACCATG AGAATTGCAG TGATTGCTT TTGCCTCCTA 120
 GGCATCACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAGAGCAG 180
 CTTTACACCA AATACCAGTA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240
 CAGAACTCTC TAGCCCCACA GACCTTCTCA AGTAAGTCCA ACGAAAGCCA TGACCCATG 300
 GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360
 AACGACTCTG ATGATGATGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420
 TCTGATGAAT CTGATGAAC TGTCACTGAT TTCTCCACGG ACCTGCCAGC AACCGAAGTT 480
 TTCCTCCAG TTTGCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540
 GGACTGAGGT CAAAATCTAA GAAGTTTCGC AGACCTGACA TCCAGTACCC TGATGCTACA 600
 GACGAGGACA TCACCTCACA CATGGAAAGC GAGGAGTTGA ATGGTGCATA CAAGGCCATC 660
 CCGTGTGCC AGGACCTGAA CGCGCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT 720
 GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780
 TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCGG ATGTGATGTA TAGTCAGGAA 840
 CTTTCCAAAG TCAGCCGTGA ATTCCACAGC CATGAATTC ACAGCCATGA AGATATGCTG 900
 GTTGTAGACC CCAAAGTAA GGAAGAAGAT AAACACCTGA AATTTCTGAT TTCTCATGAA 960
 TTGATAGTG CATCTTCTGA GGTCAATTAA AAGGAGAAAA AATACAATT CTCACTTTGC 1020
 ATTTAGTCAA AAGAAAAAAT GCTTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT 1080
 CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA 1140
 ATTAGTTTAT TTTGTGGCTT CATGGAAACT CCCTGTAAAC TAAAAGCTTC AGGGTTATGT 1200
 CTATGTTTAT TCTATAGAAG AAATGCAAAC TATCACTGTA TTTTAATATT TGTATTTCTC 1260
 TCATGAATAG AAATTTATGT AGAAGCAAAC AAAATACTTT TACCCACTTA AAAAGAGAAT 1320
 ATAAACATTT ATGTCACTAT AATCTTTTGT TTTTAAAGTT AGTGTATATT TTGTTGTGAT 1380
 TATCTTTTGT TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGGTGTC 1440
 AATGCTTAT TGTTTTCC CCGTTGTGCC AGCAATTAAT AAAACATAAC CTTTTTACT 1500
 GCCTAAAAAA AAAAAA AAAA

Seq ID NO: 508 Protein sequence
 Protein Accession #: NP_000573

1 11 21 31 41 51
 MRIAVICFCL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLAPQTL 60
 PSKSNESH DH MDDMDEDD DHVDSQDSID SNDSDDVDDT DDSHQSDSH HSDDESDELVT 120
 DFPTDLPATE VFTPVVPTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYPA TDEDITSHME 180
 SEELNGAYKA IPVAGDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
 NEHSDVIDSQ ELSKVSREFH SHEFHSHEM LVVDPKSKEE DKHLKFRISH ELDSASSEVN

Seq ID NO: 509 DNA sequence
Nucleic Acid Accession #: AB051390.1
Coding sequence: 34..2457

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	CTGAGCCGGA	CTCCGGCACT	GCTGGCCCTG	GCGCTGCCCG	TGGCCGCGCG	GCTGGCCCTT	120
10	TCCGACGAGA	CCCTGGACAA	AGTGCCCAAG	TCAGAGGGCT	ACTGCAGCCG	TATCTGCGCG	180
	GCCAGGGCA	CGCGGCGCGA	GGGCTACACC	GAGTTACAGC	TCCGCGTGGA	GGGCGACCCC	240
	GACTTCTACA	AGCCGGGAAC	CAGCTACCGC	GTAACACTTT	CAGCTGCTCC	TCCCTCCTAC	300
	TTCAGAGGAT	TCACATTAAT	TGCCCTCAGA	GAGAACAGAG	AGGGTGATAA	GGAAGAAGAC	360
	CATGCTGGGA	CCTTCCAGAT	CATAGACGAA	GAAGAACTC	AGTTTATGAG	CAATTGCCCT	420
15	GTTCAGTCA	CTGAAAGCAC	TCCACGGAGG	AGGACCCGGA	TCCAGGTGTT	TTGGATAGCA	480
	CCACCAGCGG	GAACAGGCTG	CGTGATTCTG	AAGGCCAGCA	TCGTACAAAA	ACGCATTATT	540
	TATTTTCAAG	ATGAGGGCTC	TCTGACCAAG	AAACTTTGTG	AACAAGATTC	CACATTTGAT	600
	GGGGTGACTG	ACAAAACCCAT	CTTAGACTGC	TGTGCCTGCG	GAAGTCCCAA	GTACAGACTC	660
	ACATTTTATG	GGAATTGGTC	CGAGAAGACA	CACCCAAAGG	ATTACCCTCG	TCGGGCCAAC	720
20	CACGTGCTCG	CGATCATCGG	AGGATCCAC	TCCAAGAATT	ATGTACTGTG	GGAATATGGA	780
	GGATATGCCA	GCGAAGCGGT	CAAACAAGTT	GCAGAATTGG	GCTCACCCTG	GAAATATGAG	840
	GAAGAAATTC	GACAACAGAG	TGATGAGGTC	CTCACCGTCA	TCAAAGCCAA	AGCCCAATGG	900
	CCAGCTTGGC	AGCCTCTCAA	CGTGAGAGCA	GCACCTTCAG	CTGAATTTTC	CGTGACAGCA	960
	ACGCGCCATT	TAATGTCTTT	CCTGACCATT	ATGGGCCCTA	GTCCCGACTG	GAAAGTAGGC	1020
25	TTATCTGCGA	AAGATCTGTG	CACCAAGGAA	TGTGGCTGGG	TCCAGAAGGT	GGTGCAAGAC	1080
	CTGATTCCCT	GGGACGCTGG	CACCGACAGC	GGGGTGACCT	ATGAGTCACC	CAACAAACCC	1140
	ACCATTCCCC	AGGAGAAAAT	CCGGCCCTCG	ACCAGCCTGG	ACCATCTCTA	GAGTCCCTTC	1200
	TATGACCCAG	AGGGTGGGTC	CATCACTCAA	GTAGCCAGAG	TTGTCTATCGA	GAGAATCGCA	1260
	CGGAAGGGTG	AACAATGCAA	TATTTGTACCT	GACAATGTCTG	ATGATATTGT	AGCTGACCTG	1320
30	GCTCCAGAAAG	AGAAAGATGA	AGATGACACC	CCTGAAACCT	GCATCTACTC	CAACTGGTCC	1380
	CCATGTGTCG	CTGTCAGCTC	CTCCACCTGT	GACAAAGGCA	AGAGGATGCG	ACAGCGCATG	1440
	CTGAAAGCAC	AGCTGGACCT	CAGCGTCCCC	TGCCCTGACA	CCCAGGACTT	CCAGCCCTGC	1500
	ATGGGCCCTG	GCTGCAGTGA	CGAAGACGGC	TCCACCTGCA	CCATGTCCGA	GTGGATCACC	1560
	TGGTCGCGCT	CGAGCATCTC	CTCGCGCATG	GGCATGAGGT	CCCGGGAGAG	GTATGTGAAG	1620
35	CAGTTCCCGG	AGGACGGCTC	CGTGTGCACG	CTGCCCACTG	AGGAAACGGA	GAAGTGACAG	1680
	GTCAACGAGG	AGTGCTCTCC	CAGCAGCTGC	CTGATGACCG	AGTGGGGCGA	GTGGGACGAG	1740
	TGCAGCGCCA	CCTGCGGCAT	GGGCATGAAG	AAGCGGCACC	GCATGATCAA	GATGAACCCC	1800
	GCAGATGGCT	CCATGTGCAA	AGCCGAGACA	TCACAGGCAG	AGAAGTGCA	GATGCCAGAG	1860
	TGCCACACCA	TCCCATGCTT	GCTGTCCCCA	TGGTCCGAGT	GGAGTGACTG	CAGCGTGACC	1920
40	TGCGGGAAGG	GCAATGCCAA	CCGACGCGG	ATGCTCAAGT	CTCTGGCAGA	ACTTGGAGAC	1980
	TGCAATGAGG	ATCTGGAGCA	GGTGAGGAAG	TGCATGCTCC	CTGAATGCCC	CATTGACTGT	2040
	GAGCTCACCG	AGTGGTCCCC	TGTGTGCGAA	TGTAACAAGT	CATGTGGGAA	AGGCCACGTG	2100
	ATTGCAACCC	GGATGTGCAA	AATGGAGCCT	CAGTTTGGAG	GTGCACCCCTG	CCAGAGACT	2160
	GTGCAGCGAA	AAAAGTGCCG	CATCCGAAAA	TGCCCTTGAA	ATCCATCCAT	CCAAAAGCTA	2220
45	CGCTGGAGGG	AGGCCCGAGA	GAGCCGCGCG	AGTGAGCAGC	TGAAGGAAGA	GTCTGAAGGG	2280
	GAGCAGTTCC	CAGGTTGTAG	GATGCGCCCA	TGGACGGCCT	GGTCAGAATG	CACCAACTG	2340
	TGCGGAGGCT	GAATTCAGGA	ACGTTACATG	ACTGTAAAGA	AGAGATTCAA	AAGCTCCAG	2400
	TTTACCAGCT	GCAAAGACAA	GAAGGAGATC	AGAGCATGCA	ATGTTCTATC	TTGTTAGCAA	2460
	GGGTACGAGT	TCCCCAGGGC	TGCACCTTAG	ATTCCAGAGT	CACCAATGGC	TGGATTATTT	2520
50	GCTTGTTTAA	GACAATTTAA	ATTGTGTACG	CTAGTTTTC	TTTTTGCACT	GTGGTTGCGC	2580
	CAGTAGTCTT	GTGGATGCCA	GAGACATCCT	TTCTGAATAC	TTCTTGATGG	GTACAGGCTG	2640
	AGTGGGGCGC	CCTCACCTTC	AGCCAGCCTC	TTCTGTCAGA	GGAGTAGTGT	CAGCCACCTT	2700
	GTAATAAGCT	GAACATGTCT	CCTCTGGAGC	TTCCACCTGG	CCAGGGAGGA	CGGAGACTTT	2760
	GCCTACTTCC	ACATGGGAGG	GCAACCATGT	CTGGAAGTGA	CTATGCGCTG	GTCCCAAGGT	2820
55	CGCGGAGGTA	GGAAACATTC	ACAGATGAAG	ACAGCAGATT	CCCCACATTC	TCACTTTTGG	2880
	CCTGTTCAAT	GAACCAATTG	TTTGCCCATC	TCTTCTTAGT	GGAACCTTTAG	GTCTCTTTTC	2940
	AAGTCTCCTC	AGTCATCAAT	AGTTCTCTGG	GAAGAACAGA	GCTGGTAGAC	TTGAAGAGGA	3000
	GCATTGATGT	TGGGTGGCTT	TTGTTCTTTC	ACTGAGAAAT	TCGGAAATACA	TTTGCTCTAC	3060
	CCCTGATATT	GGTTCCTGAT	GCCCCCCCAA	CAAAAATAAA	TAAATAAAT	ATGGCTGCTT	3120
60	TATTTAAATA	TAAGGTAGCT	AGTTTTTACA	CCTGAGATAA	ATAATAAGCT	TAGAGTGTAT	3180
	TTTTCCCTTG	CTTTTGGGGG	TTGAGAGGAG	TATGTACAAT	TCTTCTGGGA	AGCCAGCCTT	3240
	CTGAACCTTT	TGTTACTAAA	TCCTTATTGG	AACCAAGACA	AAGGAAGCAA	AATTGGTCTC	3300
	TTTAGAGACC	AATTGGCCTA	AATTTTAAAA	TCTTCTTACA	CACATCTAGA	CGTTCAAGTT	3360
	TGCAATCAG	TTTTTAGCAA	GAAAACATTT	TTGCTATACA	AACATTTTGC	TAAGTCTGCC	3420
65	CAAAGCCCCC	CCAATGCATT	CCTTCAACAA	AATACAATCT	CTGTACTTTA	AAGTTATTTT	3480
	AGTCATGAAA	TTTTTATATG	AGAGAGAAAA	AGTTACCGAG	ACAGAAAAACA	AATCTAAGGG	3540
	AAAGGAATAT	TATGGGATTA	AGCTGAGCAA	GCAATTCTGG	TGGAAAAGTCA	AACCTGTCTG	3600
	TGCTCCACAC	CAGGGCTGTG	GTCCCTCCAG	ACATGCATAG	GAATGGCCAC	AGGTTTACAC	3660
	TGCTTCCCA	GCAATATATA	GCACACCAGA	TTGAGGGAGA	CTGACCAACA	AGGATAGTGT	3720
70	TAAAAGGACA	TTTTCTCAGT	TGGGTCCATC	AGCAGTTTTT	CTTCTGCAAT	TATTGTGTGA	3780
	AAACTATTGT	TTCAATTCTT	CTTTTATAGG	CCTTATTACT	GCTTAATCCA	AATGTGTACC	3840
	ATTGGTGAGA	CACATACAAT	GCTCTGAATA	CACTACGAAT	TTGTATTAAA	CACATCAGAA	3900
	TATTTCCAAA	TACAACATAG	TATAGTCTTG	AATATGTACT	TTTAACACAA	GAGAGACTAT	3960
	TCAATAAAAA	CTCACTGGGT	CTTTCATGTC	TTTAAGCTAA	GTAAGTGTTC	AGAAGGTTCT	4020
75	TTTTTATATT	GTCCCTCCAC	TCCATCATTT	TCAATAAAAG	ATAGGGCTTT	TGCTCCCTTG	4080
	TTCTTGAGAG	GACCATTAAT	ACATCTCTGA	ACTACCTTTG	TATCCAACAT	GTTTAAATTC	4140
	CTTAATGAA	TGCTTTTCTC	CCAAAAAAG	CACAATATAA	AGAAACACAA	GATTTAATTA	4200
	TTTTTCTACT	TGGGGGGAAG	AAAGTCTCTA	TGTAGAAGCA	CCCACTTTTG	CAATGTTGTT	4260
	CTAAGCTATC	TATCTAAGCT	TCAGCCCATG	ATAAGTTTCC	TTAAGCTGGT	GATTCTTAAT	4320
80	CAAGGACAAG	CCACCCTAGT	GTCTCATGTT	TGTATTGGT	CCCAAGTTGG	TACATTTTAA	4380
	AATCTTGATT	TTGGAGACTT	AAAACAGGT	TAATGGCTAA	GAATGGGTAA	CATGACTCTT	4440
	GTGGGATTGT	TATTTTTTGT	TTGCAATGGG	GAATTTATAA	GAAGCATCAA	GTCTCTTTCT	4500
	TACCAAGCTG	TTGTTAGGTT	GTTTATAGTT	CTTTTGGCTA	ACAAATCATT	TTGGAAGTAA	4560
	AGATTTTCTA	CTACAAAAAT	G				

Seq ID NO: 510 Protein sequence
Protein Accession #: BAB18461.1

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5 1      11      21      31      41      51
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FSLRVEGDPD FYKPGTSYRV TLSAAPPSTF RGFTLIALRE NREGDKEDH AGTFQIIDEE    120
ETQFMSNCPV AVTESTPRRR TRIQVFWIAP PAGTGCVLK ASIVQKRIIY FQDEGSLTKK    180
LCEQDSTFDG VTDKPIILDCC ACGTAKYRLT FYGNWSEKTH PKDYPRRANH WSAIIGGSHS    240
KNYVLWEYGG YASEGVKQVA ELGSPVKMEE EIRQSSDEVL TVIKAKAQWP AWQPLNVRAA    300
PSAEFSVDRT RHLMSFLTMM GPSPDWNVGL SAEDLCTKEC GWVQKVVQDL IPWDAGTDSG    360
VTYESPNKPT IPQEKIRPLT SLDHPQSPFY DPEGGSITQV ARVVIERIAR KGEQCNIVPD    420
NVDDIVADLA PEEKDEDDTP ETCIYSNWSP WSACSSSTCD KGRMRQRML KAQLDLSVPC    480
PDTQDFQPCM GPGCSDEDDGS TCTISEWITW SPCSISCGMG MRSRERYVKQ FPDGDSVCTL    540
PTEETEKCTV NEECSPSSCL MTEWGEWDEC SATCGMGMKK RHRMIKMNP DGSMDKAETS    600
QAEKCMPEEC HTIPCLLSFW SEWSDCSVTC GKGMRTQRQM LKSLAELGDC NEDLEQVEKC    660
MLPECPIDCE LTEWSQWSEC NKSCGKGHVI RTRMIQMEPQ FGGAACPETV QRKKCRIRKC    720
LRNPSIQKLR WREARESRRS EQLKESEGE QFPGCRM RPW TAWSECTKLC GGGIQUERYMT    780
VKKRFKSSQF TSCDKKKEIR ACNVHPC

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Seq ID NO: 511 DNA sequence
Nucleic Acid Accession #: NM_003108.1
Coding sequence: 76..1401

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25 1      11      21      31      41      51
   |      |      |      |      |      |
GGGGTGGGAG GGGGAGGGGG ACCTCCGCAC GAGACCCAGC GGCCCGGGTT GGAGCGTCCA    60
GCCCTGCAAC GGATCATGGT GCAGCAGGCG GAGAGCTTGG AAGCGGAGAG CAACCTGCCC    120
CGGGAGGCGC TGGACACGGA GGAGGGCGAA TTCATGGCTT GCAGCCCGGT GGCCCTGGAC    180
GAGAGCGACC CAGACTGGTG CAAGACGCGC TCGGGGCACA TCAAGCGGCC GATGAACCGC    240
TTCATGGTAT GGTCCAAGAT CGAACGCGAG AAGATCATGG AGCAGTCTCC GGACATGCAC    300
AAGCCCGAGA TCTCCAAGAG GCTGGGCAAG CGCTGAAAA TGCTGAAGGA CAGCGAGAAG    360
ATCCCGTTCA TCCGGGAGGC GGAGCGGCTG CGGCTCAAGC ACATGGCCGA CTACCCCGAC    420
TACAAGTACC GGCCCGCGAA AAGGCCCAAA ATGGACCCCT CGGCCAAGCC CAGCGCCAGC    480
CAGAGCCGAG AGAAGAGCGC GGCCGCGGCG GCGCGGCGGA GCGCGGCGG AGGCGCGGGC    540
GGTGCCAAGA CCTCCAAGGG CTCCAGCAAG AAATGCGGCA AGCTCAAGGC CCCCGCGGCC    600
GCGGGCGCCA AGGCGGGGCG GGGCAAGGCG GCCCAGTCCG GGGACTACGG GGGCGCGGGC    660
GACGACTACG TGCTGGGCGC CCTGCGCGTG AGCGGCTCGG GCGGCGGCGG CGCGGGCAAG    720
ACGGTCAAGT GCGTGTTCCT GGATGAGGAC GACGACGACG ACGACGACGA CGACGAGCTG    780
CAGCTGCAGA TCAACAGGGA GCCGACGAG GAGGACGAGG AACCACCGCA CCAGCAGCTC    840
CTGCAGCCGC CGGGGACGCA GCCGTCGAG CTGCTGAGAC GCTACAACGT CGCCAAAGTG    900
CCCGCCAGCC CTACGCTGAG CAGCTCGGCG GAGTCCCCCG AGGGAGCGAG CCTCTACGAC    960
GAGGTGCGGG CCGGCGCGCC CTGCGGCGCC GGGGGCGGCA GCGGCCTCTA CTACAGCTTC    1020
AAGAACATCA CCAAGCAGCA CCCGCCGCGC CTGCGCGAGC CCGCGCTGTC GCCCGCGTCC    1080
TCGCGCTCGG TGTCACCTCT CTGCTCCAGC AGCAGCGGCA GCAGCAGCGG CAGCAGCGGC    1140
GAGGACGCGC ACGACCTGAT GTTCGACCTG AGCTTGAATT TCTCTCAAAG CGCGCACAGC    1200
GCCAGCGAGC AGCAGCTGGG GGGCGGCGCG GCGGCGGGA ACCTGTCCCT GTCGCTGGTG    1260
GATAAGGATT TGGATTCTGT CAGCGAGGGC AGCTTGGGCT CCCACTTCGA GTTCCCCGAC    1320
TACTGCAGCG CGGAGCTGAG CGAGATGATC GCGGGGGACT GGCTGGAGGC GAACTTCTCC    1380
GACCTGGTGT TCACATATTG AAAGGCGCCC GCTGCTCGCT CTTTCTCTCG GAGGGTGCAG    1440
AGCTGGGTTT CTGCGGAGGA AGTTGTAGTG GTGATGATGA TGATGATGAT AATGATGATG    1500
ATGATGGTGG TGTTGATGGT GCGGTGGGTA GGGTGGAGGG GAGAGAAGAA GATGCTGATG    1560
ATATTGATAA GATGTCGTGA CGCAAGAAAA TTGAAAAACA TGATGAAAAT TTTGGTGGAG    1620
TTAAAGTGAA ATGAGTAGTT TTTAAACATT TTTCTGTGTC TTTTCTGTCT CCCCCTCCCT    1680
TCCTTTATCG TGCTCTCAAG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCCAA    1740
AAAATGTGTT TTTGTAATTA CTATTTCTTT TTCTGAAAT TCGTGATTGC AACAAAGGCA    1800
GAGGGGGCGG CGCGGCGGAG GGGAGGTAGG ACCCGCTCCG GAAGGCGCTG TTTGAAGCTT    1860
GTCGCTCTTT GAAGTCTGGA AGACGCTCTG AGAGGACCCCT TTTGGCAGCA CAACTGTTAC    1920
TCTAGGAGAT TGGTGGAGAT ATTTTTTTTT CTTAAGAGAA CTTAAGAAGC TGGTGATTTT    1980
TTTTTAACAA AAAAAGGG

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Seq ID NO: 512 Protein sequence
Protein Accession #: NP_003099.1

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65 1      11      21      31      41      51
   |      |      |      |      |      |
MVQQAESLEA ESNLPREALD TEEGEFMACS PVALDESDPD WCKTASGHIK RPMNAFMVWS    60
KIERRKIMEQ SPDMDHNAEIS KRLGKRWKML KDSEKIPFIR EAERLRLKHM ADYPDYKYRP    120
RKKPKMDPSA KPSASQSPEK SAAGGGGSSA GGGAGGAKTS KGSSKKCGKL KAPAAAGAKA    180
GAGKAAQSGD YGGAGDDYVL GSLRVSSGGG GGAGKTVKCV FLDEDDDDDD DDDELQLQIK    240
QEPDEEDEEP FHQQLLPFG QQPSQLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVVRAG    300
ATSGAGGGSR LYYSFKNITK QHPPPLAQPA LSPASSRSVS TSSSSSSGSS SGSSGEDADD    360
LMFDLSLNFQ QSAHSASEQQ LGGGAAAGNL SLSLVDKDLD SFSEGSLSGSH FEFPDYCTPE    420
LSEMIAGDWL EANFSDLVFT Y

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Seq ID NO: 513 DNA sequence
Nucleic Acid Accession #: CAT Cluster

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80 1      11      21      31      41      51
   |      |      |      |      |      |
GGTCGACCTA AATCTGATAA CTGGCTTATT ATGTAATTTA TTGGTGTTAT TATAGTAGAG    60
ATTGGTAATC TACAGTAAGA TTTTCAGTTA GGATTTGAGA TTATGATAAT AACTAATAGA    120
ATATTTCTAA ATTGGAATTA GAAGATTGTT GTATGACAGA GAGTCAGGAC TTGCCATTGG    180

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GCAAACATCA AAGTCATTGT TTGGTGTGTA ATAGTACAAA ATCATCTTGC TTAACAGAGA 240
 AAGGATATCT GTTGCTCCCG AATGAAACAA TTTTCTTGAA ATAGAGGGCC CAGAATTGGT 300
 CTCTGACAAAT TAATAAGAC ATCAAAGATA GCAAAATGAT TTTATATCT TAGGGCCAAT 360
 5 ACTACCAATT TAATAATTAA AACAAGTTCT GGTGAGCTCT GAACTTGGCA GAATTGGTGG 420
 CAACATAGAC TTTGGATTCT CCAAAATCCC CACATAAAAC AAAGGGGATC AACTAGATAG 480
 AAAAACCAGA AACCTTTGGA AATATCTGTT TAAAAAATAA AAAAAGTCGA CGCGGGCC

Seq ID NO: 514 DNA sequence

Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 | | | | |
 15 GGAGCCACAG TGAAAGTCAA GAATGTGAGT GATTCACAT TTAATATCTA CATTTTGGCA 60
 GGGCAGTTAC TCTTTTGTAG TATAACATTG AGCTGATAGC ACATAGTGTA GACAAGTGAA 120
 TACAGGATTC TCTGGGTGTG ATTCCCAGAA GTCTGGAGGT CATTTGGATA TTTGTGGGCC 180
 CTTGGCTTCA CTCTGACTTG TGTGACACAT AAAAATTGTG ATGAAATGTC CTATAGATGT 240
 CCTGCAGGTC TTAAGAAGAAC CTTTCCAAAC TATGAAACAG CCCAGCAGCA CTGAGTTAGA 300
 20 GGTAATTTCT GAACCCCTGA AACTATAAAC TATTCTAACT GCACATAGAA TTGGCAAGTA 360
 GCATTCTATG TCTATGAACA GTATGTCTTT TCTATATAAC AGAGAAAATC TTTTAAAGCA 420
 AACTACTCAG TTTAAAACCT AATTCTTCTC ATAATCTCAG TACTTTTGAA TGAAGACATA 480
 TCAATGCAAC AGTACACTCT TATTGAGGCA TTTGAAAGAA AGAATTCGAG ATCTAGTTTG 540
 TATCAGATAT TATAAATTAG TATGGTTTAG TCTTTGTCTAT GAAATTTCTAC TTAATTTTGG 600
 25 GACTATAGGT TTAAGAATGT AAGCAGAAGT TCTGCACCAA TCAGAATAAG CTACATTATG 660
 CTTGAGTGAC AACTACTGTA ATGACAAAAT ATCAGTGGCT TAATACAATG GTTTTCTCT 720
 CATACTTGT CATAAAGAGT CAGCAAGGAC CCTGCTCATT ATGGTCCCTC AGGGACCCAG 780
 GGGTGTGGGA AGCTCCACCA TTTTAGATAG CTCCTTCAA AGTCAGCCAT CTTTGGCAGT 840
 CCATGTCCCC CAACAGGCTG GCAAAATTG GCTCTGGATG GCTTCAAGGA TTGAGCATCG 900
 30 GGCAGTTTAA ATGCTTTCAA CATGGAAGT GGACACCGGC CACTCCCACT CACATCCCTT 960
 GGGCCAGAAC TAGGTCACTG GGCCCGGACC TAACCTCGGA GGGTTGGGGA ATTGTAATTC 1020
 CTCATGTAC CCAAAGTGGG GAGAAGCCAG ATACTGAGAA ACATCAATAA TGGCTAACAG 1080
 AAATCCATTC TACCATTCCC TTTGCTTAA GTGAAAGAT GAGTACTTTC ATCAATTTGT 1140
 AAATCTACT TTTGAAGTAA ATCTGGTAG CTGTCATGGG GGCTGGATT CCAGAAGGCC 1200
 35 ATATGTAATT TGGGAATGAC ATTCACCTAA GCTCATAGAA TATCATTATT TGATGTAATA 1260
 TGCCCTCAT TGAATACAG GACCAAAATG CACTAACCA AAAACCCCCC TCCCCACGGG 1320
 GCCCGGGTCT CTTATTTCCC TCCATCCCTT TAAATGAGGC ATTCTATGAT TTGGAATGGA 1380
 AGCCCAAGTT TAGTCGTAAG AATTTTACTT AATTCAAGAA TTATTTCTAC TGAATATGTG 1440
 CCAGTTCTGA AAGGAATGCA AAGTCAAAAT TTGCATCTTC TTTGCTCAAG GGCCTTTAGA 1500
 40 TGTAACAAAC CAGAGCTGAT ACAAGGCTGA CAATGACATT ATGATTAAAT TATGTTAAAC 1560
 AACTTATTA ATTGTGAATC AAAAAAAAT TATGTTCTTT ATTTTATGGT TTTGCATAGT 1620
 CCTGACTCAC TGCCTACATA CCCCTCTTGT TCCTCAGTTC TTATCCCTGA TTTCTTACAG 1680
 GATGGCTTAA GACAGCTGTA GATGTTTTTA TTTAGCAAAA AAAAAAATAA AAAAGTCGAC 1740
 GCGCCGCGA ATTTAGTAG

Seq ID NO: 515 DNA sequence

Nucleic Acid Accession #: NM_012427

Coding sequence: 43..924

1 11 21 31 41 51
 | | | | |
 50 CTTGTGGTTC CTCTCTACTT GGGGAAATCA GGTGCAGCGG CCATGGCTAC AGCAAGACCC 60
 CCCTGGATGT GGGTGTCTCTG TGCTCTGATC ACAGCCTTGC TTCTGGGGGT CACAGAGCAT 120
 GTTCTCGCCA ACAATGATGT TTCCTGTGAC CACCCCTCTA ACACCGTGCC CTCTGGGAGC 180
 55 AACCAGGACC TGGGAGCTGG GGGCGGGGAA GACGCCCGGT CGGATGACAG CAGCAGCCGC 240
 ATCATCAATG GATCCGACTG CGATATGCAC ACCCAGCCGT GGCAGGCCGC GCTGTTGCTA 300
 AGGCCCAACC AGCTCTACTG CGGGGCGGTG TTGGTGCATC CACAGTGGCT GCTCACGGCC 360
 GCCCACTGCA GAAAGAAAGT TTTCAAGATC CGTCTCGGCC ACTACICCTT GTCACCAAGT 420
 TATGAATCTG GGCAGCAGAT GTTCCAGGGG GTCAAATCCA TCCCCCACC TGGCTACTCC 480
 60 CACCCTGGCC ACTCTAACGA CCTCATGCTC ATCAAATGTA ACAGAAGAAT TCGTCCCACT 540
 AAAGATGTCA GACCCATCAA CGTCTCCTCT CATTGTCCCT CTGCTGGGAC AAAAGTGCTT 600
 GTGTCTGGCT GGGGACAAAC CAAGAGCCCC CAAGTGCACT TCCTTAAGGT CCTCCAGTGC 660
 TTGAATATCA GCGTGCTAAG TCAGAAAAGG TGCGAGGATG CTTACCCGAG ACAGATAGAT 720
 GACACCATGT TCTGCGCCGG TGACAAAGCA GGTAGAGACT CCTGCCAGGG TGATTTCTGG 780
 65 GGGCCTGTGG TCTGCAATGG CTCCTGCAG GGAATCGTGT CCTGGGGAGA TTACCCTTGT 840
 GCCCGGCCCA ACAGACCGGG TGTCTACACG AACCTCTGCA AGTTCAACAA GTGGATCCAG 900
 GAAACCATCC AGGCCAACTC CTGAGTCATC CCAGGACTCA GCACACCGGC ATCCCCACCT 960
 GCTGCAGGGA CAGCCCTGAC ACTCCTTTCA GACCCTCATT CCTTCCAGGA GATGTTGAGA 1020
 ATGTTTATCT TCCAGCCCC TGACCCCATG TCTCCTGGAC TCAGGGTCTG CTTCCCCCAC 1080
 70 ATTGGGCTGA CCGTGTCTCT CTAGTTGAAC CCTGGGAACA ATTTCCAAAA CTGTCACGGG 1140
 CGGGGGTTC GTCTCAATCT CCCTGGGGCA CTTTCATCCT CAAGCTCAGG GCCCATCCCT 1200
 TCTCTGCAGC TCTGACCTAA ATTTAGTCCC AGAAATAAAC TGAGAAGTGG AAAAAAATAA

Seq ID NO: 516 Protein sequence

Protein Accession #: NP_036559

1 11 21 31 41 51
 | | | | |
 75 MATARPPPMW VLICALITALL LGVTEHVLN NDVSCDHPSN TVPSGSNQDL GAGAGEDARS 60
 DDSSSRING SDCHMHTQPW QAALLLRPNQ LYCGAVLVHP QWLLTAHCR KKVFRVRLGH 120
 80 YSLSPVYESG QMFPQGVKSI PHPGYSHPGH SNDLMLIKLN RRIRPTKDVR PINVSSHCP 180
 AGTKCLVSGV GTTKSPQVHF PKVLQCLNIS VLSQKRCEDA YPRQIDDTMF CAGDKAGRDS 240
 CQDGGGPPVV CNGSLQGLVS WGDYPCARP RPQVYTNLCK FTKWQETIQ ANS

Seq ID NO: 517 DNA sequence
Nucleic Acid Accession #: NM_001719
Coding sequence: 123..1418

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5      1      11      21      31      41      51
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      GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
      CTGCCACCTG GGGCCGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
10     CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCTGTGCG CTCTGGGCAC 180
      CCCTGTTTCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
      GCTTTCATCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
      CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
      CCATGTTTAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
      GCCAGGGCTT CTCCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
15     GCCTGCAAGA TAGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
      TGGACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
      TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
      ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
      AGCACTTGGG CAGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCCTCGG 780
20     AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC 840
      GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
      AGTTGGCGGG CTTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGTTGGCTT 960
      TCTTCAAGGC CACGAGGTTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA 1020
25     GCCAGAACCG CTCGAAGACG CCCAAGAAC ACCAAGCCCT GCGGATGGCC AACGTGGCAG 1080
      AGAACAGCAG CAGCGACGAG AGGCAGGCCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
      GAGACCTGGG CTGGCAGGAC TGGATCATCG CCGCTGAAGG CTACGCCGCC TACTACTGTG 1200
      AGGGGGAGTG TGCCCTCCCT CTGAATCCTT ACATGAACGC CACCAACCCAC GCCATCGTGC 1260
      AGACGCTGGT CCACTTCATC AACCCGAAAA CGGTGCCCAA GCCCTGCTGT GCGCCCAACG 1320
30     AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
      ACAGAAACAT GGTGTTCGGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCCT 1440
      TTGGGGCCAA GTTTTCTCG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
      CTGCCTTTTG TGAGACCTTC CCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
      AAACATGAGC AGCATATGGC TTTTGTATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
35     TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAACA ACAACGCATA AAGAAAAATG 1680
      CCGGGGCCAG GTCACTGGCT GGGAAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
      TTATGAGCGC TACCAAGCCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
      GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
      CAATAAACG AATGAATG

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Seq ID NO: 518 Protein sequence
Protein Accession #: NP_001710

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45     1      11      21      31      41      51
      |      |      |      |      |      |
      MHVRSRLAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRLRSQE RREMQREILS 60
      ILGLPHRPRP HLQGHNSAP MFMLDLNAM AVEEGGSPGG QGFSYPYKAV FSTQGPPLAS 120
      LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHRFRFDL SKIPEGEAVT AAEFRYKYD 180
      IRERFDNETF RISVYQLQE HLGRESLFL LDSRTLWASE EGWLVDITA TSNHWVNP 240
      HNLGLQLSVE TLDQGSINPK LAGLGRHGP QNKQPFMVA FKATEVHFRS IRSTGSKQRS 300
50     QNRSKTFKNG EALRMANVA NSSSDQRCAC KHELYVSFR DLGWQDWIIA PEGYAAYYCE 360
      GECAPPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
      RNMVVRACGC H

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Seq ID NO: 519 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 264..782

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60     1      11      21      31      41      51
      |      |      |      |      |      |
      CCCTGCTCCA GTCACACCCG GAAGCTGACT GGTCCACGCA CAGCTGAAGC ATGAGGAAAC 60
      TCATCGCGGG ACTAATTTTC CTTAAATTT AGACTTGCAC AGTAAGGACT TCAACTGACC 120
      TTCCTCAGAC TGAGAACTGT TTCCAGTATA TACATCAAGT CACTGAGATC TCCAGCACCC 180
      TGCCGGTGGC ACTACTGAGA GACGAGGTGC CAGGGTGGTT CCTGAAAGTG CCTGAGCCCC 240
65     AACTTATCAG CAGGAGCTC ATCATGCTGA CAGAAGTCAT GGAGGTCTGG CATGGCTTAG 300
      TGATCGCGGT GGTGTCCCTC TTCCTGCAGG CCTGCTTCTT CACCGCCATC AACTACCTGC 360
      TCAGCAGGCA CATGGCCAC AAGAGTGAAC AGATACTGAA AGCGGCCAGT CTCAGGTTTC 420
      CCAGGCCAG CCCTGGCCAC CATCATCCAC CTGTGTCAA AGAGATGAAG GAGACTCAGA 480
      CAGAGAGAGA CATCCCAATG TCTGATTCCC TTACAGGCA TGACAGCGAC ACACCCTCAG 540
70     ATAGCTTGA TAGCTCTGC AGTTCGCCTC CTGCCTGCCA GGCCACAGAG GATGTGGATT 600
      ACACACAAGT CGTCTTTTCT GACCTGGAG AACTAAAAA TGACTCCCCG CTGGACTATG 660
      AGAACAATAA GGAATATCAC GATTATGTCA ATGTCAATCC AGAAAGACAC AAGCCAGTT 720
      TCTGGTATT TGTCAACCTT GCTCTGTCTG AGCCAGCGGA ATATGATCAA GTGGCCATGT 780
      GAATTCCAAA TATTTTAAAT GGGGTCCAGT TCTCTATGGA TTCTTACATT TAATTTGTAG 840
75     GGAATGCCA TTTTCCCCC TTAACAAGG CATGGGGCTC ACAAGTCTAT GGAGACAGGC 900
      CAAAAGAAAT GTGGAGAAGA AAAGTGTATA ATACACAGAG GTCCTCAAGA CCCATGGACT 960
      CCTGTCTGT ACCCAAAAAA GCTGTTCGTT CCTCAAAAAA AAAACAAGG CTTGGCTGGG 1020
      AAAACAGGCC AATGCCCCG CAAGAAAGGT TGAGATCAGA TGTTAGGAAG AACTTTCAGG 1080
      TAAAGTATGA GAACTATGGA GTCCATCAGC AGAGATAGTA GTGAAGTCTC TCCCAGGGA 1140
80     AAATTTAAA AAGGTTGAA CAGCTGTTGT AGAGTTCTAT TTGGCAATCT CATGGTTAAA 1200
      TGACTTCCCT TTGAGCTCTT TAATTATTGG CAATAAACAA CTCTTTAAA AGTTTAAA 1260
      AAAATAGCAA CCACCACCA

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Seq ID NO: 520 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
 5 MLTEVMEVWH GLVIAVVSFL LQACFLTAIN YLLSRHMAHK SEQILKAASL QVPRPSPGHH 60
 HPPAVKEMKE QTQTERDIPMS DSLYRHSDST PSDSLDSSCS SPPACQATED VDYTQVVFSD 120
 PGELEKNDSP L DYENIKEITD YVNVNPERHK PSFWYFVNPA LSEPAEYDQV AM

Seq ID NO: 521 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 107..328

1 11 21 31 41 51
 15 CTGCTCTGTC TGAGCCAGCG GAATATGATC AAGTGGCCAT GTGAATTCCA AATATTTTAA 60
 ATGGGGTCCA GTTCTCTATG GATTCTTACA TTTAATTTGT AGGGAAATGC CATTTTTCCC 120
 CCTTAAACAA GGCATGGGCG TCACAAGTCT ATGGAGACAG GCCAAAAAGA ATGTGGAGAA 180
 GAAACTGAT AAATACACAG AGGTCTCTCA GACCCATGGA CTCTGGTCT GTACCCAAAA 240
 AAGCTGTTCT TCCCTCAAAA ACAAAAACAA GGCTTGGCTG GGAAACAGG CCAATGCCCC 300
 20 GGCAAGAAAG GTTGAGATCA GATGTTAGGA AGAACTTTCA GGTAAAGTAT GAGAACTATG 360
 GAGTCCATCA GCAGAGATAG TAGTGAAGTC TCTCCACAG GAAAATTTTA AAAAGGTTGA 420
 ATCAGCTGTT GTAGAGTTCT ATTTGGCAAT CTCATGGTTA AATGACTTCC CTTTGAGCTC 480
 TTTAATTATT GGCAATAAAC AACTTCTTTA AAAGTTTAA ATAAATAGC AACCACCACC 540
 A

Seq ID NO: 522 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51
 30 MPFFPLKQGM GLTSLWRQAK KNVEKTKDKY TEVLKTHGLL VCTQKSCSFL KNKNKAWLGK 60
 QANAPARKVE IRC

Seq ID NO: 523 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 211..1895

1 11 21 31 41 51
 40 GGATCTGAGG GGCGCCAGT CACTTCCTCC ACGTTCTCGT GCTGGGCGGG AGGAGCGGAT 60
 GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTTT TTGGGTCGGA 120
 GAGGAATTAT CTGATAAAAT TCCTGGGTTA ATATTTTAA AAACGGAGAG TTTTFAAAAA 180
 TGATTTTTTT CCCTCGAAAA TGACCTTTTT ATGCTTCGAA GCAGTTTGTC AACCAGCATA 240
 GTGCTTTTTT TTTTCTCTTC TTTTCTACG ATAAATGAAA GCATTCTCTC AAGAAAAAGG 300
 45 CACAGGTTCC TTGAACAGCT GGATTCTGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360
 CTGTGTCTGA AAGCGAAAGT ACAATGTGAA CTCACATCA CAGCTCACT CCAGGAGGGA 420
 GAAGGTAATT GTTTCCTGTA ATGGGATGGA CTCATTGTGT GGCCAGAGG AACAGTGGGG 480
 AAAATATCGG CTGTTCCATG CCCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540
 TTCCGACACT GTAACCCCAA TGGAAACATGG GATTTTATGC ACAGCTTAAA TAAACATGG 600
 50 GCCAATTATT CAGACTGCCT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660
 TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCCTTG 720
 GCTGTGGCTA TTCTCATCAT TGGTTACTTC AGACGATTGC ATTGCACTAG GAACTATATC 780
 CACATGCACT TATTTGTGTC TTTCTATGCT AGAGCTACAA GCATCTTTGT CAAAGACAGA 840
 GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900
 55 CAAAATTTCA TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT 960
 GTTGTGATGT TTATTTACTT CCTGGCTACA AATTATTATT GGATCCTGGT GGAAGGTCTC 1020
 TACCTGCATA ATCTCATCTT TGTGGCTTTC TTTTCGGACA CCAAAATACCT GTGGGGCTTC 1080
 ATCTTGATAG GCTGGGGGTT TCCAGCAGCA TTTGTTGCAG CATGGGCTGT GGCACGAGCA 1140
 ACTCTGGCTG ATGCGAGGTG CTGGGAACCT AGTGCTGGAG ACATCAAGTG GATTTATCAA 1200
 60 GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATTCTGT TTCTGAATAC GGTTAGAGTT 1260
 CTAGCTACCA AATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGAA GCAATACAGG 1320
 AAACCTGGCA AATCGACACT GGTCTGGTC CTAGTCTTTG GAGTGCATTA CATCGTGTTC 1380
 GTATGCCTGC CTCACCTCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440
 TTTCTCAACT CTTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500
 65 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCCGTGGA CTGGAAGAAG 1560
 ACACCGCCAT GTGGCAGCCG CAGATGCGGC TCAGTGCTCA CCACCGTGAC GCACAGCACC 1620
 AGCAGCCAGT CACAGGTGGC GGCAGCACA CGCATGCTGC TTATCTCTGG CAAAGCTGCC 1680
 AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740
 TCAGAGCAGG ACTGCTGCC ACACCTTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800
 70 CAGGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGAATCTAA CCCAGACACT 1860
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 524 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51
 75 MLRSSLSLSI VLFSSFSST INESISRRKR HRFLEQLDSD GTITIEBQIV LVLKAKVQCE 60
 LNIATQLQEG EGNCFEPWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW 120
 80 DFMHSLNKTW ANYSDCLRFL QPDISIGKQE FFERLYVMYT VGYSISFGSL AVAILIIGYF 180
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 KSQYIGCKIA VVMFIYFLAT NYWILVEGL YLHNLIFVAF FSDTKYLWGF ILIGWGFPAA 300
 FVAAWAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILPLNTRVR LATKIWTNA 360
 VGHDTRKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL FFNSFQGFVV 420
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Seq ID NO: 525 DNA sequence
Nucleic Acid Accession #: NM_005048
Coding sequence: 143..1795

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    MHLFVSFMLR ATSFVFKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240
65  VMFIYFLATN YYWILVEGLY LHNLIFFVAF SDTKYLWGF I LIGWGFPAF VAAWAVARAT 300
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    QAEVKMWSR WNLVDWKRT PPCGSRRCS VLTVTHTSTS SQSQVAASR MVLISGKAAK 480
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Seq ID NO: 527 DNA sequence
Nucleic Acid Accession #: XM_036683
Coding sequence: 38..3655

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    CAGCAAAAT ATAGAAGGAC GCTATCTCTC CCATACCTCT TCTGCGAGTC ACAAAGAGAG 240
    GTCAGCGAGG GACGTGTCTT CCAACCCTGA GCAGTTGTTC TTTAATATCA CGGCATTGG 300
80  AAAAGATTTT CATCTGCGAC TAAAGCCCAA CACTCAACTA GTAGCTCCTG GGGCTGTTGT 360
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5	ACAGATGGAG	GAAGAAAAAG	GAAGGATTCA	TGTTGTCTAC	AAGAGATCAG	CTGTAGAACA	660
	GGCTCCCATTA	GACATGTCCA	AAGACTTTCA	CTACAGAGAG	TCGGACCTGG	AAGGCCCTTGA	720
	TGATCTAGGT	ACTGTTTATG	GCAACATCCA	CCAGCAGCTG	AATGAAACAA	TGAGACGCCG	780
	CAGACACGCG	GGAGAAAACG	ATTACAATAT	CGAGGTACTG	CTGGGAGTGG	ATGACTCTGT	840
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10	GAATGAAATT	TACCATGATG	AGTCCCTCGG	AGTGCATATA	AATGTGGTCC	TGGTGCGCAT	960
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GACAAGCACA	TGGACTTTTT	TTATAATAGG	AGCAACACTG	ATACTGTCTGA	TGACTGGACA	120
GGAAACAAAG	TTGTGATGTT	TTTGTGTGTT	GGGACGTTTT	TCTGCCTGTT	TATTTTTTTT	180
TCTAATTCTC	TGGTCATCGC	GGCAGTGATC	AAAAACAGAA	AATTTCAITTT	CCCTTCTTAC	240
TACCTGTGG	CTAATTTAGC	TGCTGCCGAT	TTCTTCGCTG	GAATTGCCTA	TGTATTCTCTG	300
ATGTTTAAAC	CAGGCCCAGT	TTCAAAAAC	TTGACTGTCA	ACCGCTGGTT	TCTCCGTCAG	360
GGGCTTCTGG	ACAGTAGCTT	GACTGCTTCC	CTCACCACCT	TGCTGGTTAT	CGCGTGGAG	420
AGGCACATGT	CAATCATGAG	GATGCGGGTC	CATAGCAACC	TGACCAAAAA	GAGGGTGACA	480
CTGCTCATTT	TGCTTGTCTG	GGCCATCGCC	ATTTTTATGG	GGGCGGTCCC	CACACTGGGC	540
TGGAATTGCC	TCTGCAACAT	CTCTGCCCTG	TCTTCCCTGG	CCCCCATTTA	CAGCAGGAGT	600
TACCTTGTTT	TCTGGACAGT	GTCACACCTC	ATGGCCTTCC	TCATCATGGT	TGTGGTGATC	660
CTGCGGATCT	ACGTGTACGT	CAAGAGGAAA	ACCAACGTCT	TGTCTCCGCA	TACAAGTGGG	720
TCCATCAGCC	GCCGGAGGAC	ACCCATGAAG	CTAATGAAGA	CGGTGATGAC	TGTCTTAGGG	780
GCGTTTGTGG	TATGCTGGAC	CCCGGGCCTG	GTGGTTCTGC	TCCTCGACGG	CCTGAAGTGC	840
AGGCAGTGTG	GCGTGCAGCA	TGTGAAAAGG	TGGTTCCTGC	TGCTGGCGCT	GCTCAACTCC	900
GTGCTGAACC	CCATCATCTA	CTCTACAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
ATGATCTGCT	GCTTCTCTCA	GGAGAACCAC	GAGAGGCGTC	CCTCTCGCAT	CCCTCCACA	1020
GTCTCAGCA	GGAGTGACAC	AGGCAGCCAG	TACATAGAGG	ATAGTATTAG	CAAAGGTGCA	1080
GTCTGCAATA	AAAGCACTTC	CTAAACTCTG	GATGCCTCTC	GGCCACCCCA	GGTGATGACT	1140
GTCTTAGG						

Seq ID NO: 532 Protein sequence

Protein Accession #: NP_036284

25
30

1	11	21	31	41	51	
MNECHYDKHM	DDFYNRSNTD	TVDDWTGTLK	VIVLCVGTFF	CLFIFFSNLS	VIAAVIKNRK	60
FHFPPFYLLA	NLAAADFFAG	IAYVFLMFNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
LVIIVERHMS	IMRMRVHSLN	TKKRVTLLIL	LWVAIAIFMG	AVPTLGNWCL	CNISACSSLA	180
PIYSRSYLVF	WTVSNLMAFL	IMVVYLRIY	VYVKRKTINV	SPHTSGSISR	RRTPMKLMKT	240
VMTVLGAFVV	CWTPGLVVL	LDGLNCRQCG	VQHVKRWFLL	LALLNSVVP	IISYKDEDM	300
YGTMKMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK	STS	

Seq ID NO: 533 DNA sequence

Nucleic Acid Accession #: NM_002821

Coding sequence: 150..3362

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45
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55
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75
80

1	11	21	31	41	51	
AACTCCCGCC	TCGGGACGCC	TCGGGGTCGG	GCTCCGGCTG	CGGCTGCTGC	TGCGGCGCCC	60
GCGCTCGGT	GCGTCCGCCT	CCTGTGCCCG	CCGCGGAGCA	GTCTGCGGCC	CGCCGTGCGC	120
CCTCAGCTCC	TTTTCCTGAG	CCGCGCGCGA	TGGGAGCTGC	CGCGGGATCC	CCGGCCAGAC	180
CCGCGCGGTT	GCCTCTGCTC	AGCGTCCCTG	TGCTGCCGCT	GCTGGGCGGT	ACCCAGACAG	240
CCATTGTCTT	CATCAAGCAG	CCGTCTCTCC	AGGATGCACT	GCAAGGGCGC	CGGGCGCTGC	300
TTGCTGTGTA	GGTTGAGGCT	CCGGGCCCCG	TACATGTGTA	CTGGCTGCTC	GATGGGGCCC	360
CTGTCCAGGA	CACGGAGCGG	CGTTTCGCCC	AGGGCAGCAG	CCTGAGCTTT	GCAGCTGTGG	420
ACGGGCTGCA	GGACTCTGGC	ACCTTCCAGT	GTGTGGCTCG	GGATGATGTC	ACTGGAGAAG	480
AAGCCCGCAG	TGCCAAGCGC	TCCTTCAACA	TCAAATGGAT	TGAGGCAGGT	CCTGTGGTCC	540
TGAAGCATCC	AGCCTCGGAA	GCTGAGATCC	AGCCACAGAC	CCAGGTCACA	CTTCGTGTC	600
ACATTGATGG	GCACCCCTCG	CCCACTTACC	AATGGTTCG	AGATGGGACC	CCCTTTCTG	660
ATGGTCAGAG	CAACACACAC	GTCAAGCAGA	AGGAGCGGAA	CCTGACGCTC	CGGCCAGCTG	720
GTCTCAGACA	TAGTGGGCTG	TATTCCTGCT	GCGCCACAG	TGCTTTTGGC	CAGGCTTGCA	780
GCAGCCAGAA	CTTCACCTTG	AGCATTGCTG	ATGAAAGCTT	TGCCAGGGTG	GTGCTGGCAC	840
CCCAGGACGT	GGTAGTAGCG	AGGTATGAGG	AGGCCATGTT	CCATTGCCAG	TTCTCAGCCC	900
AGCCACCCCC	GAGCCTGCAG	TGGCTCTTTG	AGGATGAGAC	TCCCATCACT	AACCCGAGTC	960
GCCCCCACA	CCTCCGACAG	GCCACAGTGT	TTGCCAACGG	GTCTCTGCTG	CTGACCCAGG	1020
TCCGCGCCAG	CAATGCAGGG	ATCTACCGCT	GCATTGGCCA	GGGCGAGAGG	GGCCACCCA	1080
TCATCTGGA	AGCCACACTT	CACCTAGCAG	AGATTGAAGA	CATGCCGCTA	TTTGAGCCAC	1140
GGGTGTTTAC	AGCTTGGCAG	GAGGAGCGTG	TGACCTGCCT	TCCCCCAAG	GGTCTGCCAG	1200
AGCCACAGCT	GTGGTGGGAG	CACGCGGGAG	TCCGGCTGCC	CACCCATGGC	AGGGTCTACC	1260
AGAAGGGCCA	CGAGCTGGTG	TTGGCCAATA	TTGCTGAAAG	TGATGCTGGT	GTCTACACCT	1320
GCCACGCGGC	CAACCTGGCT	GGTCAGCGGA	GACAGGATGT	CAACATCACT	GTGGCCACTG	1380
TGCCCTCCTG	GCTGAAGAAG	CCCCAAGACA	GCCAGCTGGA	GGAGGGCAAA	CCCGGCTACT	1440
TGGATTGCCT	GACCCAGGCC	ACACCAAAAC	CTACAGTTGT	CTGGTACAGA	AACCAGATGC	1500
TCATCTCAGA	GGACTCACGG	TTCGAGGTCT	TCAAGATGG	GACCTTGCGC	ATCAACAGCG	1560
TGGAGGTGTA	TGATGGGACA	TGGTACCGTT	GTATGAGCAG	CACCCAGGCC	GGCAGCATCG	1620
AGGCGCAAGC	CCGTGTCCAA	GTGCTGGAAA	AGCTCAAGTT	CACACCACCA	CCCCAGCCAC	1680
AGCAGTGAT	GGAGTTTGAC	AAGGAGGCCA	CGGTGCCCTG	TTCAGCCACA	GGCCGAGAGA	1740
AGCCCACTAT	TAAGTGGGAA	CGGGCAGATG	GGAGCAGCCT	CCCAGAGTGG	GTGACAGACA	1800
ACGCTGGGAC	CCTGCATTTT	GCCCAGGTGA	CTCGAGATGA	CGCTGGCAAC	TACACTTGCA	1860
TTGCTCCAA	CGGGCCGAG	GGCCAGATTC	GTGCCCATGT	CCAGCTCACT	GTGGCAGTTT	1920
TTATCACCTT	CAAAAGTGGAA	CCAGAGCGTA	CGACTGTGTA	CCAGGGCCAC	ACAGCCCTAC	1980
TGCAGTGCAG	GGCCACGGGG	GACCCCAAGC	CGCTGATTCA	GTGGAAAGGC	AAGGACCGCA	2040
TCCTGGACCC	CACCAAGCTG	GGACCCAGGA	TGCACATCTT	CCAGAATGGC	TCCCTGGTGA	2100
TCCATGACGT	GGCCCTCGAG	GACTCAGGCC	GCTACACCTG	CATTGCAAGC	AACAGCTGCA	2160
ACATCAAGCA	CACGAGGCC	CCCTCTATG	TCGTGGACAA	GCCTGTGCCG	GAGGAGTCGG	2220
AGGGCCCTGG	CAGCCCTCCC	CCCTACAAGA	TGATCCAGAC	CATTGGGTTG	TCGGTGGGTG	2280
CCGCTGTGGC	CTACATCAAT	GCCGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
AAGCCAAGCG	GCTGCAGAA	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCCTCAAG	2400
GAGGGCCTTT	GCAGAACGGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
GCTTGGGCTC	CGGCCCGCGG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
TCCCACGGTC	TAGCCTGCAG	CCCATCACCA	CGTGGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCTGGTGA	CTTGTGAAGA	2640

GCCTGCAGAC GAAGSATGAG CAGCAGCAGC TGGACTTCCG GAGGGAGTTG GAGATGTTTG 2700
 GGAAGCTGAA CCACGCCAAC GTGGTGCGGC TCCTGGGGCT GTGCCGGGAG GCTGAGCCCC 2760
 ACTACATGGT GCTGGAAATAT GTGGATCTGG GAGACCTCAA GCAGTTCCTG AGGATTTCCA 2820
 AGAGCAAGGA TGAAAAATTG AAGTCACAGC CCCTCAGCAC CAAGCAGAAG GTGGCCCTAT 2880
 GCACCCAGGT AGCCTCGGGC ATGGAGCACC TGTCCAACAA CCGCTTTGTG CATAAGGACT 2940
 TGGCTGCGCG TAACCTGCCTG GTCAGTGCCC AGAGACAAGT GAAGGTGTCT GCCCTGGGCC 3000
 TCAGCAAGGA TGTGTACAAC AGTGAGTACT ACCACTTCCG CCAGGCCTGG GTGCCGCTGC 3060
 GCTGGATGTC CCCCAGAGCC ATCCTGGAGG GTGACTTCTC TACCAAGTCT GATGTCCTGG 3120
 CCTTCGGTGT GCTGATGTGG GAAGTGTTTA CACATGGAGA GATGCCCAT GGTGGGCAGG 3180
 CAGATGATGA AGTACTGGCA GATTTGCAGG CTGGGAAGGC TAGACTTCCT CAGCCCGAGG 3240
 GCTGCCCTTC CAAACTCTAT CGGCTGATGC AGCGCTGCTG GGCCCTCAGC CCCAAGGACC 3300
 GGCCCTCCTT CAGTGAGATT GCCAGCSCCC TGGGAGACAG CACCGTGGAC AGCAAGCCGT 3360
 GAGGAGGGAG CCGCTCAGG ATGGCTGGG CAGGGGAGGA CATCTCTAGA GGAAGCTCA 3420
 CAGCATGATG GGCAAGATCC CTGTCTCTCT GGGCCCTGAG GTGCCCTAGT GCAACAGGCA 3480
 TTGCTGAGGT CTGAGCAGGG CCTGGCCTTT CCTCCTCTC CTCACCCCTCA TCCTTTGGGA 3540
 GGCTGACTTG GACCCAACT GGGCGACTAG GGCTTTGAGC TGGGCAGTTT CCCCTGCCAC 3600
 CTCTTCTCT ATCAGGGACA GTGTGGGTGC CACAGGTAAC CCCAATTTCT GGCTTCAAC 3660
 TTCTCCCTT GACCCGGTCC AACTCTGCCA CTCATCTGCC AACTTTGCC GTGGGAGGCT 3720
 AGGCTTGGGA GTAGCTGGT TTGTGGGGAG TTCTTAATA TTCTCAAGT CTGGGCACAC 3780
 AGGTTAATG AGTCTTGTG CCACTGGTCC ACTTGGGGT CTAGACCAGG ATTATAGAGG 3840
 ACACAGCAAG TGAGTCTCT CCACTCTGGG CTTGTGCACA CTGACCAGA CCCACGTCTT 3900
 CCCCACCTT CTCTCTTTC CTCATCTTAA GTGCCCTGGA GATGAAGGAG TTTTCAGGAG 3960
 TTTTGGACAC TATATAAAC GCCCTTTTGT TATGACCAC GGGCGGCTT TATATGTAAT 4020
 TGCAGCGTGG GGTGGGTGG CATGGGAGT AGGGGTGGGC CCTGGAGATG AGGAGGGTGG 4080
 GCCATCCTTA CCCCACTT TTATTGTTGT CGTTTTTGT TGTGTTTGT TTTTGTGTTT 4140
 TGTGTTTGT TTTACACTG CTGCTCTCAA TAAATAAGCC TTTTTTA

Seq ID NO: 534 Protein sequence
 Protein Accession #: NP_002812

1 11 21 31 41 51
 MGAARGSPAR PRRLLPLLSVL LLPLLGGTQT AIVFIKQPSS QDALQRRAL LRCEVEAPGP 60
 VHVYLLDGA PVQDTERRF QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANASFN 120
 IKWIEAGPVV LKHPASEAEI PQQTQVTLRC HIDGHPRTY QWFRDGTPLS DQGSNHTVSS 180
 KERNLTLRPA GPEHSGLYSC CAHSAFGQAC SQONFTLSIA DESFARVLA PQDVVVARVE 240
 EAMFHCQFSA QPPPSLQWLF EDETPTNRS RPPHLRRATV FANGSLLLTQ VRPRNAGIYR 300
 CIGQQQRGPP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPFGKLP EPSVWWEHAG 360
 VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGOR RQDVNITVAT VPSWLKKPQD 420
 SQLEEGKPGY LDCLTQATPK PTVVWYRNQM LISEDSTRFEV FKNGTLRINS VEYVDGTWYR 480
 CMSSTPAGSI EAQARQVLE KLKFTPPPQP QQCMFEDKEA TVPCSATGRE KPTIKWERAD 540
 GSSLPEWVTD NAGTLHFARV TRDDAGNYTC IASNGPQGI RAHVQLTVAV FITFKVEPER 600
 RTVYQGHATL LQCEAQGDPK PLIQWKQKDR ILDPKLGPR MHIFQNGSLV IHDVAPEDSG 660
 RYTCIAGNSC NIKHTEAPLY VVDKPVPEES EGGSPPPYK MIQTIGLSVG AAVAYIIAIVL 720
 GLMFYCKKRC KAKRLQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780
 KRHSTDCKMH FPRSSLPFIT TLGKSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ 840
 LDFRRELEMF GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSQ 900
 PLSTKQKVAL CTQVALGMEH LSNRNFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960
 YHFRQAWVPL RWSPEAILE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEVILADLQ 1020
 AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDSKP

Seq ID NO: 535 DNA sequence
 Nucleic Acid Accession #: NM_013952
 Coding sequence: 161..1357

1 11 21 31 41 51
 TTCAGAAGGA GGAGAGACAC CGGGCCCAGG GCACCCCTCGC GGGCGGGCGG ACCCAAGCAG 60
 TGAGGGCCTG CAGCCGGCCG GCCAGGGCAG CGGCAGGCGC GGCCCGGACC TACGGGAGGA 120
 AGCCCCGAGC CCTCGGGCGG CTGCGAGCGA CTCGCCGCGC ATGCCTCACA ACTCCATCAG 180
 ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG AGGGGCCTTT GTGAATGGCA GACCTCTGCC 240
 GGAAGTGGTC CGCCAGCGCA TCGTAGACCT GGCCACCAG GGTGTAAGGC CCTGCACAT 300
 CTCTCGCCAG CTCGCGCTCA GCCATGGCTG CGTCAGCAAG ATCCTTGGCA GGTACTACGA 360
 GACTGGCAGC ATCCGGCCTG GAGTGATAGG GGGCTCCAAG CCCAAGGTGG CCACCCCAA 420
 GGTGGTGGAG AAGATTGGGG ACTACAAACG CCAGAACCTT ACCATGTTTG CCTGGGAGAT 480
 CCGAGACCGG CTCCTGGCTG AGGGCGTCTG TGACAATGAC ACTGTGCCCA GTGTCAGCTC 540
 CATTAATAGA ATCATCCGGA CCAAAGTGCA GCAACCATC AACCTCCCTA TGGACAGCTG 600
 CGTGGCCACC AAGTCCCTGA GTCCCGGACA CACGCTGATC CCCAGCTCAG CTGTAACCTC 660
 CCGGAGTCA CCCCAGTCGG ATTCCTGGG CTCACCTAC TCCATCAATG GGCTCCTGGG 720
 CATCGCTCAG CCTGGCAGCG ACAAGAGGAA AATGGATGAG AGTGATCAGG ATAGCTGCCG 780
 ACTAAGCATT GACTACAGA GCAGCAGCAG CGGACCCCGA AAGCACCTTC GCACGGATGC 840
 CTTAGCCAG CACCACTCG AGCCGCTCGA GTGCCCATTT GAGCGGCAGC ACTACCCAGA 900
 GGCCTATGCC TCCCCAGGC ACACCAAAGG CGAGCAGGGC CTCTACCCGC TGCCCTTGCT 960
 CAACAGCACC CTGGACGACG GGAAGGCCAC CCTGACCCCT TCCAACACGC CACTGGGGCG 1020
 CAACCTCTCG ACTCACAGA CCTACCCCGT GGTGGCAGCT CCGCCCTTTT GGATCTGCAG 1080
 CAAGTGGGCT CCGGGGTCCC GCCTTCAAT GCCTTTCCCC ATGCTGCCTC CGTGTACGGG 1140
 CAGTTACGGG GCAAGGCCCT CCTCTCAGGG CGAGAGATGG TGGGGCCAC GCTGCCCGGA 1200
 TACCACCCG ACATCCCCAC CAGCGGACAG GGCAGCTATG CCTCCTCTGC CATCGCAGGC 1260
 ATGGTGGCAG GAAGTGAATA CTCTGGCAAT GCCTATGGCC ACACCCCTTA CTCCTCTAC 1320
 AGCAGAGGCT GGGGCTTCCC CAACTCCAGC TTGCTGAGTT CCCCATATTA TTACAGTTCC 1380
 ACATCAAGGC CGAGTGACCC GCCCACCCT GCCACGGCCT TTGACCATCT GTAGTTGCCA 1440
 TGGGACAGT G

Seq ID NO: 536 Protein sequence
Protein Accession #: NP_039246

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5      1      11      21      31      41      51
|      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
10    SINGLLGIAQ PGSDKRKMDD SDQDSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF 240
ERQHYPEAYA SPSHTKGEQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAA 300
PPFWICSKSA PGSRPSMPFP MLPPCTGSSR ARPSSQGERW WGRPCPDTHP TSPPADRAAM 360
PPLPSQAWWQ EVNTLAMPMA TPPTPPTARP GASPTPAC

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Seq ID NO: 537 DNA sequence
Nucleic Acid Accession #: NM_003466.1
Coding sequence: 11..1363

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20    1      11      21      31      41      51
|      |      |      |      |      |
GAATTCGGCG ATGCTCTACA ACTCCATCAG ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG 60
AGGGGCCTTT GTGAATGGCA GACCTCTGCC GGAAGTGGTC CGCCAGCGCA TCGTAGACCT 120
GGCCACCACG GGTGTAAGGC CCTGCGACAT CTCTCGCCAG CTCGCGCTCA GCCATGGTTG 180
CGTCAGCAAG ATCCTTGGCA GGTACTACGA GACTGGCAGC ATCCGGCCTG GAGTGATAGG 240
GGGCTCCAAG CCAAGGTGG CCACCCCAA GGTGGTGGAG AAGATTGGGG ACTACAAACG 300
25    CCAGAACCTT ACCATGTTTG CCTGGGAGAT CCGAGACCGG CTCTGGCTG AGGGCGTCTG 360
TGACAATGAC ACTGTGCCCA GTGTGAGCTC CATTAAATAGA ATCATCCGGA CCAAAGTGCA 420
GCAACCATTG AACCTCCCTA TGGACAGCTG CGTGGCCACC AAGTCCCTGA GTCCCGGACA 480
CACGCTGATC CCCAGCTCAG CTGTAACCTC CCGGAGTCA CCCAGTCCG ATTCCCTGGG 540
CTCCACCTAC TCCATCAATG GGCTCCTGGG CATCGCTCAG CCTGGCAGCG ACAAGAGGAA 600
30    AATGGATGAC AGTGATCAGG ATAGCTGCCG ACTAAGCATT GACTCACAGA GCAGCAGCAG 660
CGGACCCCGA AAGCACTTTC GCACGGATGC CTTCAGCCAG CACCACCTCG AGCCGCTCGA 720
GTGCCCATTT GAGCGGCAGC ACTACCCAGA GGCTATGCC TCCCCCAGCC ACACCAAAGG 780
CGAGCAGGGC CTCTACCCGC TGCCCTTGGT CAACAGCACC CTGGACGACG GGAAGGCCAC 840
CCTGACCCCT TCCAACACGC CACTGGGGCG CAACCTCTCG ACTCACAGA CCTACCCCGT 900
35    GGTGGCAGAT CCTCACTCAC CCTTCGCCAT AAAGCAGGAA ACCCCCGAGG TGTCCAGTTC 960
TAGCTCCACC CTTCCTCTTT TATCTAGCTC CGCTTTTGTG GATCTGCAGC AAGTCGGCTC 1020
CGGGGTCCCG CCTTCAATG CCTTTCCCA TGCTGCCTCC GTGTACGGGC AGTTTACGGG 1080
CCAGGCCCTC CTCTCAGGGC GAGAGATGGT GGGGCCACG CTGCCCGGAT ACCACCCCA 1140
CATCCCCACC AGCGGACAGG GCAGCTATGC CTCTCTGCC ATCGCAGGCA TGGTGGCAGG 1200
40    AAGTGAATAC TCTGGCAATG CCTATGGCCA CACCCCTTAC TCCTCTACA GCGAGGCTG 1260
GCGCTTCCCC AACTCCAGCT TGCTGAGTTC CCCATATTAT TACAGTTCCA CATCAAGGCC 1320
GAGTGACACG CCCACACTG CCACGGCCTT TGACCATCTG TAGTTGAAGC TT

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Seq ID NO: 538 Protein sequence
Protein Accession #: NP_003457

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50    1      11      21      31      41      51
|      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRKMDD SDQDSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF 240
ERQHYPEAYA SPSHTKGEQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAD 300
55    PHSPPFAIKQE TPVSSSSST PSSLSSSAFL DLQQVGSVGP PFNAFPHAAS VYQQTGQAL 360
LSGREMVGPT LPGYPPHPT SQGGSYASSA IAGMVAGSEY SGNAYGHTPY SSYSEAWRFP 420
NSSLSSPFYY YSSTSRSAP PTTATAFDHL

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Seq ID NO: 539 DNA sequence
Nucleic Acid Accession #: NM_006799
Coding sequence: 19..963

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65    1      11      21      31      41      51
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GCCGCGGGAG AGGAGGCCAT GGGCGCGCGC GGGGCGCTGC TGCTGGCGCT GCTGCTGGCT 60
CGGGCTGGAC TCAGGAAGCC GGAGTCGAG GAGGCGGCGC CGTTATCAGG ACCATGCGGC 120
CGACGGGTCA TCACGTCGCG CATCGTGGGT GGAGAGGACG CCGAACTCGG GCGTTGGCCG 180
TGGCAGGGGA GCCTGCGCCT GTGGGATTCC CACGTATGCG GAGTGAGCCT GCTCAGCCAC 240
CGCTGGGCAC TCACGGCGGC GCACTGCTTT GAAACCTATA GTGACCTTAG TGATCCCTCC 300
GGGTGGATGG TCCAGTTTGG CCAGCTGACT TCCATGCCAT CCTTCTGGAG CCGCAGGCC 360
70    TACTACACCC GTTACTTCGT ATCGAATATC TATCTGAGCC CTCGCTACCT GGGGAATTCA 420
CCCTATGACA TTGCTTTGGT GAAGCTGTCT GCACCTGTCA CCTACACTAA ACACATCCAG 480
CCCATCTGTC TCCAGGCCTC CACATTTGAG TTTGAGAACC GGACAGACTG CTGGGTGACT 540
GGCTGGGGGT ACATCAAAGA GGATGAGGCA CTGCCATCTC CCCACACCTC CCAGGAAGTT 600
75    CAGGTGCGCA TCATAACAA CTCTATGTGC AACCACCTCT TCCTCAAGTA CAGTTTCCGC 660
AAGGACATCT TTGGAGACAT GGTTTGTGCT GGCAATGCCC AAGGCGGGAA GGATGCCTGC 720
TTCGGTGACT CAGGTGGACC CTGGCCCTGT AACAGAATG GACTGTGGTA TCAGATTGGA 780
GTCGTGAGCT GGGGAGTGGG CTGTGGTCCG CCCAATCGGC CCGGTGTCTA CACCAATATC 840
AGCCACCACT TTGAGTGTG CCAGAAGCTG ATGGCCCGA GTGGCATGTC CCAGCCAGAC 900
80    CCTCCTGGC CGTACTCTT TTTCCCTCTT CTCTGGGCTC TCCCACTCCT GGGGCCGCTC 960
TGAGCCTACC TGAGCCCATG CAGCTGGGG CCACTGCCAA GTCAGGCCTT GGTTCCTCTC 1020
TGCTTTGTTT GGTAAATAAC ACATTCAGT TGATGCCTTG CAGGGCATTC TTCAAA

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Seq ID NO: 540 Protein sequence
Protein Accession #: NP_006790

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1      11      21      31      41      51
|      |      |      |      |      |
5  MGARGALLLA LLLARAGLRK PESQEAAPLS GPCGRRVITS RIVGGEDAEL GRWPWQGSRLR 60
    LWDSHVCVGS LLSHRWALTA AHCFETYSDL SDPSGWMVQF GQLTSMPSFW SLQAYYTRYF 120
    VSNLYLSPRY LGNSPYDIAL VKLSAPVYTF KHIQPICLQA STFEFENRTD CWVTGWGYIK 180
    EDEALPSPHT LQEVQVAIIN NSMCNHLFLK YSFRKDIFGD MVCAGNAQGG KDACFGDSSG 240
    PLACNKNLW YQIGVVSQGW GCGRPNRPGV YTNISHHFEW IQKLMAQSGM SQPDPSPWPLL 300
    FFPLLWALPL LGPV

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Seq ID NO: 541 DNA sequence
Nucleic Acid Accession #: NM_014344
Coding sequence: 131..1444

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15 1      11      21      31      41      51
    |      |      |      |      |      |
    GCGGCCGCGA TGGGGCCGAA GCGCCCCGAAG CCCCAGGAGCC CACAAACTGC CGGGCCCGCC 60
    TCGCCGCGCG GACCCGGGTG CCTGGGCTCG GCTTGAAGCG GCGGCGGCGC ACCGGCACAG 120
    CCGCGGGAGC ATGGGCAGGA GGATGCGGGG CGCCGCGGCC ACCGCGGGGC TCTGGCTGCT 180
20  GCGCGTGGGC TCGTGCTGGG CGCTGTGGGG AGGGCTCTCT CCGCCGCGGA CCGAGCTGCC 240
    CGCTCCCGGG CCGCCCGAAG ACCGACTCCC ACGGCGCGCC GCCCGGAGCG GCGGCCCGGC 300
    GCCCGCGCCT CGCTTCCCTC TGCCCCCGCC CCTGGCGTGG GACGCCCGCG GCGGCTCCCT 360
    GAAAACCTTC CGGGCGCTGC TCACCCCTGGC GGCCGCGCGC GACGGCCCGC CCGGCAGTTC 420
    CCGGAGCGAG CCCAGGTGGC ACGTGTGAGC CAGGCAGCCC CGGCGGAGG AGAGCGCCGC 480
25  GGTGCACGGG GCGCTCTTCT GGAGCCGCGG CCTGGAGGAG CAGGTGCCCC CGGGCTTTTC 540
    GGAGGCCCAG GCGCGGCGGT GGCTGGAGGC GGCTGCGGCG GCCCGGATGG TGGCCCTGGA 600
    GCGCGGGGGT TGCGGGCGCA GCTCCAAACCG ACTGGCCCGT TTTGCCGACG GCACCCGCGC 660
    CTGCGTGGCG TACGGCATCA ACCCGAGACA GATTCAAGGC GAGGCCCTGT CTTACTATCT 720
    GGCGCGCCTG CTGGCCCTCC AGCGCCACGT GCCCGCGCTG GCACTGGCTC GGGTGGAGGC 780
30  TCGGGGCGCG CAGTGGGCGC AGGTGCAGGA GGAGCTGCGC GCTGCGCACT GGACCGAGGG 840
    CAGCGTGGTG AGCCTGCACAC GCTGGCTGCC CAACCTCACG GACGTGGTGG TGCCCGCGCC 900
    CTGGCGCTCG GAGGACGCGC GTCTGCGCCC CCTCCGGGAT GCCGGGGGTG AGCTGGCCAA 960
    CCTCAGCCAG GCGGAGCTGG TGGACCTAGT ACAATGGACC GACTTAATCC TTTTCGACTA 1020
35  CCTGACGGCC AACTTCGACC GGCTCGTAAG CAACCTCTTC AGCCTGCAGT GGGACCCGCG 1080
    CGTCATGCAG CGTGCCACCA GCAACCTGCA CCGCGGTCCG GCGCGGGCGC TGGTCTTTCT 1140
    GGACAATGAG GCGGGCTTGG TGCAACGGCTA CCGGCTAGCA GGCATGTGGG ACAAGTATAA 1200
    CGAGCCGCTG TTGCAGTCAG TGTGCGTGT CCGCGAGCGG ACCGCGCGGC GCGTCTGGA 1260
    GCTGCACCGC GGACAGGAGC CCGCGGCGCG GCTGCTGCGC CTCTACCGGC GCCACGAGCC 1320
40  TCGCTTCCCG GAGCTGGCGC CCCTTGCGTA CCCCACGCT CAGCTGCTAC AGCGCGCGCT 1380
    CGACTTCTCT GCCAAGCACA TTTTGCACGT TAAGGCCAAG TACGGCCGCG GGTCTGGGAC 1440
    TTAGTGTAC CCGGAGGAAA AGAGAGAGAT CTGGGGCTGG GGTATGGATG ATGGGGGGAA 1500
    GGGCGGTGCG CTCTGCCACT GTCAGGGACC AGCGGGCCAA CGCCACCCCG CAAAGGTGTC 1560
    TAAAAACTTC AGCTTTTCAC CCACCTGCCC CTTTCTTTCA ATCCACAGCT GTTTCCTTTT 1620
    AAAGTTCTGG GAGGACGAAC TCACCGAGGC GAGAAGTGTA ACATCTCTC CACCCAGCTT 1680
45  ATAAAGGAT TCTTTACTGT GCCAGCAGCG GGATTGGATC CGAAGAAACT GGCTACTGGG 1740
    GTTTGGCCCC CGAGTGGCCG TCCCTGTGGG AGATGCACCC CATTTCTGGG CCCCCTCAT 1800
    TCCCTTCCG AAAAAGGAAA ACTTGCGTTT GAGCCGTTGA GCTAATTCTG CAATTTCTTA 1860
    CCAAAACAGG CGCTGGTGGC CCGCGAGCAG GGCTGTGACA TTGGCTGGTG GAGCCCTTTC 1920
    CTGTGTTCTC CCGTGTTC CCGCGCGCGA TGGTGAGATC ACTGTTCCAA GCAGGGGGAC 1980
50  GGCTCGCGAT AGGACAAAGA GAGCAGGACC TCCAGACTCT GGGGAGCCCT GCAGACCTTG 2040
    ACAAATTGCC TGACTCATTC CTGACCTCTT GTCATTTTGG CCTGAAGGCT ACAAAATCAG 2100
    GGTCACTGT ATGCACTAAG TCAAAATATG AATTTCTTCC TCCCTCTCGC AACCGACCAA 2160
    AATTTTGACA ACGATGATGT TCACCAAGAG GAAAAAATA TCAGTTTAT GCACTTTAT 2220
    TTGTTTGTAT TTTCATTTTT TATTAAGAAA AAATTTTAT TTACAGAATT TACCTTCTCT 2280
55  GTATATATGT GCATAAAGTG TGGTGTAAT ATACTAAACA AACTTATATT TCAATAAAG 2340
    GGAGTTTAAA ATTTAAAAAA AAAAAA

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Seq ID NO: 542 Protein sequence
Protein Accession #: NP_055159

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60 1      11      21      31      41      51
    |      |      |      |      |      |
    MGRMRGAAA TAGLWLLALG SLLALWGGLL PPRTELPASR PPEDRLPRRP ARSGGPAPAP 60
    RFPLPPPLAW DARGGSLKTF RALLTLAAGA DGPPRQSRSE PRWHVSARQP RPEESAAPHG 120
    GVFWSRGLEE QVPPGFSEAQ AAAWLEAARG ARMVALERGG CGRSSNRLAR FADGTRACVR 180
    YGINPEIQIG EALSYYLARL LGLQRHVPPL ALARVEARGA QWAQVQELR AAHWTEGSVV 240
    SLTRWLPNLT DVVVPAPWRS EDGRLRPLRD AGGELANLSQ AELVDLVQWT DLILFDYLT 300
    NFDRLVSNLF SLQWDPRVMQ RATSNLHRGP GGALVFLDNE AGLVHGYYRVA GMWDKYNEPL 360
70  LQSVCLFRER TARRVLELHR GQDAAARLLR LYRRHEPRFP ELAALADPHA QLLQRRLDLF 420
    AKHILHCKAK YGRRSQT

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Seq ID NO: 543 DNA sequence
Nucleic Acid Accession #: XM_007652.4
Coding sequence: 1..1290

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75 1      11      21      31      41      51
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    CTGTTTTTAA ATGACACCAG CGCCTTTGAC TTCTCGGATG AGCGGGGGA CGAGGGGCTT 120
    TCTCGGTTCA ACAAACTTCG AGTTGTGGTG GCCGATGACG GTTCCGAAGC CCGGAAAGG 180
    CCTGTAAACG GGGCGCACCC GACCCTCCAG GCCGACGATG ATTCTTACT GGACCAAGAC 240
    TTACTTTTGA CCAACAGTCA GCTGAGTTTG AAGGTGGACT CCTGTGACAA CTGCAGCAAA 300
    CAGAGAGAGA TACTGAAGCA GAGAAAGGTG AAAGCCAGGT TGACCATTGC TGCCGTCTCT 360
80  TACTTGCTTT TCATGATTGG AGAACTGTGA GGTGGATACA TTGCAATAG CCTAGCAATC 420

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5 ATGACAGATG CACTTCATAT GTTAACTGAC CTAAGCGCCA TCATACTCAC CCTGCTTGCT 480
 TTGTGGCTAT CATCAAAATC ACCAACCAAA AGATTACCTT TTGGATTCA TCGCTTAGAG 540
 GTTTTGTGAG CTATGATAG TGTGCTGTTG GTGTATATAC TTATGGGATT CCTCTATAT 600
 GAAGCTGTGC AAAGAACTAT CCATATGAAC TATGAAATAA ATGGAGATAT AATGCTCATC 660
 ACCGAGCTG TTGAGTGTGC AGTTAATGTA ATAATGGGGT TTCTGTTGAA CCAGTCTGGT 720
 CACCGTCACT CCCATTCCCA CTCCTCGCCT TCAAAATCCC CTACCAGAGG TTCTGGGTGT 780
 GAACGTAACC ATGGGCAGGA TAGCCTGGCA GTGAGAGCTG CATTTGTACA TGCTTTGGGA 840
 GATTTGGTAC AGAGTGTGG TGTGCTAATA GCTGCATACA TCATACGATT CAAGCCAGAA 900
 10 TACAAGATTG CTGATCCCAT CTGTACATAC GTATTTTCAT TACTTGTGGC TTTTACAACA 960
 TTTTGAATCA TATGGGATAC AGTAGTTATA ATACTAGAAG GTGTGCCAAG CCATTTGAAT 1020
 GTAGACTATA TCAAAGAAGC CTTGATGAAA ATAGAAGATG TATATTCACT CGAAGATTTA 1080
 AATATCTGGT CTCTCACTTC AGGAAAATCT ACTGCCATAG TTCACATACA GCTAATTCCT 1140
 GGAAGTTTCA CTAAATGGGA GGAAGTACAG TCCAAAGCAA ACCATTTATT ATTGAACACA 1200
 15 TTTGGCATGT ATAGATGTAC TATTCACTT CAGAGTTACA GGCAAGAAGT GGACAGAACT 1260
 TGTGCAAAAT GTCAGAGTTC TAGTCCCTGA

Seq ID NO: 544 Protein sequence

Protein Accession #: XP_007652.1

20 1 11 21 31 41 51
 | | | | |
 MAGSGAWKRL KSMRLKDDAP LFLNDTSAPD FSDEAGDEGL SRFNKLRRVV ADDGSEAPER 60
 PVNGAHPFLQ ADDDSLDDQD LPLTNSQLSL KVDSCDNCSK QREILKQRKV KARLTIAAVL 120
 25 YLLFMIGELV GGYIANSLAI MTDALHMLTD LSAILITLLA LWLSKSPK RFTFGPHRLE 180
 VLSAMISVLL VYILMGFLLY EAVQRTIHMN YEINGDIMLI TAAVGVAVNV IMGFLNQSG 240
 HRHSHSHSLP SNSPTRGSGC ERNHGQDSL A VRAAFVHALG DLVQSVGVLI AAYIIRFKPE 300
 YKIADPICTY VPSLLVAFIT FRIIWDTVVI ILEGVPSHLN VDYIKEALMK IEDVYSVEDL 360
 NIWSLTSGKS TAIVHIQLIP GSSSKWEEVQ SKANHLLNT PGMRYCTIQL QSYRQEVDR 420
 CANCQSSSP

Seq ID NO: 545 DNA sequence

Nucleic Acid Accession #: AB037765.1

Coding sequence: 1..2478

35 1 11 21 31 41 51
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 ATGTTTTCCG GCTTCAATGT CTTTAGAGTT GGGATCTCTT TTGTCAATAA GTGCATTTTT 60
 TACATGCCAA CAGTAAACTC TTTACCAGAA CTGAGTCTCT AGAAATATTT TAGTACATGT 120
 40 CAACAGAGAA AAGCCTCTTT AGCCTATTTT TGTCAAGCTG ATTCCCCAAG AACATCTGTA 180
 TTTCTTGAAG AACTGAATGA GGCTGTAGA CCTCTGCAGG ACTATGGAAT TTCAGTTGCC 240
 AAGGTTAATT GTGTCAAAGA AGAAATATCA AGATACTGTG GAAAAGAAAA GGATTGTATG 300
 AAAGCATATT TATTCAGGGG CAACATATTG CTCAGAGAAAT TCCCTACTGA CACCTTGT 360
 GATGTGAATG CCATTTGCGC CCATGTCTCT TTTGCTCTCT TTTTATAGTA AGTGAATAT 420
 45 ATTACCAACC TGAAGACCT TCAGAACATA GAAAATGCTC TGAAAGGAAA AGCAATATT 480
 ATATTCTCAT ATGTAAGAGC CATTGGAATA CCAGAGCACA GAGCAGTCAT GGAAGCCGCT 540
 TTTGTGTATG GGACTACATA CCAATTGTTC TTAACCCAGG AAATGCCCC TTTGGAAAGT 600
 ATTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT TTCAATGTAA ACTAGTCTTG 660
 GACTTGACCC AGCAATGTAG AAGAACAATA ATGGAACAGC CATTGACTAC ACTGAACATT 720
 50 CACCTGTTTA TTAAGACAAT GAAAGCACCT CTGTTGACTG AAGTTGCTGA AGATCCTCAA 780
 CAAGTTTCAA TGTCCATCT CCAACTGGGC TTACTACTGG TTTTATTGT TAGCCAACAG 840
 GCTACTTATG AAGCTGATAG AAGAACTGCA GAATGGGTTG CTGGGCTCT TCTGGGAAAA 900
 GCAGGAGTTC TACTCTGTT AAGGGACTCT TTGGAAGTGA ACATTCTCA AGATGCTAAT 960
 GTGGTCTTCA AAAGAGCAGA AGAGGGAGTT CCAGTGGAAAT TTTTGTATT ACATGATGTT 1020
 55 GATTTAATAA TATCTCATGT GGAAAATAAT ATGCACATTG AGGAAATACA AGAAGATGAA 1080
 GACAAATGACA TGGAAAGTCC AGATATAGAT GTTCAGGATG ATGAAGTGGC AGAAACTGTT 1140
 TTCAGAGATA GGAAGAGAAA ATTACCTTTG GAACCTACAG TGAACCTAAC AGAAGAAACA 1200
 TTTAATGCAA CAGTGATGGC TTCTGACAGC ATAGTACTCT TCTATGCTGG TTGGCAAGCA 1260
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 60 ACTATGCTTC TTACTAGAAT AACTGTGCA GATTGGTCTG ATGTATGTAC TAAGCAAAAT 1380
 GTTACTGAAT TTCTATCAT AAAGATGTAC AAGAAAGGCG AGAACCAGT ATCTTATGCT 1440
 GGAATGTTAG GAACCGAAGA TCTCCTAAAA TTTATCCAGC TCAACAGGAT TTCATATCCA 1500
 GTGAATATAA CATCGATCCA AGAAGCAGAA GAATATTTAA GTGGGAATT ATATAAAGAC 1560
 CTCATCTTGT ATTCTAGTGT GTCAGTATTG GGACTATTTA GTCCAACCAT GAAAACAGCA 1620
 65 AAAGAAGATT TTAGTGAAGC AGGAACTAC CTAAAAGGAT ATGTTATCAC TGGAAATTTAT 1680
 TCTGAAGAAG ATGTTTTGCT ACTGTCAACC AAATATGCTG CAAGTCTTCC AGCCTGCTG 1740
 CTTGCCAGAC ACACAGAAGG CAAATAGAG AGCATCCAC TAGCTAGCAC ACATGCACAA 1800
 GACATAGTTC AAATAATAAC AGATGCACTA CTGGAATGT TTCCGGAAAT CACTGTGGAA 1860
 70 AATCTTCCCA GTTATTTTCA ACTTCAGAAA CCATTATTGA TTTTGTTCAG TGATGGCACT 1920
 GTAAATCCTC AGTATAAAAA AGCAATATTG AACTGGTAA AGCAGAAATA CTTGGATTCA 1980
 TTTACTCCAT CCTGGTTTAA TCTAAAGAAT ACTCCAGTGG GGAGAGGAAT CTTGAGGGCA 2040
 TATTTTGCAT CTCTGCCCTCC CCTTCCCTCT CTGTTTGGG TGAATCTGCA TTCAGGTGGC 2100
 CAAGTATTGT CATTTCTTTC AGACCAGGCT ATAATTGAAG AAAACCTTGT ATTGTGGCTG 2160
 75 AAGAAATTAG AAGCAGGACT AGAAAATCAT ATCACAATTT TACCTGCTCA AGAATGGAAA 2220
 CCTCTCTTTC CAGCTTATGA TTTTCTAAGT ATGATAGATG CCGCAACATC TCAACGTGGC 2280
 ACTAGGAAAG TTCCCAAGTG TATGAAAGAA ACAGATGTGC AGGAGAATGA TAAGGAACAA 2340
 CATGAAGATA AATCGGCAGT CAGAAAAGAA CCGATTGAAA CTCTGAGAAT AAAGCATTTG 2400
 80 AATAGAAGTA ATTGGTTTAA AGAAGCAGAA AAATCATTTA GACGTGATAA AGAGTTAGGA 2460
 TGCTCAAAAG TGAACATA

Seq ID NO: 546 Protein sequence

Protein Accession #: BAA92582.1

1 11 21 31 41 51
 | | | | |

MFSGFNVFRV GISFVIMCIF YMPTVNSLPE LSPQKYFSTL QPGKASLAYF CQADSPTS SV 60
 FLEELNEAVR PLQDYGISVA KVNVCKEEIS RYCGKEKDLN KAYLFKGNIL LREFPTDTLF 120
 DVNAIVAHVL FALLFSEVYK ITNLEDLQNI ENALGKGANI IFSYVRAIGI PEHRAVMEAA 180
 FVYGTYYQFV LTTEIALLES IGSEDVEYAH LYFFHCKLVL DLTQQCRRTL MEQPLTTLNI 240
 HLFIKTMKAP LLEVAEDBPQ QVSTVHLQLG LPLVFIVSQQ ATYEADRRTA EWWAVRLLGK 300
 AGVLLLLRDS LEVNIPQDAN VVFKRAEEGV PVEFLVLHDV DLIISHVENN MHIEEIQEDE 360
 DNDMEGPDID VQDDEVAETV FRDRKRKLPL ELTVELTEET FNATVMASDS IVLFYAGWQA 420
 VSMAPLQSYI DVAVLKLGTS TMLLRINCA DWSDVCTKQN VTEFPIIKMY KKGPNVPSYA 480
 GMLGTEDLLK FIQLNRISYP VNITSIQEAE EYLSGELYKD LILYSSVSVL GLFSPITMKA 540
 KEDFSEAGNY LKGYVITGIY SEEDVLLST KYAASLPALL LARHTEGKIE SIPLASTHAQ 600
 DIVQITDAL LEMFPEITVE NLPSYFRLQK PLLILFSDGT VNPQYKAIL TLVKQKYLDS 660
 FTFCWNLKLN TPVGRGILRA YFDPLPLPL LVLVNLHSGG QVFAFPSDQA IIEENLVLWL 720
 KKLEAGLENH TILPAQEWK PPLPAYDFLS MIDAATSQRG TRKVPKCMKE TDVQENDKEQ 780
 HEDKSAVRKE PIETLRIKHV NRSNWFKEAE KSFRDKELG CSKVN

Seq ID NO: 547 DNA sequence
 Nucleic Acid Accession #: NM_033102.1
 Coding sequence: 1..1662

1 11 21 31 41 51
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 ATGGTCCAGA GGCTGTGGGT GAGCCGCCTG CTGCGGCACC GGAAAGCCCA GCTCTTGCTG 60
 GTCAACCTGC TAACCTTTGG CCTGGAGGTG TGTTTGGCCG CAGGCATCAC CTATGTGCCG 120
 CCTCTGCTGC TGGAGTGGG GGTAGAGGAG AAGTTTATGA CCATGTGTCT GGGCATTTGGT 180
 CCAGTGCTGG GCCTGGTCTG TGTCCCGCTC CTAGGCTCAG CCAGTGACCA CTGGCGTGA 240
 CGCTATGGCC GCCGCCGGCC CTTTATCTGG GCACTGTCTT TGGGCATCCT GCTGAGCCTC 300
 TTTCTCATCC CAAGGGCCGG CTGGCTAGCA GGGCTGCTGT GCCCGGATCC CAGGCCCTTC 360
 GAGCTGGCAC TGCTCATCCT GGGCGTGGG CTGCTGGACT TCTGTGCCA GGTGTGCTTC 420
 ACTCCACTGG AGGCCCTGCT CTCTGACCTC TTCCGGGACC CGGACCACTG TCGCCAGGCC 480
 TACTCTGTCT ATGCCCTCAT GATCAGTCTT GGGGGCTGCC TGGGTACCT CTGCTCTGCC 540
 ATTGACTGGG ACACCTGGG CCTGGCCCCC TACCTGGGCA CCCAGGAGGA GTGCCCTCTT 600
 GGCCTGCTCA CCTCATCTT CTTCACCTGC GTAGCAGCCA CACTGTGGT GGTGAGGAG 660
 GCAGCGCTGG GCCCCACCGA GCCAGCAGAA GGGCTGTGG CCCCTCTCTT GTCGCCCCAC 720
 TGCTGTCCAT GCCGGGCGCG CTTGGCTTTC CGGAACCTGG GCGCCCTGCT TCCCGGCTG 780
 CACGAGCTGT GCTGCCGATC GCCCGCAGC CTGCGCGGGC TCTTCTGTGG TGAGCTGTGC 840
 AGCTGGATGG CACTCATGAC CTTACGCTG TTTTACACGG ATTTCTGTGG CGAGGGGCTG 900
 TACCAGGGCG TGCCAGAGC TGAGCCGGG ACCGAGGCC GAGACACTA TGATGAAGG 960
 GTTCGGATGG GCAGCTGGG GCTGTCTCTG CAGTGCAGCA TCTCCCTGGT CTTCTCTCTG 1020
 GTCATGGACC GGCTGTGTGA GCGATTGGG ACTCGAGCAG TCTATTGGC CAGTGTGGCA 1080
 GCTTTCCCTG TGCTGCCGG TGCCACATGC CTGTCACACA GTGTGCCCT GGTGACAGCT 1140
 TCAGCCGCC TCACCGGGT CACCTTCTCA GCCCTGCAGA TCCTGCCCTA CACACTGGCC 1200
 TCCTCTTACC ACCGGGAGAA GCAGGTGTTT CTGCCCAAT ACCGAGGGA CACTGGAGGT 1260
 GCTAGCAGT AGGACAGCT GATGACAGC TTCTTGCAG GCCTTAAGCC TGGAGCTCCC 1320
 TTTCCCTAATG GACACGTGGG TGCTGGAGG AGTGGCTGCT TCCACCTCC ACCCGGCTC 1380
 TGCGGGGCT CTGCTGTGA TGCTCCGTA CGTGTGGTGG TGGGTGAGCC CACCGAGGCC 1440
 AGGGTGGTTC CGGGCCGGG CATCTGCTG GACCTCGCCA TCCTGGATAG TGCTTCTCTG 1500
 CTGTCCAGG TGCGCCATC CTTGTTATG GGCTCCATTG TCCAGCTCAG CCAGTCTGTC 1560
 ACTGCCTATA TGGTGTCTGC CGCAGGCTG GGTCTGGTGC CCATTACTT TGCTACACAG 1620
 GTAGTATTG ACAAGAGCGA CTTGGCCAAA TACTCAGCGT GA

Seq ID NO: 548 Protein sequence
 Protein Accession #: NP_149093.1

1 11 21 31 41 51
 | | | | |
 MVQRLWVSRL LRHRKAQLLL VNLTFGLEV CLAAGITYVP PLLLEVGVVEE KFMTMVLGIG 60
 PVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILSL FLIPRAGWLA GLLCPDRPL 120
 ELALLILGVG LLDGCGQVCF TPLEALLSDL FRDPDHCRQA YSVYAFMISL GGCLGYLLPA 180
 IDWDSALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH 240
 CCPCRARLAF RNLGALLPLR HQLCCRMPT LRLFLVAELC SWMALMTFTL FYTDFVGEGL 300
 YQGVPRAEFG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRF TRAVYLASVA 360
 AFPVAAGATC LSHSVAVVTA SAALTGTFIS ALQILPYTLA SLYHREKQVF LPKYRGDTGG 420
 ASSEDSLMTS FLPGPKPGAP FPNHVGAGG SGLLPPPPAL CGASACDVSV RVVVGEPTEA 480
 RVVPGRGICL DLAILDSAF LSQLVAPSLFM GSIVQLSQSV TAYMVSAGL GLVAIYFATQ 540
 VVFDKSLAK YSA

Seq ID NO: 549 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1389

1 11 21 31 41 51
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 ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CCGCCGAGGA GAGATTAGA TGACAGAGAA 60
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 GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGT 180
 GGGTTTCTCT TGGGAATATT GCTTTTATC TGGGTTTCAT ATGTACAGGA CTTTCCCTT 240
 GTTTTATGTA TAAAGGAGG GGCCCTCTCT GGAACAGATA CCTACCAGTC TTTGGTCAAT 300
 AAAACTTTGC GCTTCCAGG GTATCTGCTC CTCTCTGTTT TACAGTTTGT GTATCCTTTT 360
 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAGT TTTTCAAGA 420
 ATCCAGAGG TTGATCTGTA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC 480
 ACAGTTACCT TTAATCTGCC TTTATCTTGG TACCGAAATA TAGCAAGCT TGGAAAGGTC 540
 TCCCTCATCT CTACAGGTTT AACAACTCTG ATTCTGGAA TTGTAATGGC AAGGGCAATT 600
 TCACTGGGTC CACGATATCC AAAACAGAA GACGCTTGGG TATTGTGAAA GCCCAATGCC 660
 ATTCAGCGCG TCGGGTTTAT GTCTTTTGCA TTTATTTGCC ACCATACTC CTTCTTAGTT 720

TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
 GTGATTCTCG TATTTATCTG TATATCTTT GCTACATGTG GATACTTGAC ATTTACTGGC 840
 TTCACCCAAG GGGACTTAT TGAATAATTAC TGCAGAAATG ATGACCTGGT AACATTGGGA 900
 AGATTTTGGT ATGGGTGTAC TGTCAATTTG ACATACCCCTA TGGAAATGCTT TGTGACAAGA 960
 GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTTCCA CATTGTTGTA 1020
 ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATTG TGATTGATTG CCTCGGGATA 1080
 GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCCTCA TTTTATCAT TCCATCAGCC 1140
 TGTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200
 ATGCTTCCCA TCGTGCTGT GGTGATGGTT TTTGGATTCT TCATGGCTAT TACAAATACT 1260
 CAAGACTGCA CCGATGGGCA GGAAATGTTT TACTGCTTTC CTGACAATTT CTCTCTACA 1320
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTAAA TATTAGTATC 1380
 TTTCAATGA

Seq ID NO: 550 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 MG YQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60
 GFPLGILLLF WVS YVTD FSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPF 120
 IAMISYNIIA GDTLSKVFOR IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIKALGKV 180
 SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKPNA IQAVGVMSFA FICHNSFLV 240
 YSSLEBPTVA KWSRLIHMSI VISVFICIFF ATCGYLTFTG FTQGDLFENY CRNDLVTTFG 300
 RFCYGVTVIL TYPMCEVTR EVIANVFFGG NLSGVFHIVV TVMVIIVATL VSLIDCLGI 360
 VLELNGVLCA TPLIFIPSA CYLKLSEPR THSDKIMSCV MLPIGAVVMV FGFVMAITNT 420
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Seq ID NO: 551 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1284

1 11 21 31 41 51
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 TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180
 TTGGTCAATA AAACCTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTCTC TCAGTTTGTG 240
 TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300
 TTTCAAAGAA TCCCAGGAGT TGATCCTGAA AACGTGTTTA TTGGTCGCCA CTTTATTATT 360
 GGACTTTCCA CAGTTACTCT TACTCTGCCT TTATCCTTGT ACCGAAATAT AGCAAAGCTT 420
 GGAAAGGTCT CCTCATCTC TACAGGTTA ACAACTCTGA TTCTTGAAT TGTAAATGGCA 480
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG 540
 CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTAATTTGCCA CCATAACTCC 600
 TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660
 ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATTCTTGT CTACATGTGG ATACTTGACA 720
 TTTACTGGCT TCACCCAAGG GGACTTATTT GAAATTACT GCAGAAATGA TGACCTGGTA 780
 ACATTTGGAA GATTTTGTTA TGGTGTCACT GTCATTTTGA CATACCTAT GGAATGCTTT 840
 GTGACAAGAG AGGTAATGTC CAATGTGTTT TTTGGTGGGA ATCTTTTATC GGTTTTCCAC 900
 ATTGTGTAA CAGTGTAGGT CATCACTGTA GCCACGCTTG TGTATTGCT GATTGATTGC 960
 CTCGGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCTTCAT TTTTATCATT 1020
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080
 TCTGTGTGTA TGCTTCCCAT TGGTGTCTGT GTGATGGTTT TTGGATTCTG CATGGCTATT 1140
 ACAATACTC AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTCC TGACAATTTT 1200
 TCTCTACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
 ATTAGTATCT TTCAACTCGA GTAA

Seq ID NO: 552 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 LVNKTGFFPG YLLSVLQFL YPFIAMISYN IAGDTLSKV QRIPGVDP E NVFGRHFII 120
 GLSTVFTFLP LSLYRNIAKL GKVS LISTGL TTLILGIVMA RAISLGPHIP KTEDAWVFAK 180
 PNAIQAVGV M SFAFICHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFI IFFATCGYLT 240
 FTGFTQGLD ENYCRNDLV TFRFCYGV T VILTYPMECF VTREIVANVF FGGNLSVVFH 300
 IVVTVMVITV ATLVSLLIDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360
 SCVMLPIGAV VMVFGFVMAI TQTQDCTHQ EMFYCFPDNF SLTNTSESHV QTTQLSTLN 420
 ISIFQLE

Seq ID NO: 553 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1203

1 11 21 31 41 51
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 AAAGGAGGGG CCTCTCTG AAGCAGATACC TACCACTCTT TGGTCAATAA AACTTTCGGC 120
 TTTCCAGGGT ATCTGCTCCT CTCTGTCTCT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180
 AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TTCAAAGAAT CCCAGGAGTT 240
 GATCCTGAAA ACGTGTTTAT TGGTCGCCAC TTCAATTATT GACTTTCCAC AGTTACCTTT 300
 ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGCTCT CCTCATCTCT 360
 ACAGGTTTAA CAACTCTGAT TCTTGAATT GTAATGGCAA GGGCRATTTT ACTGGGTCCA 420
 CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAGC CCAATGCCAT TCAAGCGGTC 480

GGGGTTATGT CTTTTCGATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCCTCTA 540
 GAAGAACCAC CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCCATCGT GATTTCCTGTA 600
 TTTATCTGTA TATTCCTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660
 GACTTATTAG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTGGAAG ATTTTGTAT 720
 GGTGTCACTG TCATTTTGAC ATACCCATATG GAATGCTTTG TGACAAGAGA GGTAATTGCC 780
 AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTTCCACA TTGTGTAAAC AGTGATGGTC 840
 ATCACTGTAG CCACGCTTGT GTCATTGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC 900
 AATGGTGTGC TCTGTGCAAC TCCCTCATTT TTTATCATTC CATCAGCCTG TTATCTGAAA 960
 CTGTCTGAAG AACCAAGGAC ACATCCGAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020
 GGTGCTGTGG TGATGGTTTT TGGATTGCTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080
 CATGGGCAGG AAATGTTCTA CTGCTTTCCT GACAATTTCT CTCTCACAAA TACCTCAGAG 1140
 TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200
 TAA

Seq ID NO: 554 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MG YQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYPFIAMI 60
 SYNIIAGDTL SKVFQRIQGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSILIS 120
 TGLTTLILGI VMARISLGP HIPKTEDAVV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL 180
 EEPTVAKWSR LIHMSIVISV PICIFFATCG YLTFTGFTQG DLFENYCRND DLVTFGRFCY 240
 GVTVILTYPM ECFVTREVIA NVFFGGNLSV VEHIVVTVMV ITVATLVSLI IDCLGIVLEL 300
 NGVLCATPLI FIIPSACYLK LSEEPRTSHD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360
 HQEMFYCFPD DNFSLTNTSE SHVQQTQLS TLNISIFQLE

Seq ID NO: 555 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1140

1 11 21 31 41 51
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGG TCAATAAAAC TTTCGGCTTT 60
 CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120
 TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180
 CCTGAAAACG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTCCACAGT TACCTTTACT 240
 CTGCCCTTAT CCTGTACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300
 GGTTTAACAA CTCGTATTCT TGGAAATTGA ATGGCAAGGG CAATTTACT GGGTCCACAC 360
 ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAGCCCA ATGCCATTCA AGCGGTCCGG 420
 GTTATGTCTT TTGCATTTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
 GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540
 ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTAC CCAAGGGGAC 600
 TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
 GTCACGTGTA TTTTGACATA CCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
 GTGTTTTTTG TGCGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780
 ACTGTAGCCA CGCTTGCTGC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
 GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCATTCAT CAGCCTGTTA TCTGAACTG 900
 TCTGAAGAAC CAAGGACACA CTCGATAAG ATTATGTCTT GTGTCATGCT TCCCATTTGT 960
 GCTGTGGTGA TGGTTTTTGG ATTCGTATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
 GGGCAGGAAA TGTTCTACTG CTTTCCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT 1080
 CATGTTTACG AGACAACACA ACTTTCTACT TTAAATATTA GTATCTTTCA ACTCGAGTAA

Seq ID NO: 556 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MG YQRQEPVI PPQVKNKTFG FPGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIQGV 60
 PENVFIGRHF IIGLSTVFTF LPLSLYRNI KLKGVSLIST GLTTLILGIV MARAISLGPH 120
 IPKTEDAVWF AKPNAIQAVG VMSFAFICH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180
 ICIFPATCGY LFTFTGTQGD LFNENYCRND LVTGFRFCY VTVILTYPME CFTVREVIAN 240
 VFFGGNLSV FHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL 300
 SEEPRTSHDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES 360
 HVQQTQLST LNISIFQLE

Seq ID NO: 557 DNA sequence
 Nucleic Acid Accession #: XM_057188.1
 Coding sequence: 769..4269

1 11 21 31 41 51
 ATGGGATTGC CTCTCCCTCT CACTCTGGGC TCTGTCCCA CTCTTATCTT AGTGTCACTC 60
 CTCGCCCAAG TCTGTGTCCT TCTCTCTCCC CTAAATCTCT GGCCCTCCTT TTCTGAGTTC 120
 CTGCCCTTGC CCCAATTTCT TGGTTTTTGC ATCCCCCTCT GCCCCTTGCC TCAGTCAAGT 180
 CTCCTCTGTC TGTCTCTCTC CCCCCGGCCC GGACCTCTGC ACCCCCCAGG TCGCTGTCCC 240
 TCTGTCCCTT TATCGCGGCC TGGGACCCGC CCTCTCCCG CCTCCGCTT TGGCGTCTCC 300
 AAGACTCCCT GCCCCCCAGA CCTGCCCCG CCCAGGCTA GGCTGGAAAG TGGAGGATCC 360
 GGTTTGCTCT GGGCGGGTCT GGAAGCAGAG CCGGCGGAGG GAGCGCCGGG GCCCTGGGCT 420
 GCAGGAGGTT CGCGCGGCGG CGGCAGCATG GTGGTGCCGG AGAAGGAGCA GAGCTGGATC 480
 CCCAAGATCT TCAAGAAAGAA GACCTGCACG ACGTTCATAG TTGACTCCAC AGATCCGGGG 540
 GATGGGGTCT CGCTCTATTG CCCAGGCTGT TCTCAAATCT CTGGGCTCAA GCAGTCCCTC 600
 TGCCTTGAC TCCCAAAGTG CTTGGATTGT GCCCAGCCGT CCTTGAAGTT TTGCTCAGAA 660
 GAGCAAACCT TCTGGGAAGT AGCTGCAGGT GTTGAAGTA GCTGCAGGGG AACTAGGGGA 720

5 TTCAAGGATG GAGCTGAAAT GGGTGAACGG ACAAAGTCGG TAAACTGAAT GGAGGATGCC 780
 TTGGGGGCGAG CCGTGGTGAC CGTGTGGGAC AGCGATGCAC ACACCCACGA GAAGCCACACC 840
 GATGCGCTACG GAGAGCTGGA CTTACGCGGG GCCGGCCGCA AGCAGACGAA TTTCCTCCGG 900
 CTCTCTGACC GAACGGATCC AGCTGCAGTT TATAGTCTGG TCACACGCAC ATGGGGCTTC 960
 CGTGCCCGGA ACCTGGTGGT GTCACTGCTG GGGGGATCGG GGGGCCCCGT CCTCCAGACC 1020
 TTGGTGCAGG ACCTGCTGCG TCGTGGGCTG GTGCGGGCTG CCCAGAGCAC AGGAGCCTGG 1080
 ATTGTCACTG GGGGTCTGCA CACGGGCATC GGCCGGCATG TTGGTGTGGC TGTACGGGAC 1140
 CATCAGATGG CCAGCACTGG GGGCACCAGG GTGGTGGCCA TGGGTGTGGC CCCCTGGGGT 1200
 10 TGGGTCCCGA ATAGAGACAC CCTCATCAAC CCCAAGGGCT CGTTCCTGC GAGGTACCGG 1260
 TGGCGCGGTG ACCCGGAGGA CGGGGTCCAG TTTCCCTGG ACTACAACTA CTCGGCCTTC 1320
 TTCTCTGGTG AACAGCGCAC ACACGGCTGC CTGGGGGGCG AGAACCGCTT CCCTTGGCGC 1380
 CTGGAGTCCT ACATCTCACA GCAGAAGACG GCGGTGGGAG GGACTGGAAT TGACATCCCT 1440
 GTCTGCTCC TCCTGATTGA TGGTGATGAG AAGATGTGA CGCGAATAGA GAACGCCACC 1500
 15 CAGGCTCAGC TCCCATGTCT CCTCGTGGCT GGCTCAGGGG GAGCTGCGGA CTGCCTGGCG 1560
 GAGACCTGAG AAGACACTCT GGGCCCAAGG AGTGGGGGAG CCAGGCAAGG CGAAGCCCGA 1620
 GATCGAATCA GGGCTTTCTT TCCCAAAGGG GACCTTGAGG TCCTGCAGGC CCAGGTGGAG 1680
 AGGATTATGA CCCGGAAGGA GCTCCTGACA GTCTATTCTT CTGAGGATGG GTCTGAGGAA 1740
 TTCGAGACCA TAGTTTGAAG GGCCTTGTG AAGGCTGTG GGAGCTCGGA GGCTCAGCC 1800
 20 TACCTGGATG AGCTGCTTTT GGCTGTGGCT TGGAAACCGG TGGACATTGC CCAGAGTGAA 1860
 CTCTTTGGGG GGGACATCCA ATGGCGGTCC TTCCATCTCG AAGCTTCCCT CATGGACGCC 1920
 CTGCTGAATG ACCGGCTGA GTTCGTGCGC TTGCTCATTT CCCACGGCCT CAGCCTGGGC 1980
 CACTTCTCGA CCCCAGATGG CCTGGCCCAA CTCTACAGCG CGGCGCCCTC CAACTCGCTC 2040
 25 ATCCGCAACC TTTTGGACCA GCGCTCCAC AGCGCAGGCA CCAAAGCCCC AGCCCTAAAA 2100
 GGGGGAGCTG CGGAGCTCCG GCCCCTGAC GTGGGGCATG TGCTGAGGAT GCTGCTGGGG 2160
 AAGATGTGCG CGCGAGGTA CCCCTCGGG GCGCCTCGGG ACCCTCACCC AGGCCAGGGC 2220
 TTCGGGGAGA GCATGTATCT GCTCTCGGAC AAGGCCACCT CGCGCTCTC GCTGGATGCT 2280
 GGCCTCGGGC AGGCCCCCTG GAGCGACCTG CTCTTTTGGG CACTGTTGCT GAACAGGGCA 2340
 30 CAGATGGCCA TGTACTTCTG GGAGATGGGT TCCAATGCAG TTTCTCAGC TCTTGGGGCC 2400
 TGTTTGCTGC TCCGGGTGAT GGCACGCCCT GAGCCTGACG CTGAGGAGGC AGCAGGAGG 2460
 AAAGACCTGG CGTTCAGTT TGAGGGGATG GGCCTTGACC TCTTTGGCGA GTGCTATCGC 2520
 AGCAGTGAGG TGAGGGCTGC CCGCTCTCT CTCCGTGCTG GCCCGCTCTG GGGGGATGCC 2580
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 35 CAGTCTCTGC TGACACAGAA GTGGTGGGGA GATATGGCCA GCACTACACC CATCTGGGCC 2700
 CTGTTCTCG CTTCTTTTG CCCTCCACTC ATCTACACCC GCCTCATCAC CTTCAGGAAA 2760
 TCAGAAGAGG AGCCACACAG GAGGAGGATA GAGTTTGACA TGGATAGTGT CATTAAATGGG 2820
 GAAGGGCTG TCGGAGCGGC GGACCCAGCC GAGAAGACGC CGCTGGGGGT CCCGCGCCAG 2880
 TCGGGCCGTC CGGGTGTGTC CGGGGGCCGC TCGGGGGGGC GCCGTGCTCT ACGCCGCTGG 2940
 40 TTCCACTTCT GGGGCGCGCC GGTGACCATC TTCATGGGCA ACGTGGTCAG CTACCTGCTG 3000
 TTCTCTGCTG TTTTCTCGCG GGTGCTGCTC GTGGATTTC AGCCGCGGCC GCCCGCTCC 3060
 CTGGAGCTGC TGCTCTATTT CTGGCTTTC ACGCTGCTGT GCGAGGAAC CTGCGAGGGC 3120
 CTGAGCGGAG GCGGGGGCAG CCTCGCCAGC GGGGGCCCGG GGCTTGCCA TGCTCACTG 3180
 AGCCAGCGCC TGCGCTCTA CCTCGCCGAC AGCTGGAACC AGTGCACCT AGTGGCTCTC 3240
 45 ACCTGCTTCC TCCTGGGGCT GGGCTGCCGG CTGACCCCGG GTTTGTACCA CCTGGGCCGC 3300
 ACTGTCTCT GCATCGACTT CATGGTTTTC ACGGTGCGGC TGCTTCACAT CTTACCGGTC 3360
 AACAAACAGC TGGGGCCCAA GATCGTCATC GTGAGCAAGA TGATGAAGGA CGTGTCTTTC 3420
 TTCTCTTCT TCCTCGCGCT GTGGCTGGTA GCCTATGGCG TGGCCACGGA GGGGCTCCTG 3480
 50 AGGCCACGGG ACAGTGACTT CCCAAGTATC CTGCGCCGCG TCTTCTACCG TCCCTACCTG 3540
 CAGATCTTGG GGCAGATTCC CCAGGAGGAC ATGGACGTGG CCCTCATGGA GCACAGCAAC 3600
 TGCTCGTGG AGCCCGGCTT CTGGGCACAC CCTCCTGGGG CCCAGGCGGG CACTGCGCTG 3660
 TCCAGTATG CCAACTGGCT GGTGGTGTG CTCTCGTCA TCTTCTGCT CGTGGCCAAC 3720
 ATCCTGCTGG TCAACTTGCT CATTGCCATG TTCAGTTACA CATTGGGCAA AGTACAGGGC 3780
 AACAGCGATC TCTACTGGAA GCGCGAGCGT TACCGCTCA TCCGGGAATT CCACTCTCGG 3840
 55 CCGCGCTGG CCCCGCCTT TATCGTCATC TCCCACTTGC GCCTCCTGCT CAGGCAATTG 3900
 TGCAGGCGAC CCGGAGGCC CCAGCGCTCC TCCCCGGCCC TCGAGCATTT CCGGGTTTAC 3960
 CTTTCTAAGG AAGCCGAGCG GAAGCTGCTA ACGTGGGAAT CGGTGCATAA GGAGAACTTT 4020
 CTGCTGGCAC GCGCTAGGGA CAAGCGGGAG AGCGACTCCG AGCGCTGAA GCGCACGTC 4080
 CAGAAGGTGG ACTTGGCACT GAAACAGCTG GGACACATCC GCGAGTACGA ACAGCGCTG 4140
 60 AAAGTGCTGG AGCGGGAGGT CCAGCAGTGT AGCCCGCTCC TGGGGTGGGT GGCCGAGGCC 4200
 CTGAGCCGCT CGCTCTGCT GCCCCAGGT GGGCCGCCAC CCCCTGACCT GCCTGGGTCC 4260
 AAAGACTGAG CCTGCTGCTG GACTTCAAG GAGAAGCCCC CACAGGGGAT TTTGCTCCTA 4320
 GAGTAAGGCT CATCTGGGCC TCGGCCCCCG CACCTGGTGG CCTTGTCTT GAGGTGAGCC 4380
 CCATGTCCAT CTGGGGCACT GTCAGGACCA CCTTTGGGAG TGTCATCCTT ACAAACCACA 4440
 GCATGCCCCG CTCTCCCGAG AACCACTCCC AGCCTGGGAG GATCAAGGCC TGGATCCCGG 4500
 65 GCCGTATCC ATCTGAGGCG TGCAGGGTCC TTGGGGTAAC AGGGACCACA GACCCTCAC 4560
 CACTCACAGA TTCTCACAC TGGGGAAATA AAGCCATTT AGAGGAAAAA AAAAAAAA 4620
 AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: 558 Protein sequence
 Protein Accession #: XP_057188.1

70 1 11 21 31 41 51
 MEDAFGAADV TVWDSDAHT EKPTDAYGEL DFTGAGRKHS NFLRLSDRT PAAVYSLVTR 60
 75 TWGFRAENLV VSVLGGSGGP VLQTLWQDLL RRLGLVRAAQ TGAIVITGGL HTGIGHRVGV 120
 AVRDRHQMAST GGTKVVMAMG APWGVVRNRD TLINPKGSFP ARYRWRGDPE DGVQFPLDYN 180
 YSAFFLVDDG THGCLGGENR FRLRLESYIS QKQTVGGGTG IDIPVLLLI DGDEKMLTRI 240
 ENATQAQLPC LNVAGSGGAA DCLAETLED T LAPSGGARQ GEARDIRRF FPKGDLVLQ 300
 AQVERIMTRK ELLTVYSSED GSEEFETIVL KALVKACGSS EASAYLDEL L LAVAWNVRDI 360
 80 AQSELRGDI QWRSFHLEAS LMDALLNDRP EFVRLISHG LSLGHFLTPM RLAQLYSAAP 420
 SNSLIRNLLD QASHSAGTKA PALKGGAAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480
 PGQGFESMY LLSDKATSPL SLDAQLQAP WSDLLWALL LNRAQMAMYF WEMGSNAVSS 540
 ALGACLLLRV MARLEPAEE AARRKDLAFK FEGMGVDLFG ECVRSSEVRA ARLLLRRCPL 600
 WGDATCLQLA MQADARAFA QDGVQSLLTQ KWWGDMASTT PIWALVLAFF CPPLIXTRLI 660
 TFRKSEBEPT REELEFDMDS VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGGRCGRRRC 720

LRRWFHFWGA PVTIFMGNNV SYLLELLLF S RVLLVDFQPA PPGSLELLLY FWAFTLLCEE 780
 LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840
 HLGRITVLICID FMVFTVRLHL IFTVNKQLGP KIVIVSKMMK DVFFFLFFLG VWLVAYGVAT 900
 EGLLRPRDSF PFSILRRVHY RPYLQIFGQI PQEDMDVALM BHSNCSSEFG FWAHPFGAQA 960
 5 GTCVSQYANW LVVLLLVIFL LVANILLVNL LIAMFSYTFG KVQNSDLYW KAQRVRLIRE 1020
 FHSRPAALAPP FIVISHLRLR LRQLCRRPRS PQPSPALEH FRVYLSKEAE RKLLTWESVH 1080
 KENFLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY BQRLKVLERE VQCSRVLGW 1140
 VAEALSRSAL LPPGGPPPPD LFGSKD

Seq ID NO: 559 DNA sequence
 Nucleic Acid Accession #: NM_006853.1
 Coding sequence: 26..874

1 11 21 31 41 51
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 AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC 60
 ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCCTCCAGGC 120
 CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180
 20 CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCCAG CCCTGGCAGG CAGCCCTGTT 240
 CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC 300
 AGCCCACTGC CTCAAGCCCC GCTACATAGT TCACCTGGGG CAGCACACC TCCAGAAGGA 360
 GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCCACCCCG GCTTCAACAA 420
 CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480
 25 TCCTCATCAC TGGGGTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC 540
 CAGCTGCCTC ATTTCCGGCT GGGGCAGCAC GTCCAGCCCC CAGTTACGCC TGCCTCACAC 600
 CTTCGATGTC GCCAACATCA CCATCATTGA GCACCAGAAG TGTGAGAACG CCTACCCCGG 660
 CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAAGAA GGGGGCAAGG ACTCCTGCCA 720
 GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCCTGGGG 780
 CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAAATATGT 840
 30 GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
 ACCCTCCATT TCCACTTGGT GTTTGGTTCC TGTTCACTCT GTTAATAAGA AACCTAAGC 960
 CAAGACCCCT TACGAACATT CTTTGGGCTT CCTGGACTAC AGGAGATGCT GTCACCTAAT 1020
 AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATCTGCTT GAAATATTGT 1080
 35 GACTCTGGGA ATGACAACAC CTGGTTTGTG CTCTGTTGTA TCCCAGCCCC CAAAGACAGC 1140
 TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

Seq ID NO: 560 Protein sequence
 Protein Accession #: NP_006844.1

1 11 21 31 41 51
 | | | | |
 MRILQLILLA LATGLVGGET RIIGKFECKP HSQFWQAALF EKTRLLCGAT LIAPRWLLTA 60
 AHCLKPRYIV HLGQHNLOKE EGCEQTRTAT ESFPHPGFNN SLPNDHRND IMLVKMASPV 120
 45 SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCNAYPG 180
 NITDTMVCAS VQEGGKDSQC GDSGGPLVCN QSLQGIISWG QDFCAITRKP GYITKVCKYV 240
 DWIQETMKNN

Seq ID NO: 561 DNA sequence
 Nucleic Acid Accession #: AY046419.1
 Coding sequence: 1..1743

1 11 21 31 41 51
 | | | | |
 ATGTTTACCT TCCTGTCTAT TGTCAGTCTG GCTGTCAAGT GCCTCCTGGT GGGTTATGAA 60
 55 CTGCGGATCA TCTCTGGGGC TCTTCTTCAG ATCAAAACCT TATTAGCCCT GAGCTGCCAT 120
 GAGCAGGAAA TGGTTGTGAG CTCCTCTGTC ATTTGGAGCCC TCCTTGCCCT ACTCACCGGA 180
 GGGGTCTCTG TAGACAGATA TGGGAAGAAG ACAGCAATCA TCTGTCTATC CTGCCTGCTT 240
 GGACTCGGAA GCTTAGTCTT GATCCTCAGT TTATCCTACA CGGTTCTTAT AGTGGGACGC 300
 60 ATTGCCATAG GGGTTTCCAT CTCCTCTCTT TCCATTGCCA CTGTGTGTTA CATCGCAGAG 360
 ATTGCTCCTC AACACAGAAG AGGCCTTCTT GTGTCACTGA ATGAGCTGAT GATTGTCTATC 420
 GGCATTCTTT CTGCCTATAT TTCAAATTAC GCATTTGCCA ATGTTTTCCTA TGGCTGGAAG 480
 TACATGTTTG GTCTGTGAT TCCCTTGGGA GTTTTGCAAG CAATTGCAAT GTATTTTCTT 540
 CCTCCAAGCC CTCGGTTTCT GGTGATGAAA GGACAAGAGG GAGCTGCTAG CAAGGTTCTT 600
 65 GGAAGGTTAA GAGCAGTCTC AGATACAAC T GAGGAAC TCA CTGTGATCAA ATCCTCCCTG 660
 AAAGATGAAT ATCAGTACAG TTTTGGGAT CTGTTTCTGT CAAAAGACAA CATGCGGACC 720
 CGAATAATAG TAGGACTAAC ACTAGTATTT TTTGTACAAA TCACTGGCCA ACCAAACATA 780
 TTGTTCTATG CATCAACTGT TTTGAAGTCA GTTGGATTTC AAAGCAATGA GGCAGCTAGC 840
 CTCGCTCCCA CTGGGGTTGG AGTCGTCAAG GTCATTAGCA CCATCCCTGC CACTCTTCTT 900
 70 GTAGACCATG TCGGCAGCAA AACATTCTCT TGCAATTGGT CCTCTGTGAT GGCAGCTTCG 960
 TTGGTGACCA TGGGCATCGT AAATCTCAAC ATCCACATGA ACTTCAACCA TATCTGCAGA 1020
 AGCCACAATT CTATCAACCA GTCCTTGGAT GAGTCTGTGA TTTATGGACC AGGAAACCTG 1080
 TCAACCAACA CCAATACTCT CAGAGACCAC TTCAAAGGGA TTTCTTCCCA TAGCAGAAGC 1140
 TCACTCATGC ACCATGAGAA TGAATGGAT AAGAGAGGGG AGACGACCTC AGCATCCTTG 1200
 75 CTAATGCTG GAATTAAGCCA CACTGAATAC CAGATAGTCA CAGACCTTGG GGCAGTCCCA 1260
 GCTTTTGTGA AATGGCTGTC CTTAGCCAGC TTGCTTGTGT ATGTTGCTGC TTTTCAATT 1320
 GGTCTAGGAC CAATGCCCTG GCTGGTGTCT AGCGAGATCT TTCCTGGTGG GATCAGAGGA 1380
 CGAGCCATGG CTTTAACTTC TAGCATGAAC TGGGGCATCA ATCTCCTCAT CTCGCTGACA 1440
 80 TTTTGAAGT TAACGTATCT TATTGGCCTG CCATGGGTGT GCTTATATA TACAATCATG 1500
 AGTCTAGCAT CCCTGCTTTT TGTGTTATG TTTATACCTG AGACAAAGGG ATGCTCTTTG 1560
 GAACAAATAT CAATGGAGCT AGCAAAAGTG AACTATGTGA AAAACAACAT TTGTTTATG 1620
 AGTCATCAC CAGAAGAAAT AGTGCCRAAA CAGCCTCAAA AAGAAAACC CCAGGAGCAG 1680
 CTCTTGGAGT GTAACAAGCT GTGTGGTAGG GGCCAATCCA GGCAGCTTTC TCCAGAGACC 1740
 TAA

Seq ID NO: 562 Protein sequence
Protein Accession #: AAL02327.1

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1      11      21      31      41      51
|      |      |      |      |      |
5  MFTFLSSVTA AVSGLLVGYE LGIISGALLQ IKTLALLSCH EQEMVSSSLV IGALLASLTG 60
    GVLIIDRYGRR TAILLSSCLL GLGSLVLILS LSYTVLIVGR IAIGVSIISL SIATCVYIAE 120
    IAPQHRRGLL VSLNELMIVI GILSAYISNY AFANVFHGWK YMFGLVPLG VLQAIAMYFL 180
10  PPSRFLVMK  GQEGAASKVL GRRLALSDTT EELTVIKSSL KDEYQYSFWD LFRSKDNMRT 240
    RIMIGLTLVF FVQITGQPNL LFYASTVLKS VGFQSNAAAS LASTGVGVVK VISTIPATLL 300
    VDHVGSKTFL CIGSSVMAAS LVTMGIVNLN IHMNFTHICR SHNSINQSLD ESVIYGPGNL 360
    STNNNTLRDH FKGISSHSRS SLMPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDVP 420
    AFLKWLSLAS LLVYVAAPSI GLGPMPLVL SEIFPGGIRG RAMALTSSMN WGINLLISLT 480
15  FLTITDLIGL PWVCFIYTIM SLASLLFVVM FIPETKGCSL EQISMELAKV NYVKNNICFM 540
    SHHQEELVFK QPQRKPKPEQ LLECNKLCGR QQSRLSPET

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Seq ID NO: 563 DNA sequence
Nucleic Acid Accession #: XM_059466.1
Coding sequence: 1..894

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1      11      21      31      41      51
|      |      |      |      |      |
25  ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG TCCCTGGGG 60
    CTGCTCGTCA CGGCCATCTT CACCGACCAC TGGTACGAGA CCGACCCCGG GCGCCACAAG 120
    GAGAGCTGCG AGCGCAGCCG CGCGGGCGCC GACCCCCCGG ACCAGAAGAA CCGCCTGATG 180
    CCGCTGTGCG ACCTGCCGCT GCGGGACTCG CCCCCTGCTG GCGCGCGGCT GCTCCCGGGC 240
    GCGCCGGGGG GCGCGGACCC CGAGTCCTGG CGCTCGCTCC TGGGGCTCGG CGGGCTGGAC 300
    GCGAGTGGG GCGCGCCCTT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
    CTGGGCATCG ACCGGGACAT CGACACCCCTC ATCCTGAAAG GTATTGCGCA GCGATGCACG 420
30  GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCGAA ACATTCTTTT TAATTTAACC 480
    AAGACCATAC AGCAAGATCA GTGGCACCTG CTTCATTTAA GAAGAATCAC TGCTGGCTTC 540
    CTCGGCATGG CGTAGCCCTT CCTTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC 600
    TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGAATCTGTG TCCTCATGAC AGGGATATT 660
35  TGCACCATTT CCTCTGTAC TTATGCCGCC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
    AAGCTAATTT ATAGCTGCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
    GCTGTGTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT 840
    ATTAGCCGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA

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Seq ID NO: 564 Protein sequence
Protein Accession #: XP_059466.1

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1      11      21      31      41      51
|      |      |      |      |      |
45  MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DPPDQKNRLM 60
    PLSHLPLRDS PPLGRLLLP GPGRADPESW RSLGLGLGLD AECGRPLFAT YSGLWRKCYF 120
    LGIDRIDIDL ILKGIAQRCT AIKYHFSQPI RLRNIPFNLT KTIQQDEWHL LHLRRITAGF 180
    LGMAVAVLLC GCTIVTSVFF WEESLTQHVA GLLFLMTGIF CTISLCTYAA SISYDLNRLP 240
    KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

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Seq ID NO: 565 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3315

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1      11      21      31      41      51
|      |      |      |      |      |
55  ATGTCCTTTC GGGCAGCCAG GCTCAGCATG AGGAACAGAA GGAATGACAC TCTGGACAGC 60
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70  CTAGAGAAGT ATATCTCTGA GCGCACTATT CAAGATTCCA ACTATGGTGG CAAGATCCCC 900
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Seq ID NO: 566 Protein sequence
 Protein Accession #: Eos sequence

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 40 LMDDFTRDPL YILDNNHTHL LLVDNGCHGH PTVEAKLRN LEKYISERTI QDSNYGGKIP 300
 IVCFAQGGGK ETLKAINTSI KNKIPCVVVE GSGQIADVIA SLVEVEDALT SSAVKEKLV 360
 FLPTVSRRLP EETESWIKW LKEILECSHL LTVIKMEEAG DEIVSNAISY ALYKAFSTSE 420
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 Nucleic Acid Accession #: NM_006911.1
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 65 GATGCTCCTC AGACACCTAG ACCAGTGGCA GAAATGTAC CATCTTCAT CAACAAAGAT 240
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Seq ID NO: 568 Protein sequence
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Seq ID NO: 570 Protein sequence
 Protein Accession #: XP_036453.1

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MAVLIILLPL QSCFGLFSS LRSKTATFTD ARIRTMNEVI TGIRIKMYA WEKSFSNLIT 300
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	GTGTCAGGAA	CTGTTTGATG	CACACCAGGA	TTTACATTCA	GAGGCTTGGT	TCTTGTTTTT	2940
75	GACAAAGTCC	CGCTGGTTCC	CGGTCCGTCT	GGATGCCATC	TGTGCCATGT	TTGTATCAT	3000
	CGTGTGCTTT	GGGTCCCTGA	TTCTGGCAAA	AACCTCTGGT	GCCGGGCGAG	TTGGTTTGGC	3060
	ACTGTCTCAT	GCCTCTACGC	TCATGGGGAT	GTTCAGTGG	TGTGTTTCAC	AAAGTGCTGA	3120
	AGTTGAGAAT	ATGATGATCT	CAGTAGAAG	GGTCATTGAA	TACACAGACC	TTGAAAAGAA	3180
	AGCACCTTGG	GAATATCAGA	AACGCCACCC	ACCAGCCTGG	CCCATGAAG	GAGTGATAAT	3240
80	CTTTGACAA	GTGAATCTCA	TGTACAGTCC	AGGTGGGCTC	CTGGTACTGA	AGCATCTGAC	3300
	AGCATCTATT	AAATCACAAG	AAAAGGTTGG	CATTGTGGGA	AGAACCGGAG	CTGGAAAAAG	3360
	TTCCCTCAT	TCAGCCCTTT	TTAGATTGTC	AGAACCCGAA	GGTAAATTTT	GGATTGATAA	3420
	GATCTTGACA	ACTGAAATTT	GACTTCCAGA	TTTAAGGAAG	AAAATGTCAA	TCATACCTCA	3480
	GGAACCTGTT	TTGTTCACTG	GAACAAATGG	GAAAAACCTG	GATCCCTTTA	AGGAGCACAC	3540
	GGATGAGGAA	CTTGGAATG	CCTTACAAGA	GGTACAACTT	AAAGAAACCA	TTGAAGATCT	3600

TCCTGGTAAA ATGGAATCTG AATTAGCAGA ATCAGGATCC AATTTTAGTG TTGGACAAAG 3660
 ACAACTGGTG TGCCTTGCCA GGGCAATTCT CAGGAAAAAT CAGATATTGA TTATTGATGA 3720
 AGCGACGGCA AATGTGGATC CAAGAACTGA TGAGTTAATA CAAAAAATA TCCGGGAGAA 3780
 ATTTGCCACG TGCACCGTGC TAACCATTCG ACACAGATG AACACCATTA TTGACAGCGA 3840
 CAAGATAATG GTTTTAGATT CAGGAAGACT GAAAGAATAT GATGAGCCGT ATGTTTGTCT 3900
 GCAAAATAAA GAGAGCCTAT TTTACAAGAT GGTGCAACAA CTGGGCAAGG CAGAAGCCGC 3960
 TGCCCTCACT GAAACAGCAA AACAGGTATA CTTCAAAAGA AATTATCCAC ATATTGGTCA 4020
 CACTGACCAC ATGGTTACAA ACACCTCCAA TGGACAGCCC TCGACCTTAA CTATTTTCGA 4080
 GACAGCACTG TGAATCCAAC CAAAATGTCA AGTCCGTTCC GAAGGCATT TCCACTAGTT 4140
 TTGGACTAT GTAAACACCA TGTACTTTT TTTTACTTTG GCAACAAATA TTTATACATA 4200
 CAAGATGCTA GTTCATTGTA ATATTCTCC C

Seq ID NO: 572 Protein sequence
 Protein Accession #: AAC27076.1

1 11 21 31 41 51
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 MLPVYQEVKP NPLQDANICS RVFFFWLNL FKIGHKRRLE EDDMYSVLPE DRSQHLGEEL 60
 QGFWDKEVLR AENDAQKPSL TRAIKCYWK SYLVLGIFTL IEESAKVIQF IFLGKIINYF 120
 ENYDPMDSVA LNTAYAYATV LTFCTLILAI LHHLYFYHVQ CAGMRLRVAM CHMIYRKALR 180
 LSNMAMGKTT TGQIVNLLSN DVNKFQDQTV FLHFLWAGPL QAIIVTALLW MEIGISCLAG 240
 MAVLIILLPL QSCFGLFSS LRSKTATFTD ARIRTMNEVI TGIRIIKMYA WEKSFSNLIT 300
 NLRKKEISKI LRSSCLRGMN LASFFSASKI IVFVTFTTYV LLGSVITASR VFAVATLYGA 360
 VRLTVTLLFPF SAIERVSEAI VSIRRIQTFL LLDEISQRNR QLPDSDGKMW HVQDFTAFWD 420
 KASEPTLQGL LSFTVRPGEL LAVVGPVGAG KSSLLSAVLG ELAPSHGLVS VHGRYAVSQ 480
 QPWVFSGLTR SNILFGKYE KERYEKVKA CALKKDLQLL EDGDLTVIGD RGTTLGGQK 540
 ARVNLARAVY QDADIYLLD PLSAVDAEVS RHLFELCICQ ILHEKITILV THQLQYLKAA 600
 SQILILKDKG MVQKGYTTFE LKSGIDFGSL LKKNDESEQ PVPVPGTPTLR NRTFSESSVW 660
 SQSSSRPSLK DGALESQDTE NVPVTLSEEN RSEKGVGFOA YKNYFRAGAH WIVFIFLILL 720
 NTAAQVAYVL QDWWSLYWAN QKSMNLNVTN GGGNVTEKLD LNWYLGIIYS LGTAVTVLPGI 780
 ARSLLVFYVL VNSSQTLHNK MFESILKAPV LFFDRNPIGR ILNRFKDIG HLDLPLPLTF 840
 LDFIQTLQV VGVVSVAVAV IPWIAIPLVP LGIIFIFLRR YFLETSRDVK RLESTRSPV 900
 FSHLSSSLQG LWTIRAYKAE ERCQELFDAH QDLHSEAWFL FLTTSRWFAV RLDAICAMFV 960
 IIVAFGSLIL AKTLIDAGVQG LALSIALTLM GMFQWCVQRQ AEVENMMISV ERVIEYTDLE 1020
 KEAPWEYQKR PPPAWPHEGV IIFDNVNFMY SPGGPLVLKH LTALIKSQEK VGVIGRTGAG 1080
 KSSLISALFR LSEPEGKIWI DKILTTEIGL HDLRKKMSII POEVLFTGT MRKNLDPFKE 1140
 HTDEELWNAL QEVQLKETIE DLPKMDTEL AESGSNFSVG QRQLVCLARA ILRKNQILII 1200
 DEATANVDPR TDELIQKKIR EKFAHCTVLT IAHRLNTIID SDKIMVLD SG RLKEYDEPYV 1260
 LLQNKESLFY KMVQQLGKAE AALATETAKQ VYFKRNYPHI GHTDHMTNT SNGQPSTLTI 1320
 FETAL

Seq ID NO: 573 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1365

1 11 21 31 41 51
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 ATGGAATCAA TCTCTATGAT GGGGAAGCCCT AAGAGCCTTA GTGAAACTTG TTTACCTAAT 60
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 TTTGCCAAAT CCTTGACCAT TCGACTTATT AGATGCGGCT ATCATGTGGT CATAGGAAGT 180
 AGAAATCCTA AGTTTGCTTC TGAATTTTTT CCTCATGTGG TAGATGTCAC TCATCATGAA 240
 GATGCTCTCA CAAAAACAAA TATAATATTT GTTGCTATAC ACAGAGAACA TTATACCTCC 300
 CTGTGGGACC TGAGACATCT GCTTGTGGGT AAAATCCTGA TTGATGTGAG CAATAACATG 360
 AGGATAAACC AGTACCAGA ATCCAATGCT GAATATTTGG CTTTATTATT CCCAGATTCT 420
 TTGATTGTCA AAGGATTATA TGTTGTCTCA GCTTGGGCAC TTCAGTTAGG ACCTAAGGAT 480
 GCCAGCCGGC AGGTTTATAT ATGCAGCAAC AATATTCAAG CGGCACAACA GGTATTGAA 540
 CTTGCCGCCC AGTTGGAATT CATTCCTATT GACTTGGGAT CCTTATCATC AGCCAGAGAG 600
 ATTGAAATTT TACCCCTACG ACTCTTTACT CTCTGGAGAG GGCAGTGGT GGTAGCTATA 660
 AGCTTGGCCA CATTTTTTTT CCTTATTATC TTTGTCAGAG ATGTGATTCA TCCATATGCT 720
 AGAAACCAAC AGAGTGACTT TTACAAAATT CCTATAGAGA TTGTGAATAA AACCTTACCT 780
 ATAGTTGCCA TTACTTTGCT CTCCTAGTA TACCTCGCAG GTCTTCTGGC AGCTGCTTAT 840
 CAACTTTATT ACGGCACCAA GTATAGGAGA TTTCCACCTT GGTGGAAC CTGTTACAG 900
 TGTAGAAAAC AGCTTGATT ACTAAGTTT TTCTTCGCTA TGGTCCATGT TGCCTACAGC 960
 CTCTGCTTAC CGATGAGAAG GTCAGAGAGA TATTGTGTTT TCAACATGGC TTATCAGCAG 1020
 GTTCATGCAA ATATTGAAAA CTCTTGAAT GAGGAAGAAG TTTGGAGAAT TGAATGTAT 1080
 ATCTCCTTTG GCATAATGAG CCTTGGCTTA CTTTCCCTCC TGGCAGTCAC TTCTATCCCT 1140
 TCAGTGAGCA ATGCTTTAAA CTGGAGAGAA TTCAGTTTAA TTCAGTCTAC ACTTGGATAT 1200
 GTCGCTCTGC TCATAAGTAC TTTCCATGTT TTAATTTATG GATGGAACG AGCTTTTGAG 1260
 GAAGAGTACT ACAGATTTTA TACACCACCA AACTTTGTTT TTGCTCTGT TTTGCCCTCA 1320
 ATTGTAATTC TGGATCTTTT GCAGCTTTGC AGATACCCAG ACTGA

Seq ID NO: 574 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 MESISMMSGP KSLSETCLPN GINGIKDARK VTVGVIGSGD FAKSLTIRLI RCGYHVIVGS 60
 RNPKFASEFP PHVVDVTHHE DALTKTNIIF VAIHREHYTS LWDLRHLLVG KILIDVSNM 120
 RINQYPSNA EYLASLFPDS LIVKGFNVVS AWALQLGPKD ASRQVYICSN NIQARQQVIE 180
 LARQINFIPI DLGSLSSARE IENLPLRLFT LWRGPVVVAI SLATFFFLYS FVRDVIHPYA 240
 RNRQSDFYKI PEIIVNKTLP IVAITLLSLV YLAGLLAAAY QLYYGTKYRR FPPWLETWLQ 300
 CRKQLGLLSF PFAMVHVAYS LCLPMRRSER YLFLNMAYQQ VHANIENSWN BEEVWRIEMY 360
 ISFGIMSLGL LSLLAIVTSIP SVSNALNWRE FSFIQSTLGY VALLISTFHV LIYGWKRAFE 420
 BEYRYFTFP NFVLALVLPS IVILDLLQLC RYPD

Seq ID NO: 575 DNA sequence
Nucleic Acid Accession #: NM_001873.1
Coding sequence: 3..1721

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      CCTGGGCTCC GCGGCCAGTA GTGCAGCCCC TGGAGCCGCG GCTTTGCCCG TCTCCTCTGG 120
      GTGGCCCCAG TCGCGGGGCT GACACTCATT CAGCCGGGGA AGGTGAGGCG AGTAGAGGCT 180
      GGTGCGGAAC TTGCCGCCCC CAGCAGCGCC GGCGGGCTAA GCCCAGGGCC GGGCAGACAA 240
      AAGAGGCCGC CGCGCTAGGA AGGCACGGCC GGCGGCGGCG GAGCGCAGCG ATGGCCGGGC 300
      GAGGGGGCAG CGCGCTGCTG GCTCTGTGCG GGGCACTGGC TGCCCTGCGGG TGGCTCCTGG 360
      GCGCCGAAGC CGAGGAGCCC GGGGCGCCCC CGGCGGGCAT GAGGCGGCGC CGGCGGCTGC 420
15    AGCAAGAGGA CGGCATCTCC TTGAGTACC ACCGCTACCC CGAGCTGCGC GAGGCGCTCG 480
      TGTCCGTGTG GCTGCAGTGC ACCGCCATCA GCAGGATTTA CACGGTGGGG CGCAGCTTCG 540
      AGGGCCGGGA GCTCCTGGTC ATCGAGCTGT CCGACAACCC TGGCGTCCAT GAGCCTGGTG 600
      AGCTGAATT TAAATACATT GGAATATGCG ATGGGAATGA GGCTGTTGGA CGAGAACTGC 660
      TCATTTTCTT GGGCCAGTAC CTATGCAACG AATACCAGAA GGGGAACGAG ACAATTGTCA 720
20    ACCTGATCCA CAGTACCCGC ATTACATCA TGCTTCCCT GAACCCAGAT GGCTTTGAGA 780
      AGGCAGCGTC TCAGCCTGGT GAACCAAGG ACTGGTTTGT GGGTCGAAGC AATGCCCAGG 840
      GAATAGATCT GAACCGGAAC TTCCAGACC TGGATAGGAT AGTGATCGTG AATGAGAAAG 900
      AAGGTGGTCC AAATAATCAT CTGTTGAAAA ATATGAAGAA AATTGTGGAT CAAAACACAA 960
25    AGCTTGCTCC TGAGACCAAG GCTGTCAATC ATTGGATTAT GGATATTCCT TTTGTGCTTT 1020
      CTGCCAATCT CCATGGAGGA GACCTTGTGG CCAATTATCC ATATGATGAG ACGCGGAGTG 1080
      GTAGTGCTCA CGAATACAGC TCCTCCCCAG ATGACGCCAT TTTCCAAAGC TTGGCCCGGG 1140
      CATACTCTTC TTTCAACCCG GCCATGTCTG ACCCAATCG GCCACCATGT CGCAAGAAATG 1200
      ATGATGACAG CAGCTTTGTA GATGGAACCA CCAACGGTGG TGCTTGGTAC AGCGTACCTG 1260
      GAGGGATGCA AGACTTCAAT TACCTTAGCA GCAACTGTTT TGAGATCACC GTGGAGCTTA 1320
30    GCTGTGAGAA GTTCCACCTT GAAGAGACTC TGAAGACCTA CTGGGAGGAT AACAAAAACT 1380
      CCCTCATTAG CTACCTTTAG CAGATACACC GAGGAGTTAA AGGATTGTCT CGAGACCTTC 1440
      AAGGTAACCC AATTGCGAAT GCCACCATCT CCGTGAAGG AATAGACCAC GATGTTACAT 1500
      CCGCAAGGGA TGGTGATTAC TGGAGATTGC TTATACCTGG AAACATAAAA CTTACAGCCT 1560
      CAGCTCCAGG CTATCTGGCA ATAACAAAGA AAGTGGCAGT TCCTTACAGC CCTGCTGCTG 1620
35    GGGTTGATTT TGAAGTGGAG TCATTTTCTG AAAGGAAAGA AGAGGAGAAG GAAGAATTGA 1680
      TGGAATGGTG GAAATGATG TCAGAACTT TAAATTTTTA AAAAGGCTTC TAGTTAGCTG 1740
      CTTTAAATCT ATCTATATAA TGTAGTATGA TGTAAATGGG TCTTTTTTTT AGATTTTGTG 1800
      CAGTTAATAC TTAACATTGA TTTATTTTTT AATCATTTAA ATATTATCA ACTTTCCTTA 1860
40    AAATAAATAG CCTCTTAGGT AAAAATATAA GAACTTGATA TATTTTCACT TCTTATATAG 1920
      TATTCATTTT CCTACCTATA TTACACAAAA AAGTATAGAA AAGATTAAAG TAATTTTGCC 1980
      ATCCTAGGCT TAAATGCAAT ATTCTGGTA TTATTTACAA TGCAGAAATTT TTTGAGTAAT 2040
      TCTAGCTTTC AAAAATTAGT GAAGTTCTTT TACTGTAATT GGTGACAATG TCACATAATG 2100
      AATGCTATTG AAAAGGTTAA CAGATACAGC TCGGAGTTGT GAGCACTCTA CTGCAAGACT 2160
45    TAAATGTTT AGTATAAATT GTCTTTTTTT TCTTGTGCTG ACTAACTATA AGCATGATCT 2220
      TGTTAATGCA TTTTGTATGG GAAGAAAAGG TACATGTTTA CAAAGAGGTT TTAGAAAAG 2280
      AATAAAATAT GACTTCTTGC TTGTACATAT AGGAGCAATA CTATTATATT ATGTAGTCCG 2340
      TTAACACTAC TTAAGAGTTT AGGGTTTTCT CTTGGTTGTA GAGTGGCCCA GAATTGCATT 2400
      CTGAATGAAT AAAGGTTAAA AAAAATCCC CAGTGAAAAA AAA

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Seq ID NO: 576 Protein sequence
Protein Accession #: NP_001864.1

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55    1      11      21      31      41      51
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      MAGRGSALL ALCGALAACG WLLGAEAEQEP GAPAAGMRRR RRLQEDGIS FEYHRYPELR 60
      EALVSVWLQC TAISRIYTVG RSFEGRELLV IELSDNPGVH EPGEPEFKYI GNMHGNEAVG 120
      RELLIFLAQY LCNEYQKQNE TIVNLIHSTR IHIMPSLNPD GFEXAASQPG ELKDWVFGRS 180
      NAQGDILNRR FPDILRIYVV NEKEGGPNNH LLKNMKIIVD QNTKLAPETK AVIHWIMDIP 240
      FVLNLANHGG DLVANTPYDE TRSGSAHEYS SSPDDAIFQS LARAYSSFPN AMSDPNRPCC 300
60    RKNDDSSFFV DGTNNGWAYV SVPGMQDEFN YLSSNCFEIT VELSCKEFPF EETLKYWED 360
      NKNSLISYLE QIHRGVKGFV RDLQGNPIAN ATISVEGIDH DVTSKDGIDY WRLLIPGNYK 420
      LTASAPGYLA ITKKVAVPYS PAAGVDFELE SFSEKKEEEK EELMEWKKMM SETLNF

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Seq ID NO: 577 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..933

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70    1      11      21      31      41      51
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      TTCGACAAGA GTGATGAGAA GGAGTGCCCC AAGGCTAAGT CGAAATGTGG CCCGACCTTC 120
      TTCCCTGTGT CCAGCGGCAT CCATTGCATC ATTGGTCGCT TCCGGTGCAA TGGGTTTGAG 180
      GACTGTCCCG ATGGCAGCGA TGAAGAGAAC TGCAAGCAA ACCCTCTGCT TTGCTCCACC 240
75    GCCCCTACCT ACTGCAAGAA CGGCCCTCTG ATTGACAAGA GCTTCATCTG CGATGGACAG 300
      AATAACTGTC AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCCGGCAGT 360
      GGGCAGGTGT TTGTGACTTC AGAGAACCAA CTGTGTGATT ACCCCAGCAT CACCTATGCC 420
      ATCATCGGCA GTCCTGTCAT TTTGTGCTG GTGGTGGCCC TGCTGGCACT GGTCTTGAC 480
      CACCGCGGCA AGCGGAACAA CCTCATGACG CTGCCCGTGC ACCGGCTGCA GCACCCTGTG 540
      CTGCTGTCCC GCCTGTGGGT CCTGGACCA CCCCACCACT GCAACGTGAC CTACAACGTC 600
80    AATAATGGCA TCCAGTATGT GGCCAGCCAG GCGGAGCAGA ATGCGTCGGA AGTAGGCTCC 660
      CACCCCTCCT ACTCCGAGG CTGTCTGGAC CAGAGGCTCG CGTGGTATGA CCTTCTCCA 720
      CCGCCCTACT CTCTGACAC GGAATCTCTG AACCAAGCCG ACCTGCCCCC CTACCGCTCC 780
      CGGTCCGGCA GTGCCAACAG TGCCAGCTCC CAGGCAGCCA GCAGCTCCTT GAGCGTGGAA 840
      GACACCGGCC ACAGCCCGGG GCAGCCTGGC CCCAGGAGG GCACTGCTGA GCCCAGGGAC 900

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TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 578 Protein sequence
Protein Accession #: Eos sequence

1	11	21	31	41	51	
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DCPDGSDEN	CTANPLLCST	ARYHCKNGLC	IDKSFICDGQ	NNCQDNDSE	SCSSQEPGS	120
GQVFTSENQ	LVVYPSITYA	IIGSSVIFVL	VVALLALVLH	HQRKRNLMT	LPVHRLQHPV	180
LLSRLVVLHD	PHHCNVTYNV	NNGIQYVASQ	AEQNASEVGS	PFSYSEALLD	QRPAYDLPP	240
PPYSSDTESL	NQADLPFYRS	RSGSANSASS	QAASSLLSVE	DTSHSPGQPG	PQEGTAEPRD	300
SEPSQGTEEV						

Seq ID NO: 579 DNA sequence
Nucleic Acid Accession #: AF179274.1
Coding sequence: 1..1125

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TGGCTGCTGC	TGCTGCCCGT	CATGCTACTC	ATCGTAGCCC	GCCCGGTGAA	GCTCGCTGCT	120
TTCCCTACCT	CCTTAAGTGA	CTGCCAAACG	CCCACCGGCT	GGAATTGCTC	TGGTTATGAT	180
GACAGAGAAA	ATGATCTCTT	CCTCTGTGAC	ACCAACACCT	GTAATTTTGA	TGGGGAATGT	240
TTAAGAATTG	GAGACACTGT	GACTTGCGTC	TGTCAGTTCA	AGTGCAACAA	TGACTATGTG	300
CCTGTGTGTG	GCTCCAATGG	GGAGAGCTAC	CAGAATGAGT	GTTACCTGCG	ACAGGCTGCA	360
TGCAAAACAGC	AGAGTGAGAT	ACTTGTGGTG	TCAGAAGGAT	CATGTGCCAC	AGATGCAGGA	420
TCAGGATCTG	GAGATGGAGT	CCATGAAGGC	TCTGGAGAAA	CTAGTCAAAA	GGAGACATCC	480
ACCTGTGATA	TTTGCCAGTT	TGGTGACGAA	TGTGACGAAG	ATGCCGAGGA	TGTCTGGTGT	540
GTGTGTAATA	TTGACTGTTC	TCAAACCAAC	TTCAATCCCC	TCTGCGCTTC	TGATGGGAAA	600
TCTTATGATA	ATGCATGCCA	AATCAAAGAA	GCATCGTGTC	AGAAACAGGA	GAAAATTGAA	660
GTCATGTCTT	TGGGTCGATG	TCAAGATAAC	ACAACCTACAA	CTACTAAGTC	TGAAGATGGG	720
CATTATGCAA	GAACAGATTA	TGCAGAGAAT	GCTAACAAAT	TAGAAGAAAG	TGCCAGAGAA	780
CACCACATAC	CTTGTCCCGA	ACATTACAA	GGCTTCTGCA	TGCATGGGAA	GTGTGAGCAT	840
TCTATCAATA	TGCAGGAGCC	ATCTTGCAAG	TGTGATGCTG	GTTATACTGG	ACAACACTGT	900
GAAAAAAGG	ACTACAGTGT	TCTATACGTT	GTTCCCGGTC	CTGTACGATT	TCAGTATGTC	960
TTAATCGCAG	CTGTGATTGG	AACAATTTCAG	ATTGCTGTCA	TCTGTGTGGT	GGTCTCTGTC	1020
ATCACAGGA	AATGCCCCAG	AAGCAACAGA	ATTCACAGAC	AGAAGCAAAA	TACAGGGCAC	1080
TACAGTTCAG	ACAATAACAAC	AAGAGCGTCC	ACGAGGTTAA	TCTGA		

Seq ID NO: 580 Protein sequence
Protein Accession #: NP_057276.2

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DRENDLFLCD	TNTCKFDGEC	LRIGDVTVCV	CQFKCNNDYV	PVCGSNGESY	QNECYLRQAA	120
CKQQSEILVV	SEGSCATDAG	SGSGDGVHEG	SGETSQKETS	TCDICQFGAE	CDEDAEDVWC	180
VCNIDCSQTN	FNPLCASDGK	SYDNACQIKE	ASCQKQEKIE	VMSLGRQCDN	TTTTTKSEDG	240
HYARTDYAEN	ANKLEESARE	HHIIPCEHYN	GFCMHGKCEH	SINMQEPSCR	CDAGYTQHC	300
EKKDYSVLVY	VPGEVRFQYV	LIAAVIGTIQ	IAVICVVVLC	ITRKCPRSNR	IHRQKQNTGH	360
YSSDNTTRAS	TRLI					

Seq ID NO: 581 DNA sequence
Nucleic Acid Accession #: S78203.1
Coding sequence: 1..2190

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GAGGTACCAC	CTCGACCACC	TAGCCCTCCA	AAGAAGCCAT	CTCCGACAAT	CTGTGGCTCC	120
AACATATCCAC	TGAGCATTGC	CTTCATTGTG	GTGAATGAAT	TCTGCGAGCG	CTTTCTCTAT	180
TATGGAATGA	AAGCTGTGCT	GATCCTGTAT	TTCCTGTATT	TCCGTGACTG	GAATGAAGAT	240
ACCTCCACAT	CTATATACCA	TGCCTTCAGC	AGCCTCTGTT	ATTTTACTCC	CATCCTGGGA	300
GCAGCCATTG	CTGACTCGTG	GTTGGGAAAA	TTCAAGACAA	TCATCTATCT	CTCCTTGGTG	360
TATGTGCTTG	GCCATGTGAT	CAAGTCCTTG	GGTGCCTTAC	CAATACTGGG	AGGACAAGTG	420
GTACACACAG	TCCTATCATT	GATCGGCCTG	AGTCTAATAG	CTTTGGGGAC	AGGAGGCATC	480
AAACCTGTG	TGGCAGCTTT	TGGTGGAGAC	CAGTTTGAAG	AAAAACATGC	AGAGGAACGG	540
ACTAGATACT	TCTCAGTCTT	CTACCTGTCC	ATCAATGCAG	GGAGCTTGAT	TTCTACATTT	600
ATCACACCCA	TGCTGAGAGG	AGATGTGCAA	TGTTTTGGAG	AAGACTGCTA	TGCATTGGCT	660
TTTGGAGTTC	CAGGACTGCT	CATGTAATT	GCACTTGTTG	TGTTTGCAAT	GGGAAGCAAA	720
ATATACAATA	AACCAACCCC	TGAAGGAAAC	ATAGTGGCTC	AAGTTTTCAA	ATGTATCTGG	780
TTTGTCTATT	CCAATCGTTT	CAAGAACCGT	TCTGGAGACA	TTCCAAGCG	ACAGCACTGG	840
CTAGACTGGG	CAGCTGAGAA	ATATCCAAG	CAGCTCATT	TGGATGTAAA	GGCACTGACC	900
AGGGTACTPAT	TCCTTTATAT	CCCATTGCC	ATGTTCTGGG	CTCTTTTGA	TCAGCAGGGT	960
TACAGATGGA	CTTTGCAAGC	CATCAGGATG	AATAGGAATT	TGGGGTTTTT	TGTGCTTCAG	1020
CCGACCAGGA	TGCAGGTTCT	AAATCCCTTT	CTGGTCTTTA	TCTTCATCCC	GTTGTTTGAC	1080
TTTGTCTATT	ATCGTCTGGT	CTCCAAGTGT	GGAATTAAC	TCTCATCACT	TAGGAAAAATG	1140
GCTGTTGGTA	TGATCCTAGC	GTGCCCTGCA	TTTGCACTTG	CGGCAGCTGT	AGAGATAAAA	1200
ATAAATGAAA	TGGCCCCAGC	CCAGTCAGGT	CCCCAGGAGG	TTTTCTTACA	AGTCTTGAAT	1260
CTGGCAGATG	ATGAGGTGAA	GGTGACAGTG	GTGGGAAATG	AAAACAATTC	TCTGTTGATA	1320
GAGTCCATCA	AATCCTTTCA	GAAAACACCA	CACATTATCCA	AACTGCACCT	GAAAAACAAA	1380
AGCCAGGATT	TTCACTTCCA	CCTGAAATAT	CACAAATTTGT	CTCTCTACAC	TGAGCATTTCT	1440
GTGCAGGAGA	AGAACTGGTA	CAGTCTTGTC	ATTCGTGAAG	ATGGGAACAG	TATCTCCAGC	1500

ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGGT 1560
 AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT 1620
 GAAGACTATG GTGTGTCTGC TTATAGAAGT GTGCAAGAG GAGAATACCC TGCAGTGCAC 1680
 TGTAGAACAG AAGATAAGAA CTTTCTCTG AATTGGGTC TTCTAGACTT TGGTGCAGCA 1740
 TATCTGTTTG TTATTACTAA TAACACCAAT CAGGCTCTTC AGGCCTGGAA GATTGAAGAC 1800
 ATTCCAGCCA AAAAAATGTC CATTGCGTGG CAGCTACCAC AATATGCCCT GGTACAGCT 1860
 GGGGAGGTCA TGTTCTCTGT CACAGGTCTT GAGTTTTCTT ATTCTCAGGC TCCCTCTAGC 1920
 ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCGTG 1980
 CTTGTTGTGG CACAGTCTAG TGGCCTGGTA CAGTGGGCGG AATTCATTTT GTTTTCCTGC 2040
 CTCCTGCTGG TGATCTGCCT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAAG 2100
 ACAGAGGATA TGCGGGGTCC AGCAGATAAG CACATTCCTC ACATCCAGGG GAACATGATC 2160
 AAACTAGAGA CCAAGAAAGC AAAACTCTGA

Seq ID NO: 582 Protein sequence
 Protein Accession #: AAB34388.1

1 11 21 31 41 51
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 YGMKAVLILY FLYFLHWNED TSTSIYHAFS SLCYFTPILG AAIADSWLKG FKTI IYLSLV 120
 YVLGHVILSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFGGD QFEEKHAEER 180
 TRYFSVFYLS INAGSLISTF ITPMLRGDVQ CFGEDCYALA FGVPGLLMVI ALVVVFAMGSK 240
 IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIPKRQHW LDWAAEKYPK QLIMDVKALT 300
 RVLFYLIPLP MFWALLDQGG SRWTLQAIMR NRNLGFFVLQ PDQMQLVLPF LVLIFIPLED 360
 FVIYRLVSKG GINFLSLRKM AVGMILACLA PAVAAAVEIK INEMAPAQSG PQEVFLQVLN 420
 LADDEVKVTV VGNENNSLLI ESIKSFQKTP HYSKHLHLTK SQDFHFLKY HNLSLYTEHS 480
 VQEKNWYSLV IREDGNSISS MMVKDTESEK TNGMTTVRFV NTLHKDVNIS LSTDTSLNVG 540
 EDYGVSAVRT VQRGEYPAHV CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQAWKIED 600
 IPANKMSIAW QLPQYALVTA GEVMSVSVGL EFSYSQAPSS MKSVLQAOWL LTIAGVNIIV 660
 LVVAQFSLVQ QWAEFILFSC LLLVICLIFS IMGYVYPVK TEDMRGPADK HIPHIQGNMI 720
 KLETKKTKL

Seq ID NO: 583 DNA sequence
 Nucleic Acid Accession #: NM_032642.1
 Coding sequence: 184..1263

1 11 21 31 41 51
 | | | | |
 GACCATTAGC AGGCACCCAG GCCTGTCTTT GGCTCGGAAA CGGTGGCCCC CAATGTAGCC 60
 TAGTTTGAAC CTAGGAACCTG CAGGACCAGA GAGATTCCAC TGGAGCCTGA TGGACGGGTG 120
 ACAGAGGGAA CCTACTCTG GAAACTGTCA GTCCACGGGC ACTGGGGAGG GCTGAGGCGG 180
 ACCATGCCCA GCCTGCTGCT GCTGTTCACG GCTGCTCTGC TGTCCAGCTG GGCTCAGCTT 240
 CTGACAGACG CCAACTCTCT GTGGTCATTA GCTTTGAACC CGGTGCAGAG ACCCGAGATG 300
 TTTATCATCG GTGCCACGCC CGTGTGCAGT CAGCTTCCCG GGCTCTCCCC TGGCCAGAGG 360
 AAGCTGTGCC AATTGTACCA GGAGCACATG GCCTACATAG GGGAGGGAGC CAAGACTGGC 420
 ATCAAGGAAT GCCAGCACCA GTTCCGGCAG CGCGGTGGGA ATTGCAGCAC AGCGGACAAAC 480
 GCATCTGTCT TTGGGAGAGT CATGCAGATA GGCAGCCGAG AGACCGCCTT CACCCACGCG 540
 GTGAGCGCCG CGGGCGTGGT CAACGCCATC AGCCGGGCGT GCCGCGAGGG CGAGCTCTCC 600
 ACCTGCGGCT GCAGCCGGAC GCGCGGGCCC AAGGACCTGC CCCGGGACTG GCTGTGGGGC 660
 GGCTGTGGGG ACAACGTGGA GTACGGCTAC CGCTTCGCCA AGGAGTTTGT GGATGCCCGG 720
 GAGCGAGAGA AGAATTTTGC CAAAGGATCA GAGGAGCAGG GCCGGGTGCT CATGAACCTG 780
 CAAAACAACG AGGCCGCTG CAGGGCTGTG TATAAGATGG CAGACGTAGC CTGCAAAATG 840
 CACGGCGTCT CGGGGTCTCT CAGCCTCAAG ACCTGCTGGC TGCAGCTGGC CGAGTTCCGC 900
 AAGTTCGGGG ACCGGCTGAA GGAGAAGTAC GACAGCGCGG CCGCATGCGC GGTACCCGCG 960
 AAGGGCCGGC TGGAGCTGGT CAACAGCCGC TTCACCCAGC CCACCCCGGA GGACCTGGTC 1020
 TATGTGGACC CCAGCCCCGA CTACTGCTG CGCAACGAGA GCACGGGCTC CCTGGGCACG 1080
 CAGGGCCGCT TCTGCAACAA GACCTCGGAG GGCATGGATG GCTGTGAGCT CATGTGCTGC 1140
 GGGCGTGGCT ACAACCAAGT CAAGAGCGTG CAGGTGGAGC GCTGCCATCG CAAGTTCAC 1200
 TGGTGTCTGT TCGTCAAGTG TAAGAAGTGC ACGGAGATCG TGGACCAGTA CATCTGTAAA 1260
 TAGCCCGGAG GGCCTGCTCC CGGCCCCCC TGCACCTGCT CTCACAAAGG TCTATATTAT 1320
 ATAAATCTAT ATAAATCTAT TTTATATTG TATAAGTAAA TGGGTGGGTG CTATACAATG 1380
 GAAAAGATGA AATGGAAAAG AAGAGCTTAT TTAAGAGACG CTGGAGATCT CTGAGGAGTG 1440
 GACTTTGCTG GTTCTCTCTT CTTGTTGGGT GGGAGACAGG GCTTTTCTC TCCCTCTGGC 1500
 GAGGACTCTC AGGATGTAGG GACTTGAAAA TATTTACTGT CTGTCCACCA CGGCCCTGGG 1560
 GAGGAGGTTT GTGGTTGGAT GGAGGAGATG ATCTTGTCTG GAAGCTCAGA GTCTTTGTTG 1620
 GTTAGAGGAC TGCTGTGAT CCTGGCCACT AGGCCAAGAG GCCCTATGAA GGTGGCGGGA 1680
 ACTCAGCTTC AACCTCGATG TCTTCAGGGT CTTGTCCAGA ATGTAGATGG GTTCCGTAAG 1740
 AGGCCTGGTG CTCTCTTACT CTTTCATCCA CGTGCACTTG TGCGGCATCT GCAGTTTACA 1800
 GGAACGGCTC CTTCCTTAAA ATGAGAAGTC CAAGGTCATC TCTGGCCAG TGACCACAGA 1860
 GAGATCTGCA CCTCCCGGAC TTCAGGCTG CTTTCCAGC GAGAATCTT CATCCTCCAC 1920
 GGTCACTAG CTCTACCTG AAGAGGAAAG GGGGCCATTT GACCTGACAT GTCAGGAAAG 1980
 CCCTAAACTG AATGTTTGGC CTGGGCTGC AGAAGCCAGG GTGCATGACC AGGCTGCGTG 2040
 GACGTTATAC TGTCTTCCCC CACCCCGGGG GAGGGGAAGC TTGAGCTGCT GCTGTCACTC 2100
 CTCCACCGAG GGAGGCTCA CAAACACAG GACGCTGCAA CGGGTCAGG TGGCGGGCCC 2160
 GGCGTGCTCA TCATCTCTGC CCCAGGTGTA CGGTTTCTCT CTGACATTAA ATGCCCTTCA 2220
 TGGAAAAAAA AAAAAGAAAA AAAAAAAA AA

Seq ID NO: 584 Protein sequence
 Protein Accession #: NP_116031.1

1 11 21 31 41 51
 | | | | |
 MPSSLLLFLLT ALLSSWAQLL TDANSWWSLA LNPVQRPEMF IIGAQPVCSSQ LPGLSPGQK 60
 LCQLYQEHMA YIGEGAKTGI KECQHQFRQR RWNCTADNA SVFGRVMQIG SRETAFTHAV 120

SAAGVVNAIS RACREGELST CGCSRTARPK DLPRDLWGG CGDNVEYGYR FAKEFVDARE 180
 REKNFAKGE EQGRVLMNLQ NNEAGRRAVY KMADVACKCH GVSQSCSLKT CWLQLAEPRK 240
 VGDRLEKEKYD SAAMMRVTRK GRLELVNSRF TQPTPEDLVY VDFSPDYCLR NESTGSLGTQ 300
 GRLCNKTSSEG MDGCELMCCG RGYNQFKSVQ VERCHCKFHW CCFVRCKKCT EIVDQYICK

Seq ID NO: 585 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1479

1 11 21 31 41 51
 ATGGCTTTGA ACTCAGGGTC ACCACCAGCT ATTGGACCTT ACTATGAAAA CCATGGATAC 60
 CAACCGGAAA ACCCTATCC CGCACAGCCC ACTGTGGTCC CCACTGTCTA CGAGGTGCAT 120
 CCGGCTCAGT ACTACCCGTC CCCCGTGCCC CAGTACGCCC CGAGGGTCCT GACGCAGGCT 180
 TCCAACCCCG TCGTCTGCAC GCAGCCCAAA TCCCCATCCG GGACAGTGTG CACCTCAAAG 240
 ACTAAGAAAG CACTGTGCAT CACCTTGACC CTGGGGACCT TCCTCGTGGG AGCTGCGCTG 300
 GCCGCTGGCC TACTCTGGAA GTTCATGGGC AGCAAGTGCT CCAACTCTGG GATAGAGTGC 360
 GACTCCTCAG GTACCTGCAT CAACCCCTCT AACTGGTGTG ATGGCGTGTG ACACTGCCCC 420
 GGGCGGGAGG ACAGAAATCG GTGTGTTTCG CTCTACGGAC CAAACTTCAT CCTTCAGGTG 480
 TACTCATCTC AGAGGAAGTC CTGGCACCTT GTGTGCCAAG ACGACTGGAA CGAGAACTAC 540
 GGGCGGGCGG CTGTCAGGGA CATGGGTAT AAGAATAATT TTTACTCTAG CCAAGGAATA 600
 GTGGATGACA GCGGATCCAC CAGCTTTATG AACTGAACA CAAGTGCCGG CAATGTCGAT 660
 ATCTATAAAA AACTGTACCA CAGTGATGCC TGTTCCTCAA AAGCAGTGGT TTCTTTACGC 720
 TGTATAGCCT CGGGGGTCAA CTTGAATCA AGCCCGCAGA GCAGGATCGT GGGCGGCGAG 780
 AGCGCGCTCG CCGGGGCGCTG GCCCTGGCAG GTCAACCTGC ACGTCCAGAA CGTCCACGTG 840
 TGGCGAGGCT CCATCATCAC CCCCGAGTGG ATCGTGACAG CCGCCCACTG CTGGAAGAAA 900
 CCTCTTAACA ATCCATGGCA TTGGACGGCA TTTGCGGGGA TTTTGAGACA ATCTTTTCATG 960
 TTCTATGGAG CCGGATACCA AGTAGAAAAA GTGATTCTC ATCCAAATTA TGACTCCAAG 1020
 ACCAAGAACAT ATGACATTGC GCTGATGAAG CTGCAGAACG CTCTGACTTT CAACGACCTA 1080
 GTGAAACACG TGTGTCTGCC CAACCCAGGC ATGATGCTGC AGCCAGAACA GCTCTGCTGG 1140
 ATTTCCGGGT GGGGGGCCAC CGAGGAGAAA GGAAGACCT CAGAAAGTGT GAACGCTGCC 1200
 AAGGTGCTTC TCATTGAGAC ACAGAGATGC AACAGCAGAT ATGCTATGA CAACCTGATC 1260
 ACACGACCCA TGATCTGTGC CGGCTTCTTG CAGGGGAACG TCGATTCTTG CCAGGGTGAC 1320
 AGTGGAGGGC CTCTGGTTCAC TTCGAAGAAC AATATCTGGT GGTGATAGG GGATACAAGC 1380
 TGGGGTTCTG GCTGTGCCAA AGCTTACAGA CCAGGAGTGT ACGGGAATGT GATGGTATTC 1440
 ACGGACTGGA TTTATCGACA AATGAGGGCA GACGGCTAA

Seq ID NO: 586 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MALNSGSPPA IGPIYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTA 60
 SNPVVCTQPK SPSTGTCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120
 DSSGTCINPS NWCNGVSHCP GGEDENRCVR LYGNPFIQV YSSQRKSWHP VCQDDWNENY 180
 GRAACRDMGY KNNFYSSQGI VDDSGSTSEFM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240
 CIACGVNLNS SRQSRIVGGE SALPGANFWQ VSLHVQNVHV CGGSIITPEW IVTAACVCEK 300
 PLNNPWHWTA FAGILLRQSFY FYGAGYQVEK VISHPNYDSK TKNNIDIALMK LQKPLTFNDL 360
 VKPVCLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLIIETQRC NSRYVVDNLI 420
 TPAMICAGFL QGNVDSQGD SGGPLVTSKN NIWWLIGDTS WSGGCAKAYR PGVYGVNMVF 480
 TDWIYRQMRA DG

Seq ID NO: 587 DNA sequence
 Nucleic Acid Accession #: NM_005656.1
 Coding sequence: 57..1535

1 11 21 31 41 51
 GTCATATTGA ACATTCACAGA TACCTATCAT TACTCGATGC TGTGATAAC AGCAAGATGG 60
 CTTTGAATCT AGGGTACCCA CCAGCTATTG GACCTTACTA TGAAAAACCAT GGATACCAAC 120
 CGGAAAAACC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCCG 180
 CTCAGTACTA CCCGTCCTCC GTGCCCCAGT ACGCCCGGAG GGTCTTGACG CAGGCTTCCA 240
 ACCCCGTCGT CTGCACGAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAAGACTA 300
 AGAAAGCACT GTGCATCACC TTGACCTGCG GACCTTCCT CGTGGGAGCT GCGCTGGCCG 360
 CTGGCCTACT CTGGAAGTTC ATGGGCAGCA AGTGCTCCAA CTCTGGGATA GAGTGCAGCT 420
 CCTCAGGTAC CTGCATCAAC CCCTCTAACT GGTGTGATGG CGTGTACAC TGCCCCGGCG 480
 GGGAGGACGA GAATCGGTGT GTTCGCTCT ACAGACCAAA CTTTCATCTT CAGATGTACT 540
 CATCTCAGAG GAAGTCTCTG CACCCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600
 GGGCGGCTG CAGGGACATG GGCTATAAGA ATAATTTTTC CTCTAGCCAA GGAATAGTGG 660
 ATGACAGCGG ATCCACGAGC TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT 720
 ATAAAAAAT GTACACAGT GATGCCTGTT CTTCAAAAGC AGTGGTTTCT TTAGCTGTGTT 780
 TAGCCTGCGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG 840
 CGCTCCCGGG GCGCTGGCCC TGGCAGGTCA GCCTGCACGT CCAGAACGTC CAGCTGTGCG 900
 GAGGCTCCAT CATCACCCCG GAGTGGATCG TGACAGCCGC CCACTCGGTG GAAAAACCTC 960
 TTAACAATCC ATGGCATTTG ACGGCATTTC CGGGGATTTT GAGACAATCT TTCTATGTTCT 1020
 ATGGAGCCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA 1080
 AGAACAATGA CATTGCGCTG ATGAAGCTGC AGAAGCCTCT GACTTTCAAC GACCTAGTGA 1140
 AACCAAGTGT TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT 1200
 CCGGGTGGGG GGCACCCGAG GAGAAAGGGA AGACCTCAGA AGTGTGAAC GCTGCCAAGG 1260
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAAC CTGATCACAC 1320
 CAGCCATGAT CTGTGCCGGC TTCCTGCAGG GGAACGTCGA TTCTTGCCAG GGTGACAGTG 1380
 GAGGGCCTCT GGTCACTTCG AACACAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440
 GTTCTGGCTG TCCCAAGGCT TACAGACCAG GAGTGACGG GAATGTGATG GTATTACGG 1500
 ACTGGATTAT TCGACAAATG AAGGCAACAG GCTAATCCAC ATGGTCTTCG TCCTTGACGT 1560

CGTTTTACAA GAAACAATG GGGCTGGTTT TGCTTCCCCG TGCATGATTT ACTCTTAGAG 1620
 ATGATTCAGA GGTCACTTCA TTTTATTAA ACAGTGAAC TGTCTGGCTT TGGCACTCTC 1680
 TGCACATCTG TGCAGGCTGC AGTGGCTCCC CTGCCAGACC TGTCTCTCCT AACCCCTTGT 1740
 5 CCGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGGAAGAGG 1800
 GTTGGAGGCT GCCCCATTG AGATCTTCTT GCTGAGTCC TCCAGGGGC CAATTTTGGG 1860
 TGAGCATGGA GCTGTCACTT CTGAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920
 GGAAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTTGGTAGTG 1980
 TCCCCAGCCT ACTTCACAAG GGGATTTTGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040
 10 GATGGTGGCC AGAAATAAAG GGACCAGCCC TTCATGGGTG GTGACGTGGT AGTCACTTGT 2100
 AAGGGGAACA GAAACATTTT TGTCTTATG GGGTGAGAA ATAGACAGTG CCCTTGGTGC 2160
 GAGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220
 CATTTGGGTG GGCCTCTGGG AGGGAGACTC AGCCTTCTCT CTCATCTCTC CTGACCCCTG 2280
 TCCTAGCACC CTGGAGAGTG AATGCCCTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340
 15 ATGTCGGCCT CTTGAGCCTT GATAGTCATT GGAATTTAG GTCCATGGG GAAATCAAGG 2400
 ATGCTCAGTT TAAGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
 CTGAGTTCAA AGCCATCTT

Seq ID NO: 588 Protein sequence
 Protein Accession #: NP_005647.1

1 11 21 31 41 51
 MALNSGSPPA IGPYYENHGY OPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTOA 60
 25 SNPVVCTQPK SPSGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120
 DSSGTCINPS NWCDGVSHCP GGEDENRCVR LYGNPFILOM YSSQRKSWHP VCQDDWNENY 180
 GRAACRDMGY KNNFYSSQGI VDDSGSTSEFM KLNSTAGNVD IYKKLYHSDA CSSKAVVSLR 240
 CLACGVNLNS SRQSRIVGGE SALPGAWPQV VSLHVQNVHV CGGSIITPEW IVTAAHCVKE 300
 PLNNPWHWTA FAGILRQSFM PYGAGYQVQK VISHPNYDSK TKNNIDIALMK LQKPLTFNDL 360
 30 VKPVCLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLIIETQRC NSRVVYDNL 420
 TPAMICAGFL QGNVDSQGD SGGPLVTSNN NIWVLIGDTS WSGCAKAYR PGVYGNVMVF 480
 TDWIYRQMK NG

Seq ID NO: 589 DNA sequence
 Nucleic Acid Accession #: NM_001935.1
 Coding sequence: 1..2301

1 11 21 31 41 51
 40 ATGAAGACAC CGTGAAGAT TCTTCTGGGA CTGCTGGGTG CTGCTGCGCT TGTCAACATC 60
 ATCACCGTGC CCGTGGTTCT GCTGAACAAA GGCACAGATG ATGCTACAGC TGACAGTCGC 120
 AAAAATTACA CTCTAACTGA TTACTTAAAA AATACTTATA GACTGAAGTT ATACTCCTTA 180
 AGATGGATTT CAGATCATGA ATATCTCTAC AAACAAGAAA ATAATATCTT GGTATTCAAT 240
 GCTGAATATG GAAACAGCTC AGTTTTCTTG GAGAACAGTA CATTGTGATG GTTTGGACAT 300
 45 TCTATCAATG ATTATTTCAAT ATCTCTGAT GGGCAGTTTA TTCTCTAGA ATACAACATC 360
 GTGAAGCAAT GGAGGCATTC CTACACAGCT TCATATGACA TTTATGATTT AAATAAAAGG 420
 CAGCTGATTA CAGAAGAGAG GATTCCAAAC AACACACAGT GGGTCACATG GTCACCAGTG 480
 GGTCATAAAT TGGCATATGT TTGGAACAAT GACATTTATG TTAATAATGA ACCAAATTTA 540
 CCAAGTTACA GAATCATATG GACGGGAAA GAAGATATAA TATATAATGG AATAACTGAC 600
 50 TGGGTTTATG AAGAGGAAGT CTTCACTGCC TACTCTGCTC TGTGGTGGTC TCCAAACGGC 660
 ACTTTTTTAG CATATGCCCA ATTTAACGAC ACAGAAGTCC CACTTATTGA ATACTCCTTC 720
 TACTCTGATG AGTCACTGCA GTACCCAAAG ACTGTACGGG TTCCATATCC AAAGGCAGGA 780
 GCTGTGAATC CAACTGTAAA GTTCTTTGTT GTAAATACAG ACTCTCTCAG CTCAGTCACC 840
 AATGCAACTT CCATACAAAT CACTGCTCCT GCTTCTATGT TGATAGGGGA TCACTACTTG 900
 55 TGTGATGTGA CATGGGCAAC ACAAGAAAGA ATTTCTTTGC AGTGGCTCAG GAGGATTCAG 960
 AACTATTCCG TCATGGATAT TTGTGACTAT GATGAATCCA GTGGAAGATG GAACTGCTTA 1020
 GTGGCAGGCG AACACATTGA AATGAGTACT ACTGGCTGGG TTGGAAGATT TAGGCCCTCA 1080
 GAACCTCAT TTAACCTTGA TGGTAATAGC TTCTACAAGA TCATCAGCAA TGAAGAAGGT 1140
 TACAGACACA TTTGCTATTT CCAATAGAT AAAAAAGACT GCACATTTAT TACAAAAGGC 1200
 60 ACCTGGGAAG TCATCGGGAT AGAAGCTCTA ACCAGTGATT ATCTATACTA CATTAGTAAT 1260
 GAATATAAAG GAATGCCAGG AGGAAGGAAT CTTTATAAAA TCCAACCTAG TGACTATACA 1320
 AAAGTGACAT GCCTCAGTTG TGAGCTGAAT CCGGAAAGGT GTCAGTACTA TTCTGTGTCA 1380
 TTCAGTAAAG AGGCGAAGTA TTATCAGCTG AGATGTTCCG GTCCTGGTCT GCCCTCTAT 1440
 ACTCTACACA GCAGCGTGAA TGATAAGGG CTGAGAGTCC TGGGAAGACA TTCAGCTTTG 1500
 65 GATAAAATGC TGCAGATGT CCAGATGCCC TCCAAAAAAC TGGACTTCAT TATTTTGAAT 1560
 GAAACAAAAT TTTGGTATCA GATGATCTTG CCTCCTCATT TTGATAAATC CAAGAAATAT 1620
 CCTCTACTAT TAGATGTGTA TGCAGGCCCA TGTAGTCAAA AAGCAGACAC TGTCTTCAGA 1680
 CTGAACCTGG CCCTTACCT TGCAAGCACA GAAAAATTA TAGTAGCTAG CTTTGTATGGC 1740
 70 AGAGGAAGTG GTTACCAAGG AGATAAGATC ATGCATGCAA TCAACAGAAG ACTGGGAACA 1800
 TTTGAAGTTG AAGATCAAAT TGAAGCAGCC AGACAATTTT CAAAAATGGG ATTTGTGGAC 1860
 AACAAACGAA TTGCAATTTG GGGCTGGTCA TATGGAGGGT ACGTAACCTC AATGGTCTCTG 1920
 GGATCGGGAA GTGGCGTGT CAAGTGTGGA ATAGCCGTGG CGCTGTATC CCGGTGGGAG 1980
 TACTATGACT CAGTGTACAC AGAACGTTAC ATGGGTCTCC CAACTCCAGA AGACAACCTT 2040
 75 GACCATTACA GAATTTCAAC AGTCATGAGC AGAGCTGAAA ATTTTAAACA AGTTGAGTAC 2100
 CTCCTTATTC ATGGAACAGC AGATGATAAC GTTCACTTTC AGCAGTCAGC TCAGATCTCC 2160
 AAAGCCCTGG TCGATGTTGG AGTGGATTTC CAGGCAATGT GGTATACTGA TGAAGACCAT 2220
 GGAATAGCTA GCAGCAGAG ACACCAACAT ATATATACCC ACATGAGCCA CTTCAATAAA 2280
 CAATGTTTCT CTTTACCTTA G

Seq ID NO: 590 Protein sequence
 Protein Accession #: NP_001926.1

1 11 21 31 41 51
 MKTPWKILLG LLGAAALVTI ITVPVLLNKG GTDDATADSR KTYLTLDYLK NTYRLKLYSL 60

RWISDHEYLY KQENNILVFN AEYGNSSVFL ENSTFDEFGH SINDYSISPD GQFILLEYN 120
 VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVTWSPV GHKLAYVWNN DIYVKIEPNL 180
 PSYRITWIGK EDIIYNGITD WYVEEVFSA YSALWWSPNG TFLAYAQFND TEVPLIEYSF 240
 YSDESLOQPK TVRVFPYKAG AVNPTVKFFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
 CDVTWATQER ISLQWLRRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGWVGRFRPS 360
 EPHTFLDGNF FYKIIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYIYSN 420
 EYKGMPPGRN LYKIQLSDYT KVTCLSCSELN PERCQYYSVS FSKEAKYQL RCSGPGPLPLY 480
 TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDIFIILN ETKFWYQML PPHFDKSKKY 540
 PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFDG RSGSYQGDKI MHAINRRLGT 600
 FEVEDQIEAA RQFSKMGFVD NKRIAIWGS YGGYVTSMLV GSGSGVFKCG IAVAPVSRWE 660
 YYDSVYTERY MGLPTPEDNL DHYRNSTVMS RAENFKQVEY LLIHGTADDN VHFQQAQIS 720
 KALVDVGVD FQAMWYTDDEH GIASSTAQH IYTHMSHFIF QCFSLP

Seq ID NO: 591 DNA sequence

Nucleic Acid Accession #: NM_016077.1
Coding sequence: 128..667

1 11 21 31 41 51
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 TCGCTTTGTG ATTCTTGATC CGGAACCTTG TCACCCAGGA ACCCCGGAAG AGGTAGCTCA 60
 CGCGATAGAA ACGTGTTCGC TTGCCAGAA GAAGGGAAGG CGCAGTGAG GAAAGGAGGT 120
 ACTGTAGATG CCTCCAAAT CTTGGTTAT GGAATATTG GCTCATCCA GTACACTCGG 180
 CTTGGCTGTT GGAGTTGCTT GTGGCATGTG CTGGGCTGG AGCCTTCGAG TATGCTTTGG 240
 GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT 300
 CTTGGGAGAG AGCGGGGAGT ACAAGATGAT TCTTGTGGTT CGAAATGACT TAAAGATGGG 360
 AAAAGGGAAA GTGGCTGCC AGTGCTCTCA TGCTGCTGTT TCAGCTTACA AGCAGATTCA 420
 AAGAAGAAAT CTTGAAATGC TCAAACAATG GGAATACTGT GCCAGCCCA AGGTGGTGGT 480
 CAAAGCTCCT GATGAAGAAA CCTGTATTGC ATTATTGGCC CATGCAAAA TGCTGGGACT 540
 GACTGTAAGT TTAATTCAAG ATGCTGGACG TACTCAGATT GCACCAGGCT CTCAACTGT 600
 CCTAGGGATT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCACTGGTC ACCTAAACT 660
 TTACTAGGTG GTGCTTTGATA TGACAACAAC CCCTCCATCA CAAGTGTGTT AAGCCTGTCA 720
 GATTCTAACA ACAAAAGCTG AATTTCTTCA CCAACTTAA ATGTTCTTGA GATGAAATA 780
 AAACCTATT CCACTGTTCTA AAAAA

Seq ID NO: 592 Protein sequence

Protein Accession #: NP_057161.1

1 11 21 31 41 51
 | | | | |
 MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHT DTESEASILG 60
 DSGEYKMLIV VRNDLKMKGK KVAAQCASHA VSAYKQIQRR NPMLKQWEY CGQPKVVVKA 120
 PDEETLIALL AHAKMLGLTV SLIQDAGRTQ IAPGSQTVLG IGPGPADLID KVTGHLKLY

Seq ID NO: 593 DNA sequence

Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1896

1 11 21 31 41 51
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 ATGCGCGCGG TGCCGCTGCC CGCCCGCTC CTGCGCTGC TGCTGCTGC GCTCCTGGCC 60
 GCTCCGCGCG CCCGCGCCAG CAGAGCCGAG TCCGCTCTCC CGCCGTGGCC CGAACCCGAG 120
 CGCGAGTCGC GGCACCCGCC CGGCCCGGG CCCGGGAACA CCACCCGGTT TGGGTCTGGG 180
 GCGGCGGGCG GCAGCGGCAG CTCAGCTCC AACAGCAGTG GCGACGCTT GGTGACCCGC 240
 ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAGGCAG CCGTGATCGT GCGCTTCGCC 300
 TTTACACCCC TCCTCATCGC CTGCGCTGCT CTGCGCTGCT TCAGGTCCGG AAAGAGGTGA 360
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCAGTGGG AATGGCGCCA 420
 CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
 TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGCTGCC AGACGCTACT GACAGTTCTT 540
 GTGCCCCAC CCTTCATCTT CGACATTGAC CTTCCAGCAA GATGCAGTGG AAGGCCTGAT 600
 GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAGTTGG 660
 TCAGCTGCRA CTTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTGCGT CGGAGGTGTT 720
 GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTC AGGCATCTGC 780
 TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCACCACAA TGGAGTTGCT TCTGCCACCC 840
 TTTGGGCATC CTTTAAAGT GCCCCTACT TCTACTCCC ATGGTTTTG ACAACTGCAG 900
 CTGAATCTCA TGGAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGTCTCATCT 960
 GCCAGGTGCT TGCCACTGGT CTTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
 CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTACAC ACAAAACCATG 1080
 AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGGCCAGC GGGGCACCTT TTGTGAAGAC 1140
 AGAGCAGTGA CTAAGGTTCT CCAGGCTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
 GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
 ACCATCCTG TCAGGTGGC TCGTTAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
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 GATGGCAGAT GCCAGAAGAT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
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Seq ID NO: 594 Protein sequence

Protein Accession #: FGENESH predicted

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KTRKYDIIT TPAERVMAP LNEDEDEDED STVFDIKYRV SLPAALRRQL PGCTLLTVP 180
VPPPFILDID LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV 240
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPP FGHFPKVPPT STPHGFRQLQ 300
10 LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAESDLPN PWWHFSATGS PIKTLYTQTM 360
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THPVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
ICLPCCAVEH LREAKRSSVT VLASFEQSPQ KAAAHAHEPV KRGPSCQLTR HTCPCGWGITH 540
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Seq ID NO: 595 DNA sequence
Nucleic Acid Accession #: NM_021614.1
Coding sequence: 1..1740

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25 TCCTCAGCCC CCGAGATCGT GGTGTCTAAG CCCGAGCACA ACAACTCCAA CAACCTGGCG 240
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CACGGCAGCA GCAGTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAAG 360
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Seq ID NO: 596 Protein sequence
Protein Accession #: NP_067627.1

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LLGLIIVYHA REIQLFMVND GADDWRIAMT YERIFFICLE ILVCAIHPI GNYTFTWTAR 240
LAFSYPSTT TADVDIILSI PMFLRLYLIA RVMLLHSLKF TDASSRSIGA LNKINFNTRF 300
VMKTLMTICP GTVLLVFSIS LWIIAAWTVR ACERYHDQDQ VTSNFLGAMW LISITFLSIG 360
YGDMVPNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHNF MDTQLTKRVK 420
70 NAAANVLRET WLIYKNTKLV KKIDHAKVRK HQRKFLQAIH QLRSVKMEQR KLNDQANTLV 480
DLAKTNIMY DMISDLNERS EDFEKRIVTL ETKLETIGS IHALPGLISQ TIRQQQRDFI 540
EQMESYDKH VTYNASRSR SSRRRRSSST APPTSSESS

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Seq ID NO: 597 DNA sequence
Nucleic Acid Accession #: NM_016029.1
Coding sequence: 228..1097

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CTGGTTCCCA TGAAGCGGCT ACCAAGCTG TTCTCCAGGA GTTTGGTAGA ATCGACATTC 480
TGGTCAACAA TGGTGAAGTT TCCACGCGTT CTCTGTGCAT GGATACCAGC TTGGATGTCT 540
ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTC CTTGACAAAA TGTGTTCTGC 600
CTCACATGAT CGAGAGGAAG CAAGGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA 660

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 AAAGGATTGA GAACCTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA 1080
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Seq ID NO: 598 Protein sequence
 Protein Accession #: NP_057113.1

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 KQGRIVTVNS ILGIISVPLS IGYCASKHAL RGFNGLRTE LATYPGIIVS NICPGPVQSN 240
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Seq ID NO: 600 Protein sequence
 Protein Accession #: NP_000784.2

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 ERPLVNVFSG ATUPPFTSQL PAFRKLVEEF SSVADFLIVY IDEAHPSDGW AIPGDSLSLF 180
 65 EVKKHQHQED RCAAQQLLE RFSLPQCRV VADRMNNAN IAYGVAFERV CIVQRQKIAY 240
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Seq ID NO: 601 DNA sequence
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 Coding sequence: 101..3052

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 AGCTGTTTAT GAGTTTGCCA AGGAATTGGA TGCCACCAAC ATATCCATTG ATAAAGTTGT 1980
 TGGAGCAGGT GAATTTGGAG AGGTGTGCAG TGGTCGCTTA AAACCTTCTT CAAAAAAGA 2040
 GATTT'GAGTG GCCATTAAAA CCTGAAAGT TGGCTACACA GAAAAGCAGA GGAGAGACTT 2100
 25 CCGGGAGAGAA GCAAGCATTG TGGGACAGTT TGACCAACCC AATATCATTC GACTGGAAGG 2160
 AGTTGTTACC AAAAGTAAGC CAGTTATGAT TGTCACAGAA TACATGGAGA ATGGTTCCTT 2220
 GGATAGTTTC CTACGTAAAC ACGATGCCCA GTTTACTGTC ATTACAGTAG TGGGGATGCT 2280
 TCGAGGGATA GCATCTGGCA TGAAGTACCT GTGACACATG GGCTATGTTT ACCGAGACCT 2340
 CGCTGCTCGG AACATCTTGA TCAACAGTAA CTTGGTGTGT AAGGTTTCTG ATTTGCGACT 2400
 30 TTGCGGTGTC CTGGAGGATG ACCCAGAAGC TGCTTATACA ACAAGAGGAG GGAAGATCCC 2460
 AATCAGGTGG ACATCACCAG AAGCTATAGC CTACCGCAAG TTCACGTCAG CCAGCGATGT 2520
 ATGGAGTTAT GGGATTGTTT TCTGGGAGGT GATGTCTTAT GGAGAGAGAC CATACTGGGA 2580
 GATGTCCAAT CAGGATGTAA TTAAGCTGT AGATGAGGGC TATCGACTGC CACCCCCCAT 2640
 GGACTGCCCA GCTGCCCTGT ATCAGCTGAT GCTGGACTGC TGGCAGAAAG ACAGGAACAA 2700
 35 CAGACCCCAAG TTTGAGCAGA TTGTTAGTAT TCTGGACAAG CTTATCCGGA ATCCCAGCAG 2760
 CCTGAAGATC ATCACCAGTG CAGCCGCAAG GCCATCAAAC CTTCTTCTGG ACCAAAGCAA 2820
 TGTGGATATC TCTACCTTCC GCACAACAGG TGACTGGCTT AATGGTGTCC GGACAGCACA 2880
 CTGCAAGGAA ATCTTACCGG GCGTGGAGTA CAGTTCTTGT GACACATAG CCAAGATTTT 2940
 CACAGATGAC ATGAAAAAGG TTGGTGTGAC CGTGGTTGGG CCACAGAAGA AGATCATCAG 3000
 40 TAGCATTAAG GCTCTAGAAA CGCAATCAAA GAATGGCCCA GTTCCCGTGT AAAGCACGAC 3060
 GGAAGTGCTT CTGGACGGAA GTGGTGGCTG TGAAGGCGT CAAGTCATCC TGACAGACAGA 3120
 CAATAATTCT GGAGATACTG GTGGAAGTT

Seq ID NO: 602 Protein sequence
 Protein Accession #: NP_05224.1

1 11 21 31 41 51
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 MDCQLSILL LSCSVLDSFG ELIPQPSNEV NLLDSKTIQG ELGWISYPSH GWEEISGVDE 60
 50 HYTPRTYQV CNVMDHSQNN WLRINWVPRN SAQKIYVELK FTLRDCNSIP LVLGTCKETF 120
 NLYYMESDDD HGVKFREHQF TKIDTIAADE SFTQMDLGDR ILKLNTEIRE VGPVNKKGFY 180
 LAFQDVGACV ALVSVRVYFK KCPFTVKNLA MFPDTPVMD SLSLVEVRGSC VNNKSKEEDPP 240
 RMYCSTEGEW LVPVIGKSCSN AGYEERGFMC QACRPGFYKA LDGNMKCAK PPHSSTQEDG 300
 SMNCRCENNY FRADKDPSPM ACTRPPSSPR NVISININETS VILDWSWFLD TGGRKDVTFN 360
 55 IICKKCGWNI KQCEPCSPNV RFLPRQFGLT NTVTVTDLL AHTNYTFEID AVNGVSELSS 420
 PPRQFAVSI TTNQAAAPSPV LTIKKDRTSR NSISLSWQEP EHPNGIILDY EVKYEKQEQ 480
 ETSYTLRAR GTNVTISSLK PDTIYVFIQR ARTAAGYGTN SRKFEBETSP DSFSISGESS 540
 QVVMIAISAA VAILLLTVVI YVLIGRFGY KSKHGADEKR LHFNGNHLKL PGLRITYVDPH 600
 TYEDPTQAVH EFAKELDATN ISIDKVVAG EFGVCSGRL KLPSKKEISV AIKTLKVGYT 660
 60 EKQRDRFLGE ASIMGQFDHP NIIRLEGVVT KSKPVMIVTE YMENGSLDSF LRKHDAQFTV 720
 IQLVGMRLGI ASGMKYLSDM GYVHRDLAAR NILINSNLVC KVSDFGLSRV LEDDPEAAYT 780
 TRGGKIPIRW TSPEAIAYRK FTSASDVWSY GIVLWEVMSY GERPYWEMSN QDVIKAVDEG 840
 YRLPPPMDCP AALYQLMLDC WQKDRNRNRPK FEQIVSILDK LIRNPGSLKI ITSAAARPSN 900
 LLLDQSNVDI STFRITGDWL NGVRTAHCKE IFTGVEYSSC DTIAKISTDD MKKVGVTVPV 960
 65 PQKKIISIK ALETQSKNGP VPV

Seq ID NO: 603 DNA sequence
 Nucleic Acid Accession #: NM_005727.1
 Coding sequence: 122..847

1 11 21 31 41 51
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 70 TGGAGCCTCA GCAGTTCCTT CTTTCAAGAC TCACTGCCAA GAGCCCTGAA CAGGAGCCAC 120
 CATGCAGTGC TTCAGCTTCA TTAAGACCAT GATGATCCTC TCAATTTGCG TCATCTTTCT 180
 75 GTGTGGTGCA GCCCTGTGTG CAGTGGGCAT CTGGGTGTCA ATCGATGGGG CATCTTTTCT 240
 GAAGATCTTC GGGCCTACTG CGTCCAGTGC CATGCAGTTT GTCAACGTGG GCTACTTTCT 300
 CATCGCAGCG GCGGTGTGTG TCTTTGCTCT TGGTTTCTCG GGCTGCTATG GTGCTAAGAC 360
 TGAGAGCAAG TGTGCCCTCG TGACGTTCTT CTTTCATCTC CTCCTCATCT TCATTGCTGA 420
 80 GGTTCGAGCT GCTGTGGTGC CCTTGGTGTG CACCACAATG GCTGAGCACT TCCTGACGTT 480
 GCTGTGTAGT CCTGCCATCA AGAAAGATTA TGGTTCCAG GAAGACTTCA CTCAGTGTG 540
 GAACACCAAC ATGAAAGGCG TCAAGTGCTG TGGCTTCACC AACTATACGG ATTTTGAGGA 600
 CTCACCTTAC TTCAAAGAGA CAGTGCCTT TCCCCATTTC TGTTCGAATG ACAACGTAC 660
 CAACACAGCC AATGAAACGT GCACCAAGCA AAGGCTCAC GACCAAAAAG TAGAGGGTTG 720
 CTTCAATCAG CTTTGTATGT ACATCCGAAC TAATGCAGTC ACCGTGGGTG GTGTGGCAGC 780

TGGAAATTGGG GGCCTCGAGC TGGCTGCCAT GATTGTGTCC ATGTATCTGT ACTGCAATCT 840
 ACAATAAGTC CACTTCTGCC TCTGCCACTA CTGCTGCCAC ATGGGAAC TGAAAGAGCA 900
 CCCTGGCAAG CAGCAGTGAT TGGGGGAGGG GACAGGATCT AACAAATGTCA CTGGGGCCAG 960
 AATGGACCTG CCCTTTCTGC TCCAGACTTG GGGCTAGATA GGGACCACTC CTTT TAGGCG 1020
 ATGCTGACT TTCCTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG 1080
 GTAGCCAGTT CTGTTGCCCA TTCCCCCAGT CTATTAACCC CTTGATATGC CCCCTAGGCC 1140
 TAGTGGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT 1200
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 TGTTACAATG TTAATAAA

Seq ID NO: 604 Protein sequence
 Protein Accession #: NP_005718.1

1 11 21 31 41 51
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 MQCFSEFIKTM MIFENLLIFL CGAALLAVGI WVSIDGASFL KIFGPLSSSA MQFVNVGYFL 60
 IAAGVVVFAL GFLOCYGAKT ESKCALVTFF FILLILPIAE VAAAVVALVY TTMAEHFLTL 120
 LVVPAIKKDY GSQEDFTQVW NTTMKGKLCG GFTNYTDFED SPYFKENSFA PPFCCNDNVT 180
 NTANETCTEQ KAHDQKVEGC FNQLLYDIRT NAVTVGGVAA GIGGLELAAM IVSMYLYCNL 240
 Q

Seq ID NO: 605 DNA sequence
 Nucleic Acid Accession #: NM_000729.2
 Coding sequence:

1 11 21 31 41 51
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 AGCCATGAAC AGCGGCGTGT GCCTGTGCGT GCTGATGGCG GTACTGGCGG CTGGCGCCCT 120
 GACGCAGCCG GTGCTCTCCG CAGATCCCGC GGGCTCCGGG CTGCAGCGGG CAGAGGAGGG 180
 GCCCCGTAGG CAGCTGAGGG TATCGCAGAG AACGGATGGC GAGTCCCGAG CGCACCTGGG 240
 CGCCCTGCTG GCAGATACAC TCCAGCAGGC CCGGAAAGCT CCTTCTGGAC GAATGTCCAT 300
 CGTTAAGAAC CTGCAGAAC TGGACCCAG CACAGGATA AGTGACCGGG ACTACATGGG 360
 CTGGATGGAT TTTGGCCGTC GCAGTGCCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420
 GCCGCCATCA GCCCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAAAT AAGACAACAA 480
 TCACACTCAT AACTCATTTG CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540
 TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACACGCT CACCAGAAAT 600
 TGTGCAAACT GAAGACAAAA CTGTTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT 660
 TATGCTATTA AAGTGATTTC ATTTGCCC

Seq ID NO: 606 Protein sequence
 Protein Accession #: NP_000720.1

1 11 21 31 41 51
 | | | | |
 MNSGVCLCVL MAVLAAGALT QPVPPADPAG SGLQRAEEAP RRQLRVVSQRT DGESRAHLGA 60
 LLARYIQAR KAPSGRMSIV KNLQNLDPFH RISDRDYMGW MDFGRRSAEE YEYPS

Seq ID NO: 607 DNA sequence
 Nucleic Acid Accession #: NM_001423.1
 Coding sequence: 219..692

1 11 21 31 41 51
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 ATAACCTCGG GAGGCGGGTC CTTCCTCTCA GTGCGGTGAC ATACTTCCAG AAGAGCGGAC 120
 CAGGGCTGCT GCCAGCACT GCCACTCAGA GCGCCTCTGT CGCTGGGACC CTTCAGAACT 180
 CTCTTTGCTC ACAAGTTACC AAAAAAATAA GAGCCAACAT GTTGGTATTTG CTGGCTGGTA 240
 TCTTTGTGGT CCACATCGCT ACTGTTATTA TGCTATTGTT TAGCACCATT GCCAATGTCT 300
 GGTGCTGTTT CAATACGGTA GATGCATCAG TAGGTCTTTG GAAAAACTGT ACCAACAATTA 360
 GCTGCAGTGA CAGCCTGTGA TATGCCAGTG AAGATGCCCT CAAGACAGTG CAGGCCTTCA 420
 TGATTCTCTC TATCATCTTC TGTGTCATG CCCTCCTGGT CTTGCTGTTT CAGCTCTTCA 480
 CCATGGAGAA GGGAAACCGG TTCTTCTCTT CAGGGGCCAC CACACTGGTG TGCTGGCTGT 540
 GCATCTTGT GGGGGTGTC ATCTACACTA GTCATTATGC GAATCGTGAT GGAACGCACT 600
 ATCACCACGG CTATTCTTAC ATCCTGGGCT GGATCTGCTT CTGCTTCAGC TTCTCATCTG 660
 GCGTTCTCTA TCTGGTCTG AGAAAGAAAT AAGGCCGGAC GAGTTCATGG GGATCTGGGG 720
 GGTGGGGAGG AGGAAGCCGT TGAATCTGGG AGGGAAGTGG AGGTTGCTGT ACAGGAAAAA 780
 CCGAGATAGG GGAGGGGGGA GGGGGAAGCA AAGGGGGGAG GTCAAATCCC AAACCATTAC 840
 TGAGGGGATT CTCTACTGCC AAGCCCTGCG CCTGGGGAGA AAGTAGTTGG CTAGTACTTT 900
 GATGCTCCCT TGATGGGGTC CAGAGAGCCT CCCTGCAGCC ACCAGACTTG GCCTCCAGCT 960
 GTTCTTAGTG ACACACACTG TCTGGGGCCC CATCAGCTGC CACAACACCA GCCCCACTTC 1020
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 TGGCAAGAGC AGATACTGTC TTTGTGCTGA ATACGCTAAG CTGGGAAGCC ATCTGCGCTT 1140
 TCTGACCCAA AGCAAAACAT CACATTCCAG TCTGAAGTGC CTACTGGGGG GCTTTGGCCT 1200
 GTGAGCCATT GTCCCTCTTT GGAACAGATA TTTAGCTCTG TGAATTTCAG TGACAAAAATG 1260
 GGAGAGAGAA AGAGAGTTTG TAAGGTGATG CTGGTGGGTT AGCTAAACCA AGAAGGAGAC 1320
 CTTTTCACAA TGGAAACCTT GGGGGATGTT CAGAGCCGAG TCGAGACCTC ACACACGGCT 1380
 GTCCCTCATG GAGACTCAT GCCATGGTCT TTGCTAGGCC TCTTGTGTA AGCCAAGGCA 1440
 GCTCTTCTGG AGTTTCTCTA AAGTCACTAG TGAACAATTC GGTGGTAAAA GTACCACACA 1500
 AACTATGGGA TCCAAGGGGC AGTCTTGCAA CAGTGCCATG TTAGGGTTAT GTTTTATGGA 1560
 TCCCCCTCAA TGCACTCAGT GTTCTTTTAA AGTATACAA AGGAGAGAGA TGGACATGGC 1620
 TCATTGTAGC ACAATCCTAT TACTCTTCTT CTAACATTTT TGAGGAAGTT TTGCTTAATT 1680
 ATCAATATTG AGGATCAGG CTCCCTAGCT CAGTGGTAGC TCTGGCTTAG ACACCACTG 1740
 GAGTGATCAC CTCTTGGGGA CCCTGCTTAT CCCACTTCAC AGGTGAGGCA TGGCAATTCT 1800

5 GGAAGCTGAT TAAACACAC ATAAACCAA ACCAAACAAC AGGCCCTTGG GTGAAAGGTG 1860
 CTATATAATT GTGAAGTATT AAGCCTACCG TATTTCAGCC ATGATAAGAA CAGAGTGCCT 1920
 GCATTCCCGAG GAAATACAGA AATCCCATG AGATAAATAA AATATATAGT GATGGGCAGA 1980
 TCTTTTCTTT AAAATAAAAA AGCAAAACT CTGTGTGTAC CTAGTCAGAT GGTAGACGAG 2040
 CTGTCTGCTG CCGCAGGAGC ACCTCTATAC AGGACTTAGA AGTAGTATGT TATTCTTGGT 2100
 TAAGCAGGCA TTGCTTTGCC CTGGAGCAGC TATTTTAAGC CATCTCAGAT TCTGTCTAAA 2160
 GGGGTTTTTT GGAAGACGT TTTCTTTATC GCCCTGAGAA GATCTACCCC AGGGAGAATC 2220
 TGAGACATCT TGCCTACTTT TCTTTATTAG CTTTCTCCTC ATCCATTCTT TTTATACCTT 2280
 TCCTTTTTGG GGAGTTGTTA TGCCATGATT TTTGGTATTT ATGTAAAGG ATTATTACTA 2340
 10 ATTCTATTTC TCTATGTTA TTCTAGTTAA GGAATGTGT AGGGCAAGCC ACCAAATTAC 2400
 CTAGGCTGAG GTTAGAGAGA TTGGCCAGCA AAAACTGTGG GAAGATGAAC TTTGTCATTA 2460
 TGATTTCATT ATCAGATGAT TATAGAAGGC TGTCTTAGTG CAAAAACAT ACTTACATTT 2520
 CAGACATATC CAAAGGGAAT ACTCACATTT TGTAAAGAAG TTGAACATATG ACTGGAGTAA 2580
 15 ACCATGTATT CCCTTATCTT TTACTTTTTT TCTGTGACAT TTATGTCTCA TGTAAATTGC 2640
 ATTACTCTGG TGGATTGTTT TAGTACTGTA TTGGGCTTCT TCGTTAATAG ATTATTTTCA 2700
 ATACTATAAT TGTAAATATT TTGATACAAA TGTTTATAAC TCTAGGGATA TAAAAACAGA 2760
 TTCTGATTCC CTTCAAAAAA AAAAAA

Seq ID NO: 608 Protein sequence
 Protein Accession #: NP_001414.1

1 11 21 31 41 51
 25 MLVLLAGIFV VHIAIVIMLF VSTIANVWL V SNTVDASVGL WKNCTINISCS DLSLYASEDA 60
 LKTQVAFMIL SIIFCVIALF VFVFQLFTME KGNRFFLSGA TTLVCWLCIL VGVSIYTSYH 120
 ANRDGTQYHH GSYLILGWIC FCFSLIIGVL YLVLRKK

Seq ID NO: 609 DNA sequence
 Nucleic Acid Accession #: NM_004961.2
 Coding sequence: 55..1575

1 11 21 31 41 51
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 CCTCAGACTG AATCAAAGAA TGAAGCCTCT TCCCGTGATG TTGCTATGG CCCCAGCCCC 180
 CAGCCTCTGG AAAATCAGCT CCTCTCTGAG GAAACAAAGT CAACTGAGAC TGAGACTGGG 240
 AGCAGAGTTG GCAAACTGCC AGAAGCCTCT CGCATCCTGA ACACATATCT GAGTAATTAT 300
 40 GACCACAAAC TGCGCCCTGG CATTGGAGAG AAGCCCACTG TGGTCACTGT TGAGATCGCC 360
 GTCACAGGCC TTGGTCTCT CTCTATCCTA GACATGGAAT ACACCATTTGA CATCATCTTC 420
 TCCAGACCT GGTACGACGA ACGCCTCTGT TACAACGACA CCTTTGAGTC TCTTGTCTTG 480
 AATGGCAATG TGGTAGGCGA GCTATGGATC CCGGACACCT TTTTATAGAA TTCTAAGAGG 540
 ACCCAGGAGC ATGAGATCAC CATGCCCAAC CAGATGGTCC GCATCTACAA GGATGGCAAG 600
 45 GTGTTGTACA CAATTAGGAT GACCATTTGAT GCCGGATGCT CACTCCACAT GCTCAGATT 660
 CCAATGGATT CTCACCTCTG CCTCTATCT TTCTCTAGCT TTTCTATACC TGAGAATGAG 720
 ATGATCTACA AGTGGGAAAA TTTCAAGCTT GAAATCAATG AGAAGAACTC CTGGAAGCTC 780
 TTCCAGTTTG ATTTTACAGG AGTGAGCAAC AAAACTGAAA TAATCACAAC CCCAGTTGGT 840
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 50 CAAAACTATG TCCCTTCTTC CGTGACCACG ATGCTCTCCT GGGTTTCTCT TTGGATCAAG 960
 ACAGAGTCTG CTCAGGCCCG GACCTCTCTA GGGATCACCT CTGTTCTGAC CATGACCACG 1020
 TTGGGCACCT TTTCTCGTAA GAATTTCCCG CGTGTCTCCT ATATCACAGC CTGGGATTT 1080
 TATATCGCCA TCTGCTCTGT CTCTGCTTC TGGCTCTGT TGGAGTTTGC TGTGCTCAAC 1140
 TTCTGATCT ACAACCAGAC AAAAGCCCAT GCTTCTCCTA AACTCCGCCA TCCTCGTATC 1200
 AATAGCCGTG CCCATGCCCG TACCCGTGCA CGTTCGCCG CCGTGCCCG CCAACATCAG 1260
 55 GAAGCTTTTG TTGCCAGATG TGTCAACACT GAGGGAAAGT ATGGAGAGGA GCGCCCGTCT 1320
 TGCTCAGCCC AGCAGCCCCC TAGCCAGGT AGCCCTGAGG GTCCCGCAG CCTCTGCTCC 1380
 AAGCTGGCCT GCTGTGAGTG GTGCAAGCGT TTTAAGAAGT ACTCTGCAAT GGTCCCGAT 1440
 TGTGAGGGCA GTACCTGGCA GCAGGGCCGC CTCTGCATCC ATGTCTACCG CCTGGATAAC 1500
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 60 TGCTTAACT TGTAGTTACC AGCTGTIACC CTGTGGGGCA ACCTCTCCAG TTCCCCAGGA 1620
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 AGTTTTTCTT GCCCATTTCC CCAACAGAAA GCTTGCAGAG GGTTTGTCTT TGCTGCCCT 1740
 CTCCTTACC TGGCCATTC ACTGAGTCTT CTCAGCAGAC CATTTCAAAT TATTAATAAA 1800
 TGGGCCACTT CCTCTTCTT CAAGGAGCAT CCGTGATGCT CAGTGTTCAA AACCACAGCC 1860
 65 ACTTAGTAT CAGCTCCCTA AAACCATGCC TAAGTACAGG CGGATTAGCT ATCTTCCAAC 1920
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 70 TCAGATTATT ATGTTCTCAG TTCTCTCTCC CTGCTACCCC TTTCTCTGCA GATAGATAGA 2160
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 75 ACTTTCCAG TGACTTCCC TAGCCCTGAC CCAGGCACTA GGCCTTGGTG ACTTCTGGG 2460
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 ACCCAGGGCA CACTGTCCGA GTTCTATCAC TTGCTTGACC CCGGACCCA TAAACAGTC 2580
 CACTGTTATA CCCGGGGCAC TCTAACCATC ACAATCAATC AATCAAATTC CCTTAAATTT 2640
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 80 GATAGCCTTG TGACATCTTT AGGGCAGGAT TCTTATCCCC ATTTTGAGA TGAACACCT 2760
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 ACCTTCTAGA CACATGATCA GGGCTAGACA GCTCAGTTCA CCATGATTCT CTTCTGTAC 2880
 CTCTGCTGGC ACACCACTGG CAAGGCCAG AATGGCGACC TCTCTTTAGC TCAATTTCTG 2940
 GGCCTGAGGT GCTCAGACTG CCCCCAAGAT CAAATCTCTC CTGGCTGTAG TAACCCAGTG 3000
 GAATGAATTT GGACATGCCC CAATGCTTCT ATATGCTAAG TGAAATCTGT GTCTGAATT 3060

TGTTGGGGGG TGGATAGGGT GGGGTCTCCA TCTACTTTT GTCACCATCA TCTGAAATGG 3120
GGAAATATGT AAATAATAT ATCAGCAAAG CAAAAGAAA AAAAAAAA

Seq ID NO: 610 Protein sequence
Protein Accession #: NP_004952.1

1 11 21 31 41 51
| | | | |
10 ML SKVL PVL L GILL ILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60
TGS RVGKL PE ASRI LNTILS NYDHLKLRPGI GEKPTVVTV E IAVNSLGPLS ILDMEYTIDI 120
IFSQTWYDER LCYNDTFESL VLNGNVVSQL WIPDTFFRNS KRTHEHEITM PNQMVRIYKD 180
GKVL YTI RMT IDAGCSLHML RFPMDSHSCP LSFSSFSYPE NEMIIKWENF KLEINEKNSW 240
KLFQDFDTGV SNKTEIITP VGDFMVTIF FNVSRRFYV AFQNYVFSV TMLSWVSFV 300
15 IKTESAPART SLGITSVLTM TTLGTFSRKN FPRVSYITAL DFYIAICFVF CFCALLEFAV 360
LNFLIYNQTK AHASPKLRHP RINSRAHART RARSACARQ HQEAFVCQIV TTEGSDGEER 420
PSCSAQQPPS PGSPGPRSL CSKLACCEWC KRFKKYFCMV PDCEGSTWQQ GRLCIHVYRL 480
DNYSRVFPV TFFFNVLVW LVCLNL

Seq ID NO: 611 DNA sequence
Nucleic Acid Accession #: NM_021984.1
Coding sequence: 572..1753

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GTGTAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAG ACCTCAGAAG CCCCTTTGT 240
30 CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC 300
TCAGACTGAA TCAAAAGATG AAGCCTCTTC CCGTGTATGT GTCTATGGCC CCCAGCCCCA 360
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420
CAGAGTTGGC AAAGTGCAG AAGCCTCTCG CATCCTGAAC ACTATCCTGA GTAATTATGA 480
CCACAAACTG CGCCCTGGCA TTGGAGAGAA GCCCACTGTG GTCACCTGTG AGATCTCCGT 540
35 CAACAGCCTT GGTCCCTCTCT CTATCCTAGA CATGGAATAC ACCATTGACA TCATCTTCTC 600
CCAGACCTGG TAGCAGCAAC GCCTCTGTTA CAACGACACC TTTGAGTCTC TTGTTCTGAA 660
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40 GTTGATACAA ATTAGGATGA CCATTGATGC CGGATGTCTA CTCCACATGC TCAGATTTC 840
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GATCTACAAG TGGGAAAATT TCAAGCTTGA AATCAATGAG AAGAACTCCT GGAAGCTCTT 960
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45 AGAGTCTGCT CAGGCCGGA CCTCTTAGG GATCACCTCT GTTCTGACCA TGACCACGTT 1200
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50 CTCAGCCGAG CAGCCCTCTA GCCCAGGTAG CCCTGAGGGT CCCCGCAGCC TCTGCTCAA 1560
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55 TCCAAAGCCC TTGCCAAGGG AGTTGGGGGA AAGCAGCAGC AGCAGCAGGA GCGCATAGAG 1860
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CCCCTACCTG GCCCATTCAC TGAGTTTCT CAGCAGACCA TTTCAAATTA TTAATAAATG 1980
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60 TTAGTGATCA GCTCCCTAAA ACCATGCCTA AGTACAGGCG GATTAGCTAT CTTCACAA 2100
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65 CTGGCATTAT CCCTTTAGGA AGAGGGGGGG GCAGCAAGAG AGCCTATTG GGCAGCATT 2400
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TTTCCGAGTG ACTTCCCTTA GCCCTGACCC AGGCACTAGG CCTTGGTGAC TTCTGGGGC 2640
70 CAAGAACTA AGGAACTCG GCTTTGCAAC AGGCATTACT CGCCATTGAT TGGTGCCAC 2700
CCAGGSCACA CTGTCGGAGT TCTATCACTT GCTTGACCCC TGGACCCATA AACCACTCCA 2760
CTGTTATACC CGGGGCACTA TAACCATCAC AATCAATCAA TCAAAATCCC TTAATTTGT 2820
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TAGCCTTGTG ACATCTTTAG GGCAGGATTC TTATCCCAT TTTGCAGATG AAAACCTGA 2940
75 GTCACAGATT TCTGTGGGAC TGTGGATCTC ACTGGAAGCT ATCCAAGAGC CCACTGTCAC 3000
CTTCTAGACC ACATGATAGG GCTAGACAGC TCAGTTTACC ATGATTCTCT TCTGTACCT 3060
CTGCTGGCAC ACCAGTGGCA AGGCCAGAA TGGCGACCTC TCTTTAGCTC AATTTCTGG 3120
CCTGAGGTGC TCAGACTGCC CCCAAGATCA AATCTCTCCT GGCTGTAGTA ACCCAGTGA 3180
ATGAATTTGG ACATGCCCCA ATGCTTCTAT ATGCTAAGTG AAATCTGTGT CTGTAATTG 3240
80 TTGGGGGGTG GATAGGGTGG GGTCTCCATC TACTTTTGT CACCATCATC TGAATGGGG 3300
AAATATGTAA ATAAATATAT CAGCAAAGC

Seq ID NO: 612 Protein sequence
Protein Accession #: NP_068819.1

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1      11      21      31      41      51
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MVR1YKDGKV LYTIIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWENFKLE 120
5 INEKNWSWLF QLDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTM 180
LSWVSFWIKT ESAPARTSLG ITSVLMTMTL GTFSRKNFPR VSYITALDFY IAI CFVFCFC 240
ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE 300
GSDGEERPSC SAQPPSPGSG PEGPRSLCSK LACCEWCKRF KKYFCMVPCD EGSTWQQARL 360
10 CIHVYRLDNY SRVVPVTFP FENVLYWLVC LNL

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Seq ID NO: 613 DNA sequence
Nucleic Acid Accession #: NM_021987.1
Coding sequence: 572..1657

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20 CAGAGAAGTG CTCAAATCAT AAGTGATACG CTGATGAGTT GTCAAAAAAT GACCACAGCG 180
GTGTAAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCTTTTGT 240
CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGGACC 300
TCAGACTGAA TCAAAGAAATG AAGCCTCTTC CCGTGATGTT GTCTATGGCC CCCAGCCCCA 360
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420
CAGAGTTGGC AAACCTGCCA AAGCCTCTCG CATCTGAAC ACTATCCTGA GTAATTATGA 480
25 CCACAAACTG CGCCCTGGCA TTGGAGAGAA GCCCACTGTG GTCACTGTG AGATCTCCGT 540
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CCGCATCTAC AAGGATGGCA AGGTGTTGTA CACAATTAGG ATGACCATG ATGCGGGATG 720
CTCACTCCAC ATGCTCAGAT TTCCAATGGA TTCTCACTCT TGCCCTCTAT CTTTCTCTAG 780
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AATAATCACA ACCCCAGTTG GTGACTTCAT GGTCTGACG ATTTTCTTCA ATGTGAGCAG 960
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35 CTGGGTTTCC TTTTGGATCA AGACAGAGTC TGCTCCAGCC CGGACCTCTC TAGGGATCAC 1080
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70 GTGAATCTG TGTCTGTAAT TTGTTGGGGG GTGGATAGGG TGGGTCTCC ATCTACTTTT 3180
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Seq ID NO: 614 Protein sequence
Protein Accession #: NP_068822.1

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80 VMTIFFNVSR RFGYVAFQNY VPSSVTTMLSL WVSFWIKTES APARTSLGIT SVLMTMTLGT 180
FSRKNFPRVS YITALDFYIA ICFVFCFCAL LEFAVLNFLI YNQTKAHASP KLRHPRINSR 240
AHARTRARSR ACARQHQEAF VCQIVTTEGS DGEERPSCSA QPPSPGSPSE GPRSLCSKLA 300
CCEWCKRFFK YFCMVPCDEG STWQQGRLCI HVRDLNYSR VVFPVTFPFF NVLYWLVLN 360
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Seq ID NO: 615 DNA sequence
Nucleic Acid Accession #: NM_021990.1
Coding sequence: 1309..2490

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GTGTAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCCTTTGT 240
CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGT GAGTTTCATA 300
CCTTGGCAGA TGGCCTTTAA CATTTTGTGT TAATTCAATT ATCTTACTA ATCTTCTTCT 360
TTTTCTTGGC TGTGGTGCAT GGCTGTGGAG CTCAGGGTGG ACTCCTGTTG GGCAGCCAGT 420
TCTTGGATGG CTGTCTGTGG GTGGAGGACT CCTGCCTTTC CTGTTTAGAC ACCCACAAAG 480
GCTGCTCTTT AGCCTCCTTC CCTTCATCCC TTCCCCTGC CCCAGTGCA ACGAGTATTA 540
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CTCTGGCTTT TCCTCTCAGC CCTGGCCCTC TGCCCTGCTC TCACTCCTGG TTGGTGTCTG 660
TCAGGCTGAG TAGAGGCCAA GCGACCCAAC ACTAGGCAAA CGCGGCCAGC GCTCAGACAT 720
AAATGCCCTC TTCAATTTCAC GTGTAACATT CTTTAAAAAT CTAGGTCTTG GTTTTGTGTA 780
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CAGCAAGGTT TAAAGAAAT TCACAAGCCT AATCTGTAC TGCTTTATAA TTTGCTATTA 900
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TCTAGGGTCG AGGGACCTCA GACTGAATCA AAGAATGAAG CCTCTTCCCG TGATGTTGTC 1080
25      TATGGCCCCC AGCCCCAGCC TCTGAAAAAT CAGCTCCTCT CTGAGGAAAC AAAGTCAACT 1140
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30      GAGTCTCTTG TTCTGAATGG CAATGTGGTG AGCCAGCTAT GGATCCCGGA CACCTTTTTT 1440
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TATCCTGAGA ATGAGATGAT CTACAAGTGG GAAAATTTCA AGCTTGAAT CAATGAGAAG 1680
35      AACTCCTGGA AGCTCTTCCA GTTTGATTTT ACAGGAGTGA GCAACAAAAC TGAAATAATC 1740
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40      CTGACCATGA CCACGTGGG CACCTTTTCT CGTAAGAAAT TCCCGCGTGT CTCCTATATC 1980
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GCCCGCAAC ATCAGGAAGC TTTTGTGTGC CAGATTGTCA CCACTGAGGG AAGTGATGGA 2220
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Seq ID NO: 616 Protein sequence
Protein Accession #: NP_068830.1

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MVIYKDGKLV LYTRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSPYENEM IYKWFNFKE 120
INEKNSWKLF QDFDTGSVSK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTM 180
LSWVSFWIKT ESAPARTSLG ITSVLTMITL GTFSRKNFPR VSYITALDFY IAICFVFECF 240

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ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE 300
 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCEWCKRF KRYFCMVPDC EGSTWQQGRL 360
 CIHVYRLDNY SRVVPVPTFF FPNVLYWLVC LNL

Seq ID NO: 617 DNA sequence
 Nucleic Acid Accession #: NM_004864.1
 Coding sequence: 26..952

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Seq ID NO: 618 Protein sequence
 Protein Accession #: NP_004855.1

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 HRLFRRLSPT ASRSWVTRP LRRQLSLARP QAPALHLRLS PPFSQSDQLL AESSSARPL 180
 ELHLRPQAAR GRRRARARNR DDCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC 240
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Seq ID NO: 619 DNA sequence
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Seq ID NO: 620 Protein sequence

Protein Accession #: NP_003970.1

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 KLVRGRKPLS LLVILGLAVG FSLVQDVIAI EYIVLTMRNT NVNVFSELSA PRRNEDFVLL 180
 LTYVLFLMAL TFLMSSFTFC GSFTGWRHGH AHYLTMLLS IAIWVAVITL LMLPDFDRRW 240
 DDTLLSSALA ANGMVFLLAY VSPEFWLLTK QRNPMDYPVE DAFCKPQLVK KSYGVENRAY 300
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Seq ID NO: 621 DNA sequence

Nucleic Acid Accession #: NM_002423.2

Coding sequence: 48..851

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 TGCTGTGTGC TGTGTGCCCTG CTGCTGGCCA GCCTGGCCCT GCGCTGCCT CAGGAGGCGG 120
 GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT 180
 ATGACTCAGA AACAAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAT 240
 TCTTTGGCCT ACCTATAACT GGAATGTTAA ACTCCGCGT CATAGAAATA ATGCAGAAGC 300
 CCAGATGTGG AGTGCCAGAT GTTGACAGAAT ACTCACTATT TCCAAATAGC CCAAAATGGA 360
 CTTCCAAAGT GGTACACCTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG 420
 TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTTCA 480
 GGAAAGTTGT ATGGGGAATC GCTGACATCA TGATTGGCTT TGC CGAGGA GCTCATGGGG 540
 ACTCTACCTC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCTTTGCG CTGGGACAG 600
 GTCTCGGAGG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG 660
 GGATTAACCT CCTGTATGCT GCAACTCATG AACTTGGCCA TTCTTTGGGT ATGGGACATT 720
 CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA 780
 AACTTTCCCA GGATGATATT AAAGGCATTC AGAAACTATA TGGAAAGAGA AGTAATTCAA 840
 GAAAGAAATA GAAACTTCAG GCAGAACATC CATTCACTCA TTCATTGGAT TGTATATCAT 900
 TGTGTACAAA TCAGAAATTGA TAAGCACTGT TCCTCCACTC CATTTAGCAA TTATGTACCC 960
 CTTTTTTAT GCAGTTGGTT TTTGAATGTC TTCTACTCCT TTTATTGGTT AAACCTCCTT 1020
 ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTTGTCA GTGCGCTGAT ATGTCAATAA 1080
 ATGTTACATA CACAAATAAA TAAATGTTT ATTCCATGGT AAATTTA

Seq ID NO: 622 Protein sequence

Protein Accession #: NP_002414.1

1 11 21 31 41 51
 | | | | |
 MRLTVLCVAV LLPGLALPL PQEAGGMSSEL QWEQAQDYLYK RFYLYDSETK NANSLEAKLK 60
 EMQKFFGLPI TGLMNSRVIE IMQKPRGVVP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL 120
 PHITVDRLVS KALNMWKEI PLHFRKVVWG TADIMIGFAR GAHGDSYFPD GPGNTLAHAF 180
 APGTGLGGDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYNGND 240
 PQNFKLSQDD IKGIQKLYGK RSNRKK

Seq ID NO: 623 DNA sequence

Nucleic Acid Accession #: NM_031457.1

Coding sequence: 204..956

1 11 21 31 41 51
 | | | | |
 AAACAGGAAA TAAATACGAA TGAAACTGAG CTCTAAGCAG CATGTAACCT GGCCTGCATC 60
 CAGGAAATAG AGGACTTCGG ATCCTTCTAA CCTACCACC CAACTGGCCC CAGTACATTC 120
 ATTCTCTCAG GAAAAAAAC AAGGTCCCCA CAGCAAGAA AAGGAATAGG ATCAAGAGAT 180
 ACGTGGCTGC TGGCAGAGCA AGCATGAATT CGATGACTTC AGCAGTTCCG GTGGCCCAAT 240
 CTGTGTTGGT GGTGGCACCC CACAATGTT ATCCTGTGAC CCCAGGAATT ATGTCTCACG 300
 TGCCCTGTGA TCCAAACAGC CAGCCGCAAG TCCACCTAGT TCCTGGGAAC CCACCTAGTT 360
 TGGTGTGCGA TGTGAATGGG CAGCCTGTGC AGAAGCTCT GAAAGAAGGC AAAACCTTGG 420
 GGGCCATCCA GATCATCATT GGCCTGGCTC ACATCGGCCT CGGCTCCATC ATGGCGACGG 480
 TTCTCGTAGG GGAATACCTG TCTATTTTCT TCTACGGAGG CTTTCCCTTC TGGGGAGGCT 540
 TGTGGTTTAT CATTTCAGGA TCTCTCTCCG TGGCAGCAGA AAATCAGCCA TATCTTATT 600
 GCCTGCTGTC TGGCAGTTTG GGCCTGAACA TCGTCAGTGC AATCTGCTCT GCAGTTGGAG 660
 TCATACTCTT CATCACAGAT CTAAGTATTC CCCACCCATA TGCTTACCCC GACTATTATC 720
 CTTACGCTCG GGTGTTGAAC CCTGGAATGG CGATTTCTGG CGTGTCTGCT GTCTTCTGCC 780
 TCCTGGAGTT TGGCATCGCA TGCAGCATCT CCCACTTTGG CTGCCAGTTG GTCTGCTGTC 840
 AATCAAGCAA TGTGAGTGTG ATCTATCCAA ACATCTATGC AGCAAAACCA GTGATCACCC 900
 CAGAACCGGT GACCTCACCA CCAAGTTATT CCAAGTATGC CCAAGCAAA AAGTAAGGCT 960
 ACAGATTCTG GAAGCATCTT TCACTGGGAC CAAAGAAGT CCTCTCCCT TCTGGGCTT 1020
 CCATAACCCA GGTGTTCTCT GTTCTGACAG CTGAGGAAAC GTCTCTCCCA CTGTTTGTAC 1080
 TCTCACCTTC ATTCTTCAAT TCAGTCTAGG AAACCATGCT GTTCTCTTAT CAAGAAGAAG 1140
 ACAGAGATTT TAAACAGATG TTAACCAAGA GGGACTCCCT AGGGCACATG CATCAGCACA 1200
 TATGTGGGCA TCCAGCCTCT GGGGCCTTGG CACACACACA TTCGTGTGCT CTGCTGCATG 1260

TGAGCTTGTG GGTTAGAGGA ACAAATATCT AGACATTCAA TCTTCACTCT TTCAATTGTG 1320
CATTCAATTA ATAAATAGAT ACTGAGCATT CAAAAA AAAA

Seq ID NO: 624 Protein sequence
Protein Accession #: NP_113645.1

1 11 21 31 41 51
MNSMTSAVPV ANSVLVVAPH NGYPVTPGIM SHVPLYPN SQ PQVHLVPGNP PSLVSNVNGQ 60
PVQKALKEGV TLGAIQIIIG LAHIGLGSIM ATVLVGEYLS ISFYGGFFFW GGLWFIISGS 120
LSVAENQPY SYCLLSGSLG LNIIVSAICSA VGVILFITDL SIPHPYAYPD YYPYAWGVNP 180
GMAISGVLLV FCLLEFGIAC ASSHFGCQLV CQSSNVSVI YPNIYAANPV ITPEPVTSPF 240
SYSSEIQANK

Seq ID NO: 625 DNA sequence
Nucleic Acid Accession #: NM_005221.3
Coding sequence: 1..870

1 11 21 31 41 51
ATGACAGGAG TGTTTGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG 60
TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACTTT GCCCGAGTCT 120
TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCCACACGG CTACTGCTCT 180
CCTACCTCGG CTCTCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGCGCTG 240
AACGGCTCCG CCGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC 300
TACCACCATG ACGGCGGCGC CTACAACCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360
GAAGTGACCG AGCCCCAGGT GAGAATGGTG AATGGCAAAC CAAAGAAAGT TCGTAAACCC 420
AGGACTATT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480
TACCTGCGCT TGCCGGAACG CGCCGAGCTG GCCGCTCGC TGGGATTGAC ACAAACACAG 540
GTGAAAATCT GGTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AAACCGGGGAG 600
ATGCCCCCGG AGCACAGTCC CAGCTCCAGC GACCCAATGG CGTGTAACTC GCCGCACTCT 660
CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCAC 720
CCTCCGACCT CCAACAGTCC CCCAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC 780
ACAAGTGCAG CCAAGTCAAT CAATTCCAC CTGCCGCGC CGGGCTCCTT ACAGCACCCG 840
CTGGCGCTGG CTCCCGGAC ACTCTATTAG

Seq ID NO: 626 Protein sequence
Protein Accession #: NP_005212.1

1 11 21 31 41 51
MTGVFDRRVP SIRSGDFQAP FQTSAAHHP SQESPTLPES SATDSDYISP TGGAPHGYCS 60
PTSASYGKAL NPYQYQYHGV NGSAGSYPK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120
EVTEPEVRMV NGKPKVRKP RTIYSSFQLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ 180
VKIWFQNKRS KIKKIMKNGE MPPEHSPSSS DPMACNSPQS PAVWEPQSSS RSLSHHPHAH 240
PPTSNOQPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLV

Seq ID NO: 627 DNA sequence
Nucleic Acid Accession #: NM_014420
Coding sequence: 118..792

1 11 21 31 41 51
GCACGAGAGA CGAGCTGCTG AGCTGCCAGC TTAGTGGAAG CTCTGCTCTG GTGGGAGAGC 60
AGCCTCGCTT TGGTGACGCA CAGTGCTGGG ACCCTCCAGG AGCCCCGGA TTGAAGGATG 120
GTGGCGGCGG TCCTGCTGGG GCTGAGCTGG CTCTGCTCTC CCTGGGAGC TCTGGTCTCTG 180
GACTTCAACA ACATCAGGAG CTCTGCTGAC CTGCATGGGG CCGGAAGGG CTCACAGTGC 240
CTGTCTGACA CGGACTGCAA TACCAGAAAG TTCTGCCTCC AGCCCCGCGA TGAGAAGCCG 300
TTCTGTGCTA CATGTCGTGG GTTGGCGAGG AGGTGCCAGC GAGATGCCAT GTGCTGCCCT 360
GGGACACTCT GTGTGAACGA TGTGTGACT ACCATGGAAG ATGCAACCCC AATATTAGAA 420
AGGCAGCTTG ATGAGCAAGA TGGCACACAT GCAGAAGGAA CAACTGGGCA CCCAGTCCAG 480
GAAAACCAAC CCAAAGGAA GCCAAGTATT AAGAAATCAC AAGGCAGGAA GGGACAAGAG 540
GGAGAAAGTT GTCTGAGAAC TTTTGACTGT GGCCCTGGAC TTTGCTGTGC TCGTCATTTT 600
TGGACGAAAA TTTGTAAGCC AGTCCTTTTG GAGGGACAGG TCTGCTCCAG AAGAGGGCAT 660
AAAGACACTG CTCAAGCTCC AGAAATCTTC CAGCGTTGCG ACTGTGGCCC TGGACTACTG 720
TGTCGAAGCC AATTGACCAG CAATCGGCAG CATGCTCGAT TAAGAGTATG CCAAAAAATA 780
GAAAAGCTAT AAATATTTCA AAATAAGAA GAATCCACAT TGCAAAAAA AAAAAAATA 840
A

Seq ID NO: 628 Protein sequence
Protein Accession #: NP_055235

1 11 21 31 41 51
MVAAVLLGLS WLCSPLGALV LDFNNIRSSA DLHGARKGSQ CLSDTDCNTR KFCLQPRDEK 60
PFCATCRGLR RRCQRDAMCC PGLCVNDVC TTMEDATPIL ERQLDEQDGT HAEGTTGHPV 120
QENQPKRKPS IKKSQGRKGQ EGESCLRTFD CGPGLCCARH FWTKICKPVL LEGQVCSRRG 180
HKDTAQAPEI FQRCDGPGFL LCRSGLTSNR QHARLRVCQK IEKL

Seq ID NO: 629 DNA sequence
Nucleic Acid Accession #: NM_002448.1
Coding sequence: 241..1134

1 11 21 31 41 51

	CGCGGAGTGC	TCGCCGGAAC	CTGCTCTGCG	CGCGGCGAGC	GACCGGAGGC	CAGGCCAGC	60
	ACGCCGAGGC	TGGCCTGCTG	GGGAGGGGCG	GGAGGCGCGC	GCGGGAGGGT	CCGCCCGGCC	120
5	AGGCCCGGGG	CCCTCGCAGA	GGCCGGCCCG	GCTCCCAGCC	CGCCCGGAGC	CCATGCCCGG	180
	CGGCTGGCCA	GTGCTGCGGC	AGAAGGGGGG	GCCCGGCTCT	GCATGGCCCC	GGCTGCTGAC	240
	ATGACTTCTT	TGCCACTCGG	TGTCAAAGTG	GAGGACTCCG	CCTTCGGCAA	GCCGGCGGGG	300
	GGAGGCGCGG	GCCAGGCCCC	CAGCGCGGCC	GCGGCCACGG	CAGCCGCCAT	GGGCGCGGAC	360
	GAGGAGGGGG	CCAAGCCCAA	AGTGTCCCCT	TCGCTCCTGC	CCTTCAGCGT	GGAGGCGCTC	420
10	ATGGCCGACC	ACAGGAAGCC	GGGGGCCAAG	GAGAGCGCCC	TGGCGCCCTC	CGAGGGCGTG	480
	CAGGCGGCGG	GTGGCTCGGC	GCAGCCACTG	GGCGTCCC	CGGGGTGCT	GGGAGCCCCG	540
	GACGCGCCCT	CTTCGCGCGG	GCCGCTCGGC	CATTCTCTCG	TGGGGGGACT	CCTCAAGCTG	600
	CCAGAAGATG	CGCTCGTCAA	AGCCGAGAGC	CCCGAGAAGC	CCGAGAGGAC	CCCGTGGATG	660
	CAGAGCCCCC	GCTTCTCCCC	GCCGCCGGCC	AGGCGGCTGA	GCCCCCAGC	CTGCACCCCT	720
15	CGCAAAACAC	AGACGAACCG	TAAGCCGCGG	ACGCCCTTCA	CCACCGCGCA	GCTGTGGCG	780
	CTGGAGCGCA	AGTTCGCCCA	GAAGCAGTAC	CTGTCCATCG	CCGAGCGCGC	GGAGTTCTCC	840
	AGTCTCGTCA	GCCTCACTGA	GACGAGGTG	AAGATATGGT	TCCAGAACCG	CCGCGCCAA	900
	CCAAAGAGAC	TACAAGAGCC	AGAGCTGGAG	AAGCTGAAGA	TGGCCGCCAA	GCCCATGCTG	960
	CCACCGGCTG	CCTTCGCGCT	CTCCTTCCCT	CTCGCGGCC	CGCAGCTGT	AGCGGCCGCG	1020
20	GCGGGTGCC	CGCTCTACGG	TGCCTCTGGC	CCCTTCCAGC	GCGCCGCGCT	GCCTGTGGCG	1080
	CCCGTGGGAC	TCTACACGGC	CCATGTGGGC	TACAGCATGT	ACCACCTGAC	ATAGAGGGTC	1140
	CCAGGTCCCC	ACCTGTGGGC	CAGCCGATTC	CTCCAGCCCT	GGTGTGTATC	ACCCGACGTG	1200
	CTCCCTTGCT	CGGCACGCGC	AGCCGCTTTC	CCTTAAACCC	TCACACTGCT	CCAGTTTCAC	1260
25	CTCTTTGCTC	CCTGAGTTCA	CTCTCCGAAG	TCTGATCCCT	GCCAAAAGT	GGCTGGAAGA	1320
	AGGCTTAGT	ACTCTTCTAG	CATTAGATC	TACACTCTCG	AGTTAAAGAT	GGGGAAGT	1380
	AGGGCAGAGA	GGTTAAACAGA	TTTATCTAGG	GTCCCCAGCA	GAATTGACAG	TTGAACAGAG	1440
	CTAGAGGCCA	TGTCTCCTGC	ATAGCTTTTC	CCTGTCTGTA	CACCAAGCAA	GAAAAGCGCA	1500
	GAGAAATCGG	TGTCTGACGA	TTTTGGAAAT	GAGAACCAAT	TCAAAAAA	AAAAAAGGAA	1560
	AAAAAAGGAA	GAAAAGAGAA	AAAAAAGACT	AGCCAGCCAG	GAAGATGAAT	CCTAGCTTCT	1620
30	TCCATTGGAA	AATTAAAGAC	AAGTTCAACA	ACAAAACATT	TGCTCTGGGG	GGCAGGAAAA	1680
	ACACAGATGT	GTTGCAAGG	TAGTTGAAG	GGA			

Seq ID NO: 630 Protein sequence
Protein Accession #: NP_002439.1

	1	11	21	31	41	51	
35	MTSLPLGVKV	EDSAFGKPG	GGAGQAPSAA	AATAAAMGAD	EEGAKPKVSP	SLLPFSVEAL	60
	MADHRKPGAK	ESALAPSEGV	QAAGGSAQPL	GVPPGSLGAP	DAPSSPRPLG	HFSVGGLLKL	120
	PEDALVKAES	PEKPFRTWPM	QSPRFSPPPA	RRLSPPACTL	RKHKTNRKPR	TPFTTAQLLA	180
40	LERKFRQKQY	LSIAERAEFS	SSLSLTETQV	KIWFQNRRAK	AKRLQEAEL	KLKMAAKPML	240
	PPAAGFLSFP	LGGPAAVAAA	AGASLYGASG	PFQRAALPVA	PVGLYTAHV	YSMYHLT	

Seq ID NO: 631 DNA sequence
Nucleic Acid Accession #: NM_002557.1
Coding sequence: 13..2049

	1	11	21	31	41	51	
50	CAGACCATTG	AGATGTGGAA	GCTGTTGCTG	TGGGTTGGGC	TGGTTCTTGT	GCTGAAACAC	60
	CACGATGGTG	CTGCCATATA	ACTCGTGTGT	TATTTACCA	ACTGGGCACA	CAGTCGGCCA	120
	GGCCCTGCGT	CGATCTTGCC	CCATGACCTG	GACCCCTTTC	TCTGCACCCA	CCTGATATTT	180
	GCCTTTGCCT	CAATGAACAA	CAATCAGATT	GTTGCTAAGG	ATCTCCAGGA	TGAGAAAATT	240
	CTCTACCCAG	AGTTCAACAA	ACTAAAGGAG	AGGAACAGAG	AGCTGAAAAC	ACTACTGTCC	300
55	ATCGGGGGGT	GGAACCTTGG	CACCTCAAGA	TTCACCACTA	TGTTGTCCAC	ATTTGCCAAC	360
	CGTGAAAAGT	TTATTGCTTC	AGTTATATCC	CTTCTGAGGA	CACATGACTT	TGATGGTCTT	420
	GACCTTTTCT	TCTTATATCC	TGGACTAAGA	GGCAGCCCA	TGCATGACCG	GTTGACTTTT	480
	CTCTTCTTAA	TGGAAGAGCT	CCTGTTTGCC	TTCGGGAAGG	AGGCACTGCT	CACCATGCGC	540
	CCGAGGCTGC	TGCTGTCTGC	TGCTGTTTCT	GGGGTCCCAC	ACATCGTCCA	AACATCCTAT	600
60	GATGTGCGCT	TTCTAGGAAG	ACTCCTGGAT	TTTCATCAATG	TCTTGTCTTA	TGACTTACAT	660
	GGAGTTGGG	AAAGGTTTAC	AGGACATAAT	AGCCCTCTCT	TCTCTCTGCC	TGAAGACCCC	720
	AAATCTTCGG	CATATGCTAT	GAATTATTTG	AGAAAGCTTG	GGGCACCCCT	AGAGAAGCTC	780
	ATCATGGGGA	TCCCCACCTA	TGGACGTACC	TTTCGCTTCC	TCAAAGCCTC	TAAGATGGG	840
	TTGCAGGCCA	GAGCGATCGG	ACCAGCATCT	CCAGGGAAGT	ACACCAAGCA	AGAAGGCTTC	900
65	TTGGCTTATT	TTGAGATTTG	TTCTTTTGTC	TGGGGAGCGA	AGAAGCACTG	GATTGATTAC	960
	CAGTATGTCC	CGTATGCCAA	CAAGGGGAAA	GAGTGGGTTG	GCTATGACAA	TGCCATCAGC	1020
	TTCAAGTTACA	AGGCATGGTT	TATAAGGCGA	GAGCATTTTG	GGGGGGCCAT	GGTGTGGACA	1080
	TTGGACATGG	ATGACGTGAG	GGGCACGTTT	TGTGGCACTG	GCCCTTTCCC	CCTTGTCTAC	1140
70	GTATTGAATG	ATATCTTGCT	GCGGGCTGAG	TTCAAGTTCAA	CTTCTTTACC	ACAATTTTGG	1200
	CTGTCACTG	CTGTGAATTC	TTCAAGCACT	GACCCTGAAA	GGCTGGCTGT	GACCACGGCA	1260
	TGGACCACTG	ATAGTAAGAT	TTTGCCCCCA	GGAGGAGAGG	CTGGGGTTC	TGAGATCCAC	1320
	GGAAAGTGTG	AAAATATGAC	TATAACCCCT	AGAGGTACAA	CTGTGACCCC	TACAAAGGAA	1380
	ACTGTATCCC	TTGGAAAGCA	CACGTAGCT	CTAGGAGAGA	AGACTGAGAT	CACTGGGGCA	1440
	ATGACCATGA	CTTCTGTGGT	TCATCAGTCC	ATGACCCCTG	GAGAGAAGGC	CCTGACCCCT	1500
75	GTGGGTCACT	AATCTGTGAC	CACGTGGACG	AAGACCCTGA	CCTCTGTGGG	TTATCAGTCT	1560
	GTGACCCCTG	GGGAAAAGAC	CCTGACCCCT	GTGGGTCACT	AGTCTGTGAC	CCCTGTGAGT	1620
	CATCAGTCTG	TGAGCCCTGG	AGGAACGACT	ATGACCCCTG	TCCATTTTCA	GACTGAGACC	1680
	CTTAGACAGA	ATACAGTGGC	CCCTAGAAGG	AAGGCTGTGG	CCCGTGAAAA	GGTGACTGTC	1740
	CCCTCCAGAA	ACATATCAGT	CACCCCTGAA	GGGCAGACTA	TGCCTTTAAG	AGGGGAGAA	1800
80	TTGACTTCTG	AGGTGGGCAC	TCACCCGAGG	ATGGGTAAC	TGGGTCTTCA	GATGGAAGCT	1860
	GAAACAGGGA	TGATGCTGTC	CTCCAGCCCC	GTCATCCAGC	TCCCGGAACA	AACTCCTCTA	1920
	GCTTTTGACA	ACCGCTTTGT	TCCCATCTAT	GGAAACCAAT	CCTCTGTCAA	CTCAGTAACC	1980
	CCTCAACAAA	GTCTCTTTTC	TCTAAAAAAA	GAATCCCGAG	AAAACTCTGC	TGTGGATGAA	2040
	GAAGCCTAAG	CCCTCTGGT	GTCAGAAACC	AGGGAAACCC	CTTGTCTTTT	CTTCTAAGTG	2100
	ACATGTTGGA	AGCCTTCTCA	TCCCGGGGCA	AAGCAGGCAT	CAAAACCAAT	ATAGGCCAAT	2160

CTCTTTTCCA TTAAATAAAC TGTAAACACA AGAACCCA

Seq ID NO: 632 Protein sequence
Protein Accession #: NP_002548.1

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1	11	21	31	41	51	
MWKLLEWVGL	VLVLKHHGDA	AHKLVCYFTN	WAHSRPGPAS	ILPHDLDPFL	CTHLIFAFAS	60
MNNNQIVAKD	LQDEKILYPE	FNKLKERNRE	LKTLLSIGGW	NFGTSRFTTM	LSTFANREKF	120
IASVISLLRT	HDFDGLDLFF	LYPGLRGSPM	HDRWTFLLFI	EELLFAFRKE	ALLTMRPRLL	180
LSAAVSGVPH	IVQTSYDVRF	LGRLLDINIV	LSYDLHGWE	RFTGHNSPLF	SLPEDPKSSA	240
YAMMYWRKLG	APSEKLIMGI	PTYGRTFRL	KASKNGLQAR	AIGPASPGKY	TKQEGFLAYF	300
EICSFVWGAK	KHWIDYQYVP	YANKGKEWVG	YDNAISFSYK	AWFIRREHFG	GAMVWTLDM	360
DVRGTFCTGT	PFPLVYVLND	ILVRAEFSST	SLPQFWLSSA	VNSSTDPER	LAVTTAWTTD	420
SKILPPGGEA	GVTEIHGKCE	NMTITPRGTT	VTPTKETVSL	GKHTVALGEK	TEITGAMTMT	480
SVGHQSMTPG	EKALTPVGHQ	SVTTGQKILT	SVGYQSVTPG	EKTLTPVGHQ	SVTPVSHQSV	540
SPGGTMTTPV	HFQTETLRQN	TVAPRRKAVA	REKVTVPSPN	ISVTPEGQTM	PLRGENLTSE	600
VGTHPRMGNL	GLQMEAENRM	MLSSSPVIQL	PEQTPLAFDN	RFVPIYGNHS	SVNSVTPQTS	660
PLSLKKEIPE	NSAVDEEA					

Seq ID NO: 633 DNA sequence
Nucleic Acid Accession #: NM_003885.1
Coding sequence: 98..1021

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1	11	21	31	41	51	
AAACTCAGAA	TTTTCGCGGG	CTCGGTGAGC	GGTTTATACC	CTCCGGCCGG	CAGGCTGGGC	60
GCAGGGGGCG	AGCCCCCGCC	CGGCGCGCAG	CAGCACCATG	GGCACCCTGC	TGTCCCTGTC	120
TCCACGTAC	CGGAAGGCCA	CGCTGTTTGA	GGATGGCGCG	GCCACCCTGG	GCCACTATAC	180
GGCCGTACAG	AACAGCAAGA	ACGCCAAGGA	CAAGAACCCTG	AAGCGCCACT	CCATCATCTC	240
CGTGCTGCCT	TGGAAGAGAA	TCGTGGCCGT	GTCGGCCAAG	AAGAAGAACT	CCAAGAAGGT	300
GCAGCCTAAC	AGCAGCTACC	AGAACAACAT	CACGCACCTC	AACAATGAGA	ACCTGAAGAA	360
GTCGCTGTCG	TGCGCCAACC	TGTCCACATT	CGCCAGCCCC	CCACCGGCCC	AGCCGCCTGC	420
ACCCCGGGCC	AGCCAGCTCT	CGGTTTCCCA	GACCGGGGGC	TCCTCCTCAG	TCAAGAAAGC	480
CCCTCACCTC	GCCGTACACT	CCGCAGGGAC	GCCCAAACGG	GTCATCGTCC	AGGCGTCCAC	540
CAGTGAGCTG	CTTCGCTGCC	TGGTGAGTT	TCTCTGCCGC	CGGTGCTACC	GCCTGAAGCA	600
CCTGTCCCCC	ACGGACCCCG	TGCTCTGGCT	GCGCAGCGTG	GACCGCTCGC	TGCTTCTGCA	660
GGGTGCGCAG	GACCAGGGCT	TCATCACGCC	GGCCAACGTG	GTCTTCTCT	ACATGCTCTG	720
CAGGGATGTT	ATCTCCTCCG	AGGTGGGCTC	GGATCACGAG	CTCCAGGCCG	TCCTGCTGAC	780
ATGCTGTAC	CTCTCCTACT	CCTACATGGG	CAACGAGATC	TCCTACCCGC	TCAAGCCCTT	840
CCTGGTGGAG	AGCTGCAAGG	AGGCCTTTTG	GGACCGTTGC	CTCTCTGTCA	TCAACCTCAT	900
GAGCTCAAAG	ATGTGTGAGA	TAAATGCCGA	CCCACACTAC	TTACACAGG	TCTTCTCCGA	960
CCTGAAGAAC	GAGAGCGGCC	AGGAGGACAA	GAAGCGGCTC	CTCCTAGGCC	TGGATCGGTG	1020
AGCACTGTAG	CCTGCGTCAT	GGCTCAAGGA	TTCAATGCAT	TTTAAAGAAT	TTATTATTAA	1080
ATCAGTTTTG	TGTACAG					

Seq ID NO: 634 Protein sequence
Protein Accession #: NP_003876.1

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55

1	11	21	31	41	51	
MGTVLSLSPS	YRKATLFEDG	AATVGHYTA	QNSKNAKDKN	LKRHSIISVL	PWKRIVAVSA	60
KKKNSKKVQP	NSSQNNITH	LNNENLKSL	SCANLSTFAQ	PPPAQPPAPP	ASQLSGSQTG	120
GSSSVKKAPH	PAVTSAGTPK	RVIVQASTSE	LLRCLGEFLC	RRCYRLKHL	PTDPVLNLS	180
VDRSLLQGW	QDQGFITPAN	VVFLYMLCRD	VISSEVSDH	ELQAVLLTCL	YLSYSYMGNE	240
ISYPLKPFIV	ESCKEAFWDR	CLSVINLMSS	KMLQINADPH	YFTQVFSDLK	NESQEDKKR	300
LLGLGLDR						

TABLE 79A:

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelID:	Unigene number			
	Unigene Title:	Unigene gene title			
	Seq ID No.:	Sequence identification number linking information in Table 79A to sequences in Table 80			
10	Pkey	ExAccn	UnigenelID	Unigene Title	Seq ID No.
15	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	Seq ID No. C1 & C217
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID No. C2 & C218
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C3 & C219
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C4 & C220
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. C5 & C221
20	443646	AI085198	Hs.164226	Thrombospondin 1	Seq ID No. C6 & C222
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	Seq ID No. C7 & C223
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	Seq ID No. C8 & C224
	444381	BE387335	Hs.283713	hypothetical protein BC014245	Seq ID No. C9 & C225
	421582	AI910275	Hs.350470	trefoil factor 1 (breast cancer, estroge	Seq ID No. C10 & C226
25	411789	AF245505	Hs.72157	Adican	Seq ID No. C11 & C227
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	Seq ID No. C12
	428698	AA852773	Hs.334838	KIAA1866 protein	Seq ID No. C13 & C228
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	Seq ID No. C14 & C229
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. C15 & C230
30	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	Seq ID No. C16 & C231
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	Seq ID No. C17 & C232
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	Seq ID No. C18 & C233
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	Seq ID No. C19 & C234
	432179	X75208	Hs.2913	EphB3	Seq ID No. C20 & C235
35	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	Seq ID No. C21 & C236
	409889	AW630041	Hs.56937	suppression of tumorigenicity 14 (colon	Seq ID No. C22 & C237
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C23 & C238
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C24 & C239
	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	Seq ID No. C25 & C240
40	434206	AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen i	Seq ID No. C26 & C241
	423936	U77629	Hs.135639	achaele-scute complex (Drosophila) homol	Seq ID No. C27 & C242
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	Seq ID No. C28 & C243
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	Seq ID No. C29 & C244
	415214	AI445236	Hs.125124	EphB2	Seq ID No. C30 & C245
45	443247	BE614387	Hs.333893	c-Myc target JPO1	Seq ID No. C31 & C246
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	Seq ID No. C32 & C247
	410418	D31382	Hs.63325	transmembrane protease, serine 4	Seq ID No. C33 & C248
	446342	BE298665	Hs.14846	solute carrier family 7 (cationic amino	Seq ID No. C34 & C249
	411274	NM_002776	Hs.69423	kallikrein 10	Seq ID No. C35 & C250
50	104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	Seq ID No. C36 & C251
	422260	AA315993	Hs.105484	regenerating gene type IV	Seq ID No. C37 & C252
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C38 & C253
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	Seq ID No. C39 & C254
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	Seq ID No. C40 & C255
55	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	Seq ID No. C41 & C256
	422330	D30783	Hs.115263	epiregulin	Seq ID No. C42 & C257
	408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. C43 & C258
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	Seq ID No. C44 & C259
	437852	BE001836	Hs.256897	putative GPCR	Seq ID No. C45 & C260
60	408243	Y00787	Hs.624	interleukin 8	Seq ID No. C46 & C261
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. C47 & C262
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	Seq ID No. C48 & C263
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. C49 & C264
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	Seq ID No. C50 & C265
65	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	Seq ID No. C51 & C266
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. C52 & C267
	442006	AW975183	Hs.372210	ESTs, Weakly similar to S72482 hypotheti	Seq ID No. C53 & C268
	413048	M93221	Hs.75182	mannose receptor, C type 1	Seq ID No. C54 & C269
	443324	R44013	Hs.164225	ESTs	Seq ID No. C55 & C270
70	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C56 & C271
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C57 & C272
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	Seq ID No. C58 & C273
	442652	AI005163	Hs.201378	Homo sapiens cDNA FLJ40427 fis	Seq ID No. C59 & C274
	450726	AW204600	Hs.355462	HUMPSPBA Human pulmonary surfactant-asso	Seq ID No. C60 & C275
75	416965	N26223	Hs.160436	MDAC1	Seq ID No. C61 & C276
	442275	AW449467	Hs.54795	Homo sapiens secretoglobulin, family 3A, m	Seq ID No. C62 & C277
	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C63 & C278
	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C64 & C279
	453142	AA033648	Hs.7473	Homo sapiens gap junction protein, alpha	Seq ID No. C65 & C280
80	421659	NM_014459	Hs.106511	protocadherin 17	Seq ID No. C66 & C281
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	Seq ID No. C67 & C282
	421563	NM_006433	Hs.105806	granulysin	Seq ID No. C68 & C283
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	Seq ID No. C69 & C284
	414991	C17898		Homo sapiens up-regulated by BCG-CWS (LO	Seq ID No. C70 & C285
	419833	AA251131	Hs.220697	Homo sapiens tryptophanyl-tRNA synthetas	Seq ID No. C71 & C286
	424943	AU077260	Hs.153924	death-associated protein kinase 1	Seq ID No. C72 & C287

	430890	X54232	Hs.2699	glypican 1	Seq ID No. C73 & C288
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No. C74 & C289
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	Seq ID No. C75 & C290
	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No. C76 & C291
5	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	Seq ID No. C77 & C292
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	Seq ID No. C78 & C293
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	Seq ID No. C79 & C294
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C80 & C295
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C81 & C296
10	431846	BE019924	Hs.271580	uroplakin 1B	Seq ID No. C82 & C297
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	Seq ID No. C83 & C298
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	Seq ID No. C84 & C299
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	Seq ID No. C85 & C300
15	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. C86 & C301
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. C87 & C302
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	Seq ID No. C88 & C303
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	Seq ID No. C89 & C304
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	Seq ID No. C90 & C305
	418462	BE001596	Hs.85266	integrin, beta 4	Seq ID No. C91 & C306
20	439606	W79123	Hs.58561	G protein-coupled receptor 87	Seq ID No. C92 & C307
	407720	AB037776	Hs.38002	immunoglobulin superfamily, member 9	Seq ID No. C93 & C308
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	Seq ID No. C94 & C309
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	Seq ID No. C95 & C310
25	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C96 & C311
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C97 & C312
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C98 & C313
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C99 & C314
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C100 & C315
30	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C101 & C316
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C102 & C317
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C103 & C318
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C104 & C319
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C105 & C320
35	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	Seq ID No. C106 & C321
	440659	AF134160	Hs.7327	claudin 1	Seq ID No. C107 & C322
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C108 & C323
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C109 & C324
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C110 & C325
40	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	Seq ID No. C111 & C326
	414774	X02419	Hs.77274	plasminogen activator, urokinase	Seq ID No. C112 & C327
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	Seq ID No. C113 & C328
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	Seq ID No. C114 & C329
	449101	AA205847	Hs.23016	G protein-coupled receptor	Seq ID No. C115 & C330
45	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	Seq ID No. C116 & C331
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	Seq ID No. C117 & C332
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	Seq ID No. C118 & C333
	408482	NM_000676	Hs.45743	adenosine A2b receptor	Seq ID No. C119 & C334
	426761	AI015709	Hs.172089	PORIMIN Pro-oncogene receptor inducing me	Seq ID No. C120 & C335
50	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	Seq ID No. C121 & C336
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	Seq ID No. C122 & C337
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	Seq ID No. C123 & C338
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	Seq ID No. C124 & C339
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	Seq ID No. C125 & C340
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	Seq ID No. C126 & C341
	428513	BE220806	Hs.184697	plexin C1	Seq ID No. C127 & C342
	430280	AA361258	Hs.237868	interleukin 7 receptor	Seq ID No. C128 & C343
	428486	AW583497	Hs.184604	pancreatic polypeptide	Seq ID No. C129 & C344
	457489	AI693815	Hs.127179	cryptic gene	Seq ID No. C130 & C345
	432874	W94322	Hs.279651	melanoma inhibitory activity	Seq ID No. C131 & C346
60	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C132 & C347
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C133 & C348
	404682			ortholog of mouse polydomain protein	Seq ID No. C134 & C349
	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	Seq ID No. C135 & C350
65	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C136 & C351
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C137 & C352
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C138 & C353
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	Seq ID No. C139 & C354
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	Seq ID No. C140 & C355
70	432596	AJ224741	Hs.278461	matrilin 3	Seq ID No. C141 & C356
	444006	BE395085	Hs.334762	type I transmembrane protein Fn14	Seq ID No. C142 & C357
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	Seq ID No. C143 & C358
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C144 & C359
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C145 & C360
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	Seq ID No. C146 & C361
75	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	Seq ID No. C147 & C362
	422109	S73265	Hs.1473	gastrin-releasing peptide	Seq ID No. C148 & C363
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	Seq ID No. C149 & C364
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	Seq ID No. C150 & C365
80	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	Seq ID No. C151 & C366
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	Seq ID No. C152 & C367
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	Seq ID No. C153 & C368
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	Seq ID No. C154 & C369
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	Seq ID No. C155 & C370

5	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	Seq ID No. C156 & C371
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	Seq ID No. C157 & C372
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	Seq ID No. C158 & C373
	413095	AA494359	Hs.30715	potassium voltage-gated channel, Isk-rel	Seq ID No. C159 & C374
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	Seq ID No. C160 & C375
	436729	BE621807	Hs.351316	transmembrane 4 superfamily member 1	Seq ID No. C161 & C376
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	Seq ID No. C162 & C377
	451820	AW058357	Hs.199248	ESTs	Seq ID No. C163 & C378
10	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	Seq ID No. C164 & C379
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	Seq ID No. C165 & C380
	421340	F07783	Hs.1369	decay accelerating factor for complement	Seq ID No. C166 & C381
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C167 & C382
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C168 & C383
15	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	Seq ID No. C169 & C384
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	Seq ID No. C170 & C385
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	Seq ID No. C171 & C386
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	Seq ID No. C172 & C387
	439659	AW970780	Hs.59483	leucine-rich repeat-containing G protein	Seq ID No. C173 & C388
20	411825	AK000334	Hs.352415	solute carrier family 39 (zinc transport	Seq ID No. C174 & C389
	412314	AA825247	Hs.356084	G protein-coupled receptor 27 (GPR27) (S	Seq ID No. C175 & C390
	429150	AF120103	Hs.197366	smoothened (Drosophila) homolog	Seq ID No. C176 & C391
	419073	AW372170	Hs.183918	transmembrane receptor Unc5H2 mRNA	Seq ID No. C177 & C392
	411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	Seq ID No. C178 & C393
25	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C179 & C394
	421779	AI879159	Hs.108219	wingless-type MMTV integration site fami	Seq ID No. C180 & C395
	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	Seq ID No. C181 & C396
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2 (str	Seq ID No. C182 & C397
	436972	AA284679	Hs.25640	claudin 3	Seq ID No. C183 & C398
30	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No. C184 & C399
	416370	N90470	Hs.203697	CD38 antigen (p45)	Seq ID No. C185 & C400
	437052	AA861697	Hs.120591	ESTs	Seq ID No. C186 & C401
	421481	AW391972	Hs.104696	KIAA1324 protein	Seq ID No. C187 & C402
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	Seq ID No. C188 & C403
35	426174	AA547959	Hs.115838	Homo sapiens similar to Echinoidin (LOC1	Seq ID No. C189 & C404
	410037	AB020725	Hs.58009	KIAA0918 protein	Seq ID No. C190 & C405
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	Seq ID No. C191 & C406
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	Seq ID No. C192 & C407
	418576	AW968159	Hs.302740	Epithelial calcium channel 2, CaT-like A	Seq ID No. C193 & C408
40	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C194 & C409
	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C195 & C410
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C196 & C411
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C197 & C412
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C198 & C413
45	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C199 & C414
	430144	AI732722	Hs.98927	ERGL protein; ERGIC-53-like protein	Seq ID No. C200 & C415
	408833	AW612232	Hs.254835	ESTs	Seq ID No. C201 & C416
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	Seq ID No. C202 & C417
50	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C203 & C418
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C204 & C419
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	Seq ID No. C205 & C420
	425976	C75094	Hs.334514	NG22 protein	Seq ID No. C206 & C421
	432800	BE391046	Hs.278962	AIM-1 protein	Seq ID No. C207 & C422
55	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	Seq ID No. C208 & C423
	424339	BE257148	Hs.145416	endoglycan	Seq ID No. C209 & C424
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	Seq ID No. C210 & C425
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	Seq ID No. C211 & C426
	434293	NM_004445	Hs.3796	EphB6	Seq ID No. C212 & C427
	427715	BE245274	Hs.180428	KIAA1181 protein	Seq ID No. C213 & C428
60	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	Seq ID No. C214 & C429
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	Seq ID No. C215 & C430
	422424	AI186431	Hs.296638	prostate differentiation factor	Seq ID No. C216 & C431
	432378	AI493046	Hs.146133	ESTs	Seq ID No. C432 & C433
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C434 & C435

65 TABLE 79B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

70

Pkey	CAT Number	Accession
414991	1785136_1	D78831 C17898 D78863

75 TABLE 79C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NT_position: Indicates nucleotide positions of predicted exons.

80

Pkey	Ref	Strand	NT_position
------	-----	--------	-------------

5	404682	9797231	Minus	40977-41150
	404287	2326514	Plus	53134-53281
	404287	2326514	Plus	53134-53281
	404287	2326514	Plus	53134-53281

Table 80:

Seq ID NO: C1 DNA Sequence
Nucleic Acid Accession #: NM_005814
Coding sequence: 345..1304

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	AGTAGGTGAC	ACATGAGCCC	AGCCCCAGCT	CACCTGCCAA	TCCAGCTGAG	GAGCTCACCT	180
	GCCAAATCCAG	CTGAGGCTGG	GCAGAGGTGG	GTGAGAAGAG	GGAAAATTGC	AGGGACCTCC	240
	AGTTGGGCCA	GGCCAGAAGC	TGCTGTAGCT	TTAACCAGAC	AGCTCAGACC	TGCTGGAGG	300
15	CTGCCAGTGA	CAGGTTAGGT	TTAGGGCAGA	GAAGAAGCAA	GACCATGGTG	GGGAAGATGT	360
	GGCCTGTGTT	GTGGACACTC	TGTGCAGTCA	GGGTGACCGT	CGATGCCATC	TCTGTGGAAG	420
	CTCCGCAGGA	CGTTCCTCGG	GCTTCGCAGG	GAAAGAGTGT	CACCTGCCCC	TGCACCTACC	480
	ACACTTCAC	CTCCAGTCGA	GAGGGACTTA	TTCAATGGGA	TAAGCTCCTC	CTCACTCATA	540
	CGGAAAGGGT	GGTCATCTGG	CCGTTTTCAA	ACAAAACTA	CATCCATGGT	GAGCTTTATA	600
20	AGAATCGCGT	CAGCATATCC	AACAATGCTG	AGCAGTCCGA	TGCTCCATC	ACCATTGATC	660
	AGCTGACCAT	GGCTGACAAC	GGCACCTACG	AGTGTCTGTT	CTCGCTGATG	TCAGACCTGG	720
	AGGGCAACAC	CAAGTCACGT	GTCCGCCCTG	TGGTCCCTCG	GCCACCTCC	AAACCGAAT	780
	GCGGCATCGA	GGGAGAGACC	ATAATTGGGA	ACAACATCCA	GCTGACCTGC	CAATCAAAGG	840
	AGGGCTCACC	AACCCCTCAG	TACAGCTGGA	AGAGGTACAA	CATCCTGAAT	CAGGAGCAGC	900
25	CCCTGGCCCA	GCCAGCCTCA	GGTCAGCCTG	TCTCCCTGAA	GAATATCTCC	ACAGACACAT	960
	CGGGTTACTA	CATCTGTACT	TCCAGCAATG	AGGAGGGGAC	GCAGTTCTGC	AACATCACGG	1020
	TGGCCGTGAG	ATCTCCCTCC	ATGAACGTGG	CCCTGTATGT	GGGCATCGCG	GTGGGCGTGG	1080
	TTGAGCCCT	CATTATCATT	GGCATCATCA	TCTACTGCTG	CTGCTGCCGA	GGGAAGGACG	1140
	ACAACACTGA	AGACAAGGAG	GATGCAAGGC	CGAACCAGGA	AGCCTATGAG	GAGCCACCAG	1200
30	AGCAGCTAAG	AGAAGTTTCC	AGAGAGAGGG	AGGAGGAGGA	TGACTACAGG	CAGAAGAGAG	1260
	AGAGGAGCAG	TGGGCGTGAA	TCCCGGAGCC	ACCTCGACCA	GTGACAGGCC	AGCAGCAGAG	1320
	GGCGGCGGAG	GAAGGGTTAG	GGGTTCATT	TCCCGCTTCC	TGGCCTCCCT	TCTCCTTTCT	1380
	AAGCCCTGTT	CTCCTGTCCC	TCCATCCCAG	ACATTGATGG	GGACATTTCT	TCCCCAGTGT	1440
	CAGCTGTGGG	GAACATGGCT	GGCCTGGTAA	GGGGGTCCCT	GTGCTGATCC	TGCTGACCTC	1500
35	ACTGTCTGTT	GAAGTAACCC	CTCCTGGCTG	TGACACCTGG	TGCGGGCCTG	GCCCTCACTC	1560
	AAGACCAGGC	TGCAGCCTCC	ACTTCCCTCG	TAGTTGGCAG	GAGCTCCTGG	AAGCACAGCG	1620
	CTGAGCATGG	GGCGTCCCA	CTCAGAACTC	TCCAGGGAGG	CGATGCCAGC	CTTGGGGGGT	1680
	GGGGGCTGTC	CTGCTCACCT	GTGTGCCAG	CACCTGGAGG	GGCACCAGGT	GGAGGGTTTG	1740
	CACCTCCAC	ATCTTTCTTG	AATGAATGAA	AGAATAAGTG	AGTATGCTTG	GGCCCTGCAT	1800
40	TGGCTGGGCC	TCCAGCTCCC	ACTCCCTTTC	CAACCTCACT	TCCCGTAGCT	GCCAGTATGT	1860
	TCCAAACCT	CCTGGGAAGG	CCACCTCCCA	CTCCTGTGTC	ACAGGCCCTG	GGGAGCTTTT	1920
	GCCACACAC	TTTCCATCTC	TGCCCTGTCA	TATCGTACCT	GTCCCTCCAG	GCCCATCTCA	1980
	AATACACAAG	ATTTCTCTAA	CCCTATCCTA	ATTGTCCACA	TACGTGGAAA	CAATCCTGTT	2040
	ACTCTGTCCC	ACGTCCTAAT	ATGGGCCACA	AGGCACAGTC	TTCTGTAGCG	GTGCTCTCAC	2100
45	TGTATTAGAG	CGCCAGCTCC	TTGGGGCAGG	GCCTGGGCCT	CATGGCTTGT	GCTTTCCCTG	2160
	AAGCCCTAGT	AGCTGGCGCC	CATCCTAGTG	GGCACTTAAG	CTTAATTGGG	GAAACTGCTT	2220
	TGATTGGTTG	TGCCTTCCCT	TCTCTGGTCT	CCTTGAGATG	ATCGTAGACA	CAGGGATGAT	2280
	TCCCAACCAA	ACCCAGTAT	TCATTCACTG	AGTTAAACAC	GAATTGATT	AAAGTGAACA	2340
	CACACAAGGG	AGCTTGCTTG	CAGATGGTCT	GAGTTCTTGT	GTCCTGGTAA	TTCCTCTCCA	2400
50	GGCCAGAATA	ATTGGCATGT	CTCCTCAACC	CACATGGGGT	TCCTGGTTGT	TCCTGCATCC	2460
	CGATACTCTA	GCCCTGGGCC	TGCCAGGCC	ATTTGGGCTC	TGGTTTTCTG	GTGGGGCTGT	2520
	CCTGCTGCCC	TCCACAGGCC	TCCTTCTGTT	TGTCAGAGCAT	TTCTTCTACT	CTTGAGAGCT	2580
	CAGGCAGCGT	TAGGCTCTAT	GGACCACTGG	CTGGTCTCAT	CCAAGTCTGG	CTTCTGAGCT	2640
	TTTACTATTG	CTATCTTTTC	TGGATGATCA	GAAAAATAAT	TCCATAAATC	TATTGTCTAC	2700
55	TTGGGATTTT	TTAAAAATG	TATATTTT	TATATATTGT	TAAATCCTTT	GCTTCATTCC	2760
	AAATGCTTTC	AGTAATAATA	AAATTGTGGG	TGG			2793

Seq ID NO: C2 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3150

	1	11	21	31	41	51	
60	ATGGGGAGCC	GGACGCCAGA	GTCCCTCTC	CACGCCGTGC	AGCTGCGCTG	GGGCCCCCGG	60
65	CGCCGACCCC	CGCTSSGTCC	GCTGCTGTTG	CTGCTSSGTG	CGCCGCCACC	CAGGGTCGGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCGAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGGAGTTT	CGGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
	CCCAAGGCTA	ATACCAGCCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCTC	300
	TGGGGTGCCA	GCCCAACACA	GTGCACCCCC	ATTGAATTG	ACAGCAAAGG	CTCTCGGCTC	360
70	CTGGAGTCTC	CACTGTCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCTTGCAG	420
	TGGTTCGGGG	CAACAGTTTC	AGCCCATGGC	TCCTCCATCT	TGGCATGCGC	TCCACTGTAC	480
	AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCCGCT	CAGATTTCAG	CTGGGCAGCA	600
	GGACAGGGTT	ACTGCCAAGG	AGGCTTCAGT	GCCGAGTTCA	CCAAGACTGG	CCGTGTGGTT	660
75	TTAGGTGGAC	CAGGAAGCTA	TTTCTGGCAA	GGCCAGATCC	TGCTCTGCCAC	TCAGGAGGAG	720
	ATTGCAGAA	CTTATTTACCC	CGAGTACCTG	ATCAACCTGG	TTGAGGGGCA	GCTGAGAGCT	780
	CGCCAGGCCA	GTTCCATCTA	TGATGACAGC	TACCTAGGAT	ACTCTGTGGC	TGTTGGTGAA	840
	TTCACTGGTG	ATGACACAGA	AGACTTTGTT	GCTGGTGTGC	CCAAAGGGAA	CCTCACTTAC	900
	GGCTATGTCA	CCATCTTTAA	TGGCTCAGAC	ATTGATCCCT	TCTACAACCT	CTCAGGGGAA	960
80	CAGATGGCCT	CCTACTTTGG	CTATGCACTG	GCCGCCACAG	ACGTCAATGG	GGACGGGCTG	1020
	GATGACTTGC	TGGTGGGGGG	ACCCCTGCTC	ATGGATCGGA	CCCTTGACGG	GCGGCCTCAG	1080
	GAGGTGGGCA	GGGTCTACGT	CTACCTGCAG	CACCCAGCCG	GCATAGAGCC	CACGCCACCC	1140
	CTTACCTTCA	CTGGCCATGA	TGAGTTTGGC	CGATTTGGCA	GCTCCTTGAC	CCCCCTGGGG	1200
	GACCTGGACC	AGGATGGCTA	CAATGATGTG	GCCATCGGGG	CTCCCTTTGG	TGGGGAGACC	1260
	CAGCAGGGAG	TAGTGTTTGT	ATTTCCTGGG	GGCCAGGAG	GGCTGGGCTC	TAAGCCTTCC	1320

5	CAGGTTCTGC	AGCCCCGTGTG	GGCAGCCAGC	CACACCCAG	ACTTCTTTGG	CTCTGCCCTT	1380
	CGAGGAGGCC	GAGACCTGGA	TGGCAATGGA	TATCCTGATC	TGATTGTGGG	GTCCCTTGGT	1440
	GTGGACAAGG	CTGTGGTATA	CAGGGGCCGC	CCCATCGTGT	CCGCTAGTGC	CTCCCTCACC	1500
	ATCTTCCCCG	CCATGTTCAA	CCCAGAGGAG	CGGAGCTGCA	GCTTAGAGGG	GAACCCCTGTG	1560
	GCCTGCATCA	ACCTTAGCTT	CTGCCTCAAT	GCTTCTGGAA	AACACGTTGC	TGACTCCATT	1620
	GGTTTCACAG	TGGAACCTCA	GCTGGACTGG	CAGAAGCAGA	AGGGAGGGGT	ACGGCGGGCA	1680
	CTGTTCCCTG	CCTCCAGGCA	GGCAACCCTG	ACCCAGACCC	TGCTCATCCA	GAATGGGGCT	1740
	CGAGAGGATT	GCAGAGAGAT	GAAGATCTAC	CTCAGGAACG	AGTCAGAATT	TCGAGACAAA	1800
10	CTCTCGCCGA	TTACATCGC	TCTCAACTTC	TCCTTGGACC	CCCAAGCCCC	AGTGACAGC	1860
	CACGGCTCA	GGCCAGCCCT	ACATTATCAG	AGCAAGAGCC	GGATAGAGGA	CAAGGCTCAG	1920
	ATCTTGCTGG	ACTGTGGAGA	AGACAACATC	TGTGTGCTTG	ACCTGCAGCT	GGAAGTGTTC	1980
	GGGGAGCAGA	ACCATGTGTA	CCTGGGTGAC	AAGAATGCCC	TGAACCTCAC	TTTCCATGCC	2040
	CAGAAATGTGG	GTGAGGGTGG	CGCCTATGAG	GCTGAGCTTC	GGGTCAACGC	CCCTCCAGAG	2100
15	GCTGAGTACT	CAGGACTCGT	CAGACACCCA	GGGAACCTCT	CCAGCCTGAG	CTGTGACTAC	2160
	TTTGCCGTGA	ACCAGAGCCG	CCTGCTGGTG	TGTGACCTGG	GCAACCCCAT	GAAGGCAGGA	2220
	GCCAGTCTGT	GGGGTGGCCT	TCGGTTTACA	GTCCCTCATC	TCCGGGACAC	TAAGAAAACC	2280
	ATCCAGTTTG	ACTTCCAGAT	CCTCAGCAAG	AATCTCAACA	ACTCGCAAAG	CGACGTGGTT	2340
	TCCTTTTCGGC	TCCTCCGTGGA	GGCTCAGGCC	CAGGTCACCC	TGAACGGTGT	CTCCAAGCCT	2400
20	GAGGCAGTGC	TATTCCCAGT	AAGCGACTGG	CATCCCCGAG	ACCAGCCTCA	GAAGGAGGAG	2460
	GACCTGGGAC	CTGCTGTCCA	CCATGTCTAT	GAGCTCATCA	ACCAAGGCCC	CAGCTCCATT	2520
	AGCCAGGGTG	TGCTTGAAC	CAGCTGTCCC	CAGGCTCTGG	AAGGTGACGA	GCTCCTATAT	2580
	GTGACCAGAG	TTACGGGACT	CAACTGCACC	ACCAATCACC	CCATTAACCC	AAAGGGCCTG	2640
	GAGTTGGATC	CCGAGGGTCT	CCTGCACCAC	CAGCAAAAAC	GGGAAGCTCC	AAGCCGCAGC	2700
25	TCGTCTTCCT	CGGGACCTCA	GATCCTGAAA	TGCCCCGAGG	CTGAGTGTTC	CAGGCTGCCG	2760
	TGTGAGCTCG	GGCCCCTGCA	CCAACAAGAG	AGCCAAAGTC	TGCAGTTGCA	TTTCCGAGTC	2820
	TGGGCCAAGA	TTTCTTTGCA	GCGGGAGCAC	CAGCCATTTA	GCCTGCAAGT	TGAGGCTGTG	2880
	TACAAAGCCC	TGAAGATGCC	CTACCGAATC	CTGCCTCGGC	AGCTGCCCCA	AAAAGAGCGT	2940
	CAGGTGGCCA	CAGCTGTGCA	ATGGACCAAG	GCAGAAGGCA	GCTATGGCGT	CCCACCTGTG	3000
30	ATCATCATCC	TAGCCATCCT	GTTTGGCCTC	CTGCTCTAG	GTCTACTCAT	CTACATCCTC	3060
	TACAAGCTTG	GATTCTTCAA	ACGCTCCCTC	CCATATGGCA	CGGCCATGGA	AAAAGCTCAG	3120
	CTCAAGCCTC	CAGCCACCTC	TGATGCCTGA				3150

Seq ID NO: C3 DNA Sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1410

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	ATGCACAGCT	TTCTTCCACT	GCTGCTGCTG	CTGTTCTGGG	GTGTGGTGTC	ACACAGCTTC	60
	CCAGCGACTC	TAGAAACACA	AGAGCAAGAT	GTGGACTTAG	TCCAGAAATA	CCTGGAAAAA	120
	TACTACAAAC	TGAAGAAATG	TGGGAGGCAA	GTTGAAAAGC	GGAGAAATAG	TGGCCCAAGT	180
	GTTGAAAAAT	TGAAGCAAAAT	GCAGGAATTC	TTTGGGCTGA	AAGTGACTGG	GAAACCAGAT	240
	GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCTGATGT	GGCTCAGTTT	300
45	TCCTCTCACT	AGGGGAACCC	TCGCTGGGAG	CAAACACATC	TGACCTACAG	GATTGAAAAAT	360
	TACACGCCAG	ATTTGCCCAAG	AGCAGATGTG	GACCATGCCA	TTGAGAAAAGC	CTTCCAACCT	420
	TGGAGTAATG	TCACACCTCT	GACATTACCC	AAGGTCTCTG	AGGGTCAAGC	AGACATCATG	480
	ATATCTTTTG	TCAGGGGAGA	TCATCGGGAC	AACTCTCCTT	TTGATGGACC	TGGAGGAAAT	540
	CTTGCTCATG	CTTTTCAACC	AGGCCCAGGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600
50	GAAAGGTGGA	CCAACAATTT	CAGAGAGTAC	AACTTACATC	GTGTTGCGGC	TCATGAACTC	660
	GGCCATTCTC	TTGGACTCTC	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
	ACCTTCAGTG	GTGATGTTCA	GCTAGCTCAG	GATGACATTG	ATGGCATCCA	AGCCATATAT	780
	GGACGTTCCC	AAAATCCTGT	CCAGCCCATC	GGCCCAAAA	CCCCAAAAGC	ATGTGACAGT	840
	AAGCTAACCT	TTGATGCTAT	AACTACGATT	CGGGGAGAAG	TGATGTTCTT	TAAAGACAGA	900
55	TTCTACATGC	GCACAAATCC	CTTCTACCCG	GAAGTTGAGC	TCAATTTTCT	TTCTGTTTTT	960
	TGGCCACAAC	TGCCAAATGG	GCTTGAAGCT	GCTTACGAAT	TTGCCGACAG	AGATGAAGTC	1020
	CGGTTTTTCA	AAGGGAATAA	GTACTGGGCT	GTTCAGGGAC	AGAATGTGCT	ACACGGATAC	1080
	CCCAAGGACA	TCTACAGCTC	CTTTGGCTTC	CCTAGAAGTC	TGAAGCATAT	CGATGCTGCT	1140
	CTTTCTGAGG	TGAAGGTGAT	GAAGCAAGTC	TTCTTTGTTG	CTAACAATAA	CTGGAGGTAT	1200
60	GATGAATATA	AACGATCTAT	GGATCCAGGT	TATCCCAAAA	TGATAGCACA	TGACTTTCCAT	1260
	GGAATTGGCC	ACAAAGTTGA	TGCAGTTTTC	ATGAAAGATG	GATTTTCTTA	TTTCTTTTCT	1320
	GGAACAAGAC	AATACAAATT	TGATCCTAAA	ACGAAGAGAA	TTTTGACTCT	CCAGAAAGCT	1380
	AATAGCTGGT	TCAACTGCAG	GAAAAATTAG				1410

Seq ID NO: C4 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1410

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	ATGCACAGCT	TTCTTCCACT	GCTGCTGCTG	CTGTTCTGGG	GTGTGGTGTC	ACACAGCTTC	60
	CCAGCGACTC	TAGAAACACA	AGAGCAAGAT	GTGGACTTAG	TCCAGAAATA	CCTGGAAAAA	120
	TACTACAAAC	TGAAGAAATG	TGGGAGGCAA	GTTGAAAAGC	GGAGAAATAG	TGGCCCAAGT	180
	GTTGAAAAAT	TGAAGCAAAAT	GCAGGAATTC	TTTGGGCTGA	AAGTGACTGG	GAAACCAGAT	240
75	GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCTGATGT	GGCTCAGTTT	300
	GTCCTCACTG	AGGGGAACCC	TCGCTGGGAG	CAAACACATC	TGACCTACAG	GATTGAAAAAT	360
	TACACGCCAG	ATTTGCCCAAG	AGCAGATGTG	GACCATGCCA	TTGAGAAAAGC	CTTCCAACCT	420
	TGGAGTAATG	TCACACCTCT	GACATTACCC	AAGGTCTCTG	AGGGTCAAGC	AGACATCATG	480
	ATATCTTTTG	TCAGGGGAGA	TCATCGGGAC	AACTCTCCTT	TTGATGGACC	TGGAGGAAAT	540
80	CTTGCTCATG	CTTTTCAACC	AGGCCCAGGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600
	GAAAGGTGGA	CCAACAATTT	CAGAGAGTAC	AACTTACATC	GTGTTGCGGC	TCATGCCCTC	660
	GGCCATTCTC	TTGACTCTCT	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
	ACCTTCAGTG	GTGATGTTCA	GCTAGCTCAG	GATGACATTG	ATGGCATCCA	AGCCATATAT	780
	GGACGTTCCC	AAAATCCTGT	CCAGCCCATC	GGCCCAAAA	CCCCAAAAGC	ATGTGACAGT	840
	AAGCTAACCT	TTGATGCTAT	AACTACGATT	CGGGGAGAAG	TGATGTTCTT	TAAAGACAGA	900

5
 10
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCAT TTCTGTTTTTC 960
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTTCTTGTG CTAACAAATA CTGGAGGTAT 1200
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCCT 1260
 GGAATTGGCC ACAAAAGTTGA TGCAGTTTTT ATGAAAGATG GATTTTTCTA TTTCTTTTCAT 1320
 GGAACAAGAC AATACAAAT TGCATCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG 1410

Seq ID NO: C5 DNA Sequence
 Nucleic Acid Accession #: NM_014331.2
 Coding sequence: 1..1506

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 AAGAGGAAAG TCACCTTTACT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTGGAGCA 180
 GGAATCTTCA TCTCTCTTAA GGGCGTGCTC CAGAACACGG GCAGCGTGGG CATGTCCTCG 240
 ACCATCTGGA CGGTGTGTGG GGTCTGTGCA CTATTGGAG CTTTGTCTTA TGCTGAATTG 300
 GGAACAACTA TAAAGAAATC TGGAGGTCAT TACACATATA TTTTGGAGT CTTTGGTCCA 360
 TTACCAGCTT TTGTACGAGT CTGGGTGGAA CTCCTCATAA TACGCCCTGC AGCTACTGCT 420
 GTGATATCCC TGGCATTTGG ACGCTACATT CTGGAACCAT TTTTATTCA ATGTGAAATC 480
 CCTGAACCTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTGAT GGTCTCTAAAT 540
 AGCATGAGTG TCAGCTGGAG CGCCCGGATC CAGATTTTCT TAACCTTTTG CAAGCTCACA 600
 GCAATTTCTGA TAATTATAGT CCCTGGAGTT ATGCAGCTAA TTAAGGTCA AACGCAGAAC 660
 TTTAAAGACG CGTTTTTCAGG AAGAGATTCA AGTATTACGC GGTTCGCCAT GGCTTTTTAT 720
 TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTTACTGA AGAAGTAGAA 780
 AACCCTGAAA AAACCATTC CTTTGCAATA TGTATATCCA TGGCCATTGT CACCATTGGC 840
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 CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCACAT 3000
 GCTGGTAATC TCCCTCTGTT AGGAGGCTGA GGCAGGAGAA TTGCTTGAA CCGGGAGGCG 3060
 GAGTTTGAG TGAGCCAAAG TTGACCACCT GTACTCCAGC CTGGGTGACA AAGTCAGACT 3120
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Seq ID NO: C6 DNA Sequence
 Nucleic Acid Accession #: NM_003246.1
 Coding sequence: 112..3624

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 GCCTGGGGAC TAGGCGTCTT GTTCTGATG CATGTGTGTG GCACCAACCG CATTCAGAG 180
 TCTGGCGGAG ACAACAGCTG GTTTGACATC TTTGAACTCA CCGGGGCGGC CCGCAAGGGG 240
 TCTGGGCGCC GACTGCTGAA GGGCCCCGAC CCTTCCAGCC CAGCTTTCCG CATCGAGGAT 300
 GCCAACCTGA TCCCTCTGTT GCCTGATGAC AAGTTCCAAG ACCTGGTGGG TGCTGTGCGG 360
 GCAGAAAAGG GTTTCCTCCT TCTGGCATCC CTGAGGCAGA TGAAGAAGAC CCGGGGCACG 420

5	CTGCTGGCCC	TGGAGCGGAA	AGACCACTCT	GGCCAGGTCT	TCAGCGTGGT	GTCCAATGGC	480
	AAGGCGGGCA	CCCTGGACCT	CAGCCTGACC	GTCCAAGGAA	AGCAGCACGT	GGTGTCTGTG	540
	GAAGAAGCTC	TCCTGGCAAC	CGGCCAGTGG	AAGAGCATCA	CCCTGTTTGT	GCAGGAAGAC	600
	AGGGCCGAGC	TGTACATCGA	CTGTGAAAAG	ATGGAGAATG	CTGAGTTGGA	CGTCCCCATC	660
	CAAAGCGTCT	TCACCAAGGA	CCTGGCCAGC	ATCGCCAGAC	TCCGCATCGC	AAAGGGGGGC	720
	GTCAATGACA	ATTTCAGGG	GGTGTGTCAG	AATGTGAGGT	TTGTCTTTGG	AACCACACCA	780
	GAAGACATCC	TCAGGAACAA	AGGCTGCTCC	AGCTCTACCA	GTGTCTCTCT	CACCCCTTGAC	840
	AACAACGTGG	TGAATGGTTC	CAGCCCTGCC	ATCCGCACTA	ACTACATTGG	CCACAAGACA	900
10	AAGGACTTGC	AAGCCATCTG	CGGCATCTCC	TGTGATGAGC	TGTCCAGCAT	GGTCTCTGAA	960
	CTCAGGGGCC	TGGCGCCAT	TGTGACCACG	CTGCAGGACA	GCATCCGCAA	AGTGA CTGAA	1020
	GAGAACAAAG	AGTTGGCCAA	TGAGCTGAGG	CGGCCTCCCC	TATGCTATCA	CAACGGAGTT	1080
	CAGTACAGAA	ATAACGAGGA	ATGGACTGTT	GATAGCTGCA	CTGAGTGTCA	CTGTCCAGAAC	1140
	TCAGTTACCA	TCGTCAAAAA	GGTGTCTGTC	CCCATCATGC	CCGTCTCCAA	TGCCACAGTT	1200
	CCTGATGGAG	AATGCTGTCC	TCGCTGTTGG	CCCAGCGACT	CTGCGGACGA	TGGCTGGTCT	1260
15	CCATGGTCCG	AGTGGACCTC	CTGTTCTACG	AGCTGTGGCA	ATGGAATTCA	GCAGCGCGGC	1320
	CGCTCTGCG	ATAGCCTCAA	CAACCGATGT	GAGGGCTCCT	CGGTCCAGAC	ACGGACCTGC	1380
	CACATTGAGC	AGTGTGACAA	AAAGATTAAA	CAGGATGGTG	GCTGGAGCCA	CTGGTCCCCG	1440
	TGCTCATCTT	GTTCTGTGAC	ATGTGTGAT	GGTGTGATCA	CAAGGATCCG	GCTCTGCAAC	1500
20	TCTCCCAGCC	CCCAGATGAA	TGGGAAACCC	TGTGAAGGCG	AAGCGCGGGA	GACCAAAGCC	1560
	TGCAAGAAAG	ACGCCCTGCC	CATCAATGGA	GGCTGGGGTC	CTTGGTCAAC	ATGGGACATC	1620
	TGTTCTGTCA	CCTGTGGAGG	AGGGGTACAG	AAACGTAGTC	GCTCTGCAAA	CAACCCCGCA	1680
	CCCCAGTTTG	GAGGCAAGGA	CTGCGTTGGT	GATGTAACAG	AAAACCAAGT	CTGCAACAAG	1740
	CAGGACTGTC	CAATTGATGG	ATGCCCTGCT	AATCCCTGCT	TTGCCGGCGT	GAAGTGACT	1800
25	AGCTACCCTG	ATGGCAGCTG	GAAATGTGGT	GCTTGTCCCC	CTGTTTACAG	TGGAAATGGC	1860
	ATCCAGTGCA	CAGATGTTGA	TGAGTGCAAA	GAAGTGCCCT	ATGCCCTGCT	CAACCAACAT	1920
	GGAGAGCACC	GGTGTGAGAA	CACGGAACCC	GGCTACAAC	GCCTGCCCTG	CCCCCAACGC	1980
	TTCAACGGCT	CACAGCCCTT	CGGCCAGGGT	GTCAACATG	CCACGGCCAA	CAAAACAGGT	2040
	TGCAAGCCCC	GTAACCCCTG	CACGGATGGG	ACCCAGCACT	GCAACAAGAA	CGCCAAGTGT	2100
30	AACCTACTGG	GCCACTATAG	CGACCCCATG	TACCCGTGCG	AGTGCAAGCC	TGGCTACGTC	2160
	GGCAATGGCA	TCATCTGCGG	GGAGGACACA	GACCTGGATG	GCTGGCCCAA	TGAGAACCTG	2220
	GTGTGCGTGG	CCAATGCGAC	TTACCACTGC	AAAAAGGATA	ATTGCCCAA	CCCTCCCAAC	2280
	TCAGGGCAGG	AAGACTATGA	CAAGGATGGA	ATTGGTGATG	CCTGTGATGA	TGACGATGAC	2340
	AATGATAAAA	TTCAGATGTA	CAGGGACAAC	TGTCCATTCC	ATTACAACCC	AGCTCAGTAT	2400
35	GACTATGACA	GAGATGATGT	GGGAGACCGC	TGTGACAACT	GTCCCTACAA	CCACAACCCA	2460
	GATCAGGCAG	ACACAGACAA	CAATGGGGAA	GGAGACGCCT	GTGCTGCAGA	CATTGATGGA	2520
	GACGGTATCC	TCAATGAACG	GGACAACCTG	CAGTACGTCT	ACAATGTGGA	CCAGAGAGAC	2580
	ACTGATATGG	ATGGGGTTGG	AGATCAGTGT	GACAATTGCC	CCTTGGAACA	CAATCCGGAT	2640
	CAGCTGGACT	CTGACTCAGA	CCGCATTGGA	GATACCTGTG	ACAACATCA	GGATATTGAT	2700
40	GAAGATGGCC	ACCAGAACAA	TCTGGACAAC	TGTCCCTATG	TGCCCAATGC	CAACCAAGCT	2760
	GACCATGACA	AAGATGGCAA	GGGAGATGCC	TGTGACCACG	ATGATGACAA	CGATGGCATT	2820
	CCTGATGACA	AGGACAACCT	CAGACTCGTG	CCCAATCCCG	ACCAGAAGGA	CTCTGACGGC	2880
	GATGGTCGAG	GTGATGGCTG	CAAAGATGAT	TTTGACCATG	ACAGTTGTCC	AGACATCGAT	2940
	GACATCTGTC	CTGAGAAATG	TGACATCAGT	GAGACCGATT	TCCGCCGATT	CCAGATGATT	3000
45	CCCTCTGGAC	CCAAAGGGAC	ATCCCAAAAT	GACCCTAACT	GGGTTGTACG	CCATCAGGGT	3060
	AAAGAAGTCT	CTCAGACTGT	CAACTGTGAT	CCTGGACTCG	CTGTAGTTTA	TGATGAGTTT	3120
	AATGCTGTGG	ACTTTCAGTG	CACCTTCTTC	ATCAACACCG	AAAGGGACGA	TGACTATGCT	3180
	GGATTTGTCT	TTGGCTACCA	GTCCAGCAGC	CGCTTTTATG	TTGTGATGTG	GAAGCAAGTC	3240
	ACCCAGTCTC	ACTGGGACAC	CAACCCACAG	AGGGCTCAGG	GATACTCGGG	CCTTCTGTG	3300
50	AAAGTTGTAA	ACTCCACACC	AGGGCCTGGC	GAGCACCTGC	GGAAACGCCCT	GTGGCAGACA	3360
	GGAAACACCC	CTGGCCAGGT	GCGCACCTCG	TGGCATGACC	CTCGTCACAT	AGGCTGGAAA	3420
	GATTTACCCG	CCTACAGATG	GCGTCTCAGC	CACAGGCCAA	AGACGGGTTT	CATTAGAGTG	3480
	GTGATGTATG	AAGGGAAGAA	AATCATGGCT	GACTCAGGAC	CCATCTATGA	TAAAACCTAT	3540
	GCTGGTGGTA	GACTTAGGTT	GTTTGTCTTC	TCTCAAGAAA	TGGTGTCTTC	CTCTGACCTG	3600
55	AAATACGAAT	GTAGAGATCC	CTAATCATCA	AATTTGTTGAT	TGAAAGACTG	ATCATAAACC	3660
	AAATGCTGTA	TTGCACCTTC	TGGAACATATG	GGCTTGAGAA	AACCCCAAGG	ATCACTTCTC	3720
	CTTGGCTTCC	TTCTTTTCTG	TGCTTGCATC	AGTGTGGACT	CCTAGAACGT	GCGACCTGCC	3780
	TCAAGAAAAT	GCAAGTTTTC	AAAACAGACT	CATCAGCATT	CAGCCCTCAA	TGAATAAGAC	3840
	ATCTTCCAAG	CATATAAACA	ATTGCTTTGG	TTTCTTTTGG	AAAAAGCATC	TACTTGCTTC	3900
60	AGTTGGGAAG	GTGCCCATTC	CACTCTGCCT	TTGTACAGAA	GCAGGGTGCT	ATTGTGAGGC	3960
	CATCTCT						3967

Seq ID NO: C7 DNA Sequence
Nucleic Acid Accession #: NM_002192
Coding sequence: 86..1366

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70	AATCACAACA	ACTTTTGTCT	CCAGGATGCC	CTTGCTTTGG	CTGAGAGGAT	TTCTGTTGGC	120
	AAGTTGCTGG	ATTATAGTGA	GGAGTTCCCC	CACCCACAGG	TCCGAGGGGC	ACAGCGCGGC	180
	CCCGCACTGT	CCGTCTGTGT	CGCTGGCCGC	CCTCCCAAAG	GATGTACCCA	ACTCTCAGCC	240
	AGAGATGGTG	GAGGCCGTCA	AGAAGCATAT	TTTAAACATG	CTGCACCTGA	AGAAGAGACC	300
	CGATGTCAAC	CAGCCGGTAC	CCAAGGCGGC	GCTTCTGAAC	GCGATCAGAA	AGCTTCATGT	360
75	GGGCAAGTCC	GGGAGAGAAC	GGTATGTGGA	GATAGAGGAT	GACATTGGAA	GGAGGGCAGA	420
	AATGAATGAA	CTTATGAGAG	AGACCTCGGA	GATCATCACG	TTTGCCGAGT	CAGGAACAGC	480
	CAGGAAGACG	CTGCACCTTC	AGATTTCCAA	GGAAGGCAGT	AGCCTGTCTAG	TGGTGGAGCG	540
	TGCAGAAGTC	TGGCTCTTCC	TAAAAGTCCC	CAAGGCCAAC	AGGACCAGGA	CCAAAGTCAC	600
	CATCCGCCCT	TTTCAGCAGC	AGAAGCACCC	GCAGGGCAGC	TTGGACACAG	GGGAAGAGGC	660
80	CGAGGAAGTG	GGCTTAAAGG	GGGAGAGGAG	TGAACCTGTT	CTCTTGAAA	AAGTAGTAGA	720
	CGCTCGGAAG	AGCACCTGGC	ATGTCTTCCC	TGTCTCCAGC	AGCATCCAGC	GGTTGCTGGA	780
	CCAGGGCAAG	AGCTCCCTGG	ACGTTCCGGT	TGCCTGTGAG	CAGTGCCAGG	AGAGTGGCGC	840
	GAGCTTGGTT	CTCTCTGGGA	AGAAAGAGAA	GAAAGAGAGG	GAGGGGGAAG	GGAAAAAGAA	900
	GGGCGGAGGT	GAAGGTGGGG	CAGGAGCAGA	TGAGGAAAAG	GAGCAGTCGC	ACAGACCTTT	960
	CCTCATGCTG	CAGGCCCGGC	AGTCTGAAGA	CCACCTCAT	CGCCGGCCTC	GGCGGGCCTT	1020

5 GGAGTGTGAT GGCAAGGTCA ACATCTGCTG TAAGAAACAG TTCTTTGTCA GTTTCAGGA 1080
 CATCGGCTGG AATGACTGGA TCATTGCTCC CTCTGGCTAT CATGCCAACT ACTGCGAGGG 1140
 TGAGTGCCCG AGCCATATAG CAGGCACGTC CGGGTCCTCA CTGTCTTCC ACTCAACAGT 1200
 CATCAACCAC TACCGCATGC GGGGCCATAG CCCCTTTGCC AACCTCAAAT CGTGCTGTGT 1260
 GCCCACCAG CTGAGACCCA TGTCCATGTT GTACTATGAT GATGGTCAAA ACATCATCAA 1320
 AAAGGACATT CAGAACATGA TCGTGAGGGA GTGTGGGTGC TCATAGAGTT GCCCAGCCCA 1380
 GGGGAAAGG GAGCAAGAGT TGTCCAGAGA AGACAGTGGC AAAATGAAGA AATTTTAAAG 1440
 GTTTCAGT TAACCAGAAA AATAGAAATT AAAACAAAA CAAAAACAAA AAAAAACAA 1500
 10 AAAAAACAA AAGTAAATTA AAAACAAACC TGATGAAACA GATGAAACAG ATGAAGGAAG 1560
 ATGTGGAAT CTTAGCCTGC CTTAGCCAGG GCTCAGAGAT GAAGCAGTGA AGAGACAGAT 1620
 TGGGAGGAA AGGGAGAAAT GTGTACCTT TATTTCTTCT GAAATCACAC TGATGACATC 1680
 AGTTGTTAA ACGGGTATT GTCTTTCCC CCCTTGAGGT TCCTTGATGA GCTTGAATCA 1740
 ACCAATCTGA TCTGCAGTAG TGTGGACTAG AACAACCAA ATAGCATCTA GAAAGCCATG 1800
 15 AGTTGAAAG GGGCCATCAC AGGCACCTTC CTAGCCTAAT 1840

Seq ID NO: C8 DNA Sequence
 Nucleic Acid Accession #: NM_000095.1
 Coding sequence: 26..2299

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 25 CCTGGCTGCC CTGGCGCGGT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC 120
 GCAGATGCTT CGGGAAGTGC AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180
 GCGGCAGCAG GTCAGGAGAGA TCACGTTCCCT GAAAAACACG GTGATGGAGT GTGACGGGTG 240
 CGGGATGCAG CAGTCAGTAC GCACCGGCCT ACCCAGCGTG CGGCCCTGTC TCCACTGCGC 300
 30 GCCCGGCTTC TGCTTCCCCG GCGTGGCCTG CATCCAGACG GAGAGCGGCG GCCGCTGCGG 360
 CCCCTGCCCC GCGGGCTTCA CCGGCAACGG CTCGCACTGC ACCGACGTCA ACGAGTGCAA 420
 CGCCACCCCC TGCTTCCCCC GAGTCCGCTG TATCAACACC AGCCCCGGGT TCCGCTGCGA 480
 GGTCTGCCCC CGGGGTACA GCGGCCCCAC CCACAGGGG GTGGGGCTGG CTTTCGCCAA 540
 35 GGCCAAACAG CAGGTTTGCA CGACATCAA CGAGTGTGAG ACCGGGCAAC ATAAGTGGT 600
 CCCCAACTCC GTGTGCATCA ACACCCGGGG CTCTTCCAG TGCGGCCCGT GCCAGCCCGG 660
 CTTCTGGGG GACCAAGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCGACG 720
 CTGCGCCAGC GAGTGCACAG AGCATGCAGA CTGCGTCTTA GAGCGCGATG GCTCGCGGTC 780
 40 GTGCGTGTGT GCGTGTGGCT GGGCCGCAAA CGGATCCTC TGTGGTCCG ACACCTGACCT 840
 AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCGGAGCCG CAGTGCCGTA AGGACAACTG 900
 CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCGTC 960
 CGATCCGGAT CCGGACGCGG ACGGGTCCC CAATGAAAAG GACAACTGCC CGCTGGTGCG 1020
 45 GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGCG ACAACTGCCG 1080
 GTCCCAAGAG AACGACGACC AAAAGGACAC AGACCAAGGAC GGCCTGGGCG ATGCGTGCGA 1140
 CGACGACATC GACGGCGACC GGATCCGCAA CCAGGCCGAC AACTGCCCTA GGGTACCCAA 1200
 CTGAGACAGC AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCA 1260
 50 GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320
 CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACTGTC CCACGGTGCC 1380
 TAACAGTGCC CAGGAGGACT CAGACACGTA TGGCCAGGGT GATGCTGCG ACGACGACGA 1440
 CGCAATGAC GAGTCCCTG ACAGTCGGGA CAACTGCCGC CTGGTGCTTA ACCCCGCCA 1500
 GGAGGACGCG GACAGGACG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
 55 GTGTTAGAC AAGATCGAGC TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG 1620
 GGCCTTCCAG ACAGTCTGTG TGGACCGGA GGTGTGCGCG CAGATTGACC CCAACTGGGT 1680
 GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAAATGAAC AGCGACCCAG GCCTGGCTGT 1740
 GGGTTACACT GCTTCAATG GCGTGAATT CGAGGCGACG TTCCATGTGA ACACGGTCC 1800
 GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT 1860
 60 CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCTTCCGTG CTGTGGCCGA 1920
 GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGAAAC AGCTGCGGAA 1980
 CGCTCTGTGG CATACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040
 AAACGTGGGT TGAAGGACA AGAAGTCTTA TCGTTGGTTC CTGCAGCACC GGGCCCAAGT 2100
 GGGCTACATC AGGGTGCAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
 CTTGGACACA ACCATGCGGG GTGGCGCCT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
 65 CATCTGGGCC AACCTGCGTT ACCGTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
 TCAGCTGCGG CAGCCTAGG GACCAGGGTG AGGACCCGCC GGATGACAGC CACCCTCACC 2340
 GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCTGAGG GGGAGTGAG 2400
 AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAAGG 2439

Seq ID NO: C9 DNA Sequence
 Nucleic Acid Accession #: XM_057014
 Coding sequence: 143..874

70 1 11 21 31 41 51
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 75 CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCGCC TCCAGCTCCG 120
 CGCTGCCCCG CAGCCGGGAG CCATGCGACC CCAGGGCCCC GCGCCTCCC CGCAGCGGCT 180
 CCGCGGCGCT CTGCTGCTCC TGCTGCTGCA GCTGCCGCG CGCTCGAGCG CCTCTGAGAT 240
 CCCCAGGGGG AAGCAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
 80 AATGTGCTTA CAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAAATG 360
 CATTCGGGGT ACACCTGGGA TCCCAGTTCG GGATGGATT CAAAGGAGAA AGGGGGAATG 420
 TCTGAGGGAA AGCTTTGAGG AGTCTTGAC ACCCACTAC AAGCAGTGT CATGGAGTTC 480
 ATTGAATAT GGCATAGATC TTGGGAAAT TCGGAGTGT ACATTTACAA AGATGCGTTC 540
 AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACCTCGG CTAAATGCA GAAATGCATG 600
 CTGTACGCGT TGGTATTTC CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTG 660
 AGCTATATAT TATTTGACCA AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG 720

CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780
 CTGGGTGGC ACTTGTTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
 TTCTCGCATC ATTATTGAAG AACTACCCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
 TTTTCTTAT ATGCTTGGGA ATGGTTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
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 TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAGTG GTTTCATAT TTTTCTTAGT 1080
 TGGTTAGAAT ACTTCTCTTCA TAGTCACATT CTCTCAACCT ATAATTGGGA ATATTGTTGT 1140
 GGTCCTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAAGC TACCAATCTT 1200
 TGTACAATTT GTAAATGTTA AGAATTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
 CAACCTTAAA AAAAAAAAAA AAAA 1284

Seq ID NO: C10 DNA Sequence
 Nucleic Acid Accession #: NM_003225
 Coding sequence: 41..295

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 GCCTCCCGT TGTGCAATA AGGGCTGCTG TTTGACGAC ACCGTTTCGT GGGTCCCGTG 240
 GTGCTTCTAT CCTAATACCA TCGACGTCCC TCCAGAAGAG GAGTGTGAAT TTTAGACACT 300
 TCTGCAGGGA TCTGCTGCA TCTGACGGG GTGCCGTCCC CAGCACGGTG ATTAGTCCCA 360
 GAGCTCGGCT GCCACCTCCA CCGGACACCT CAGACACGCT TCTGCAGCTG TCGCTCGGCT 420
 CACAACACAG ATTGACTGCT CTGACTTTGA CTACTCAAAA TTGGCCTAAA AATTAAAGA 480
 GATCGATATT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 540

Seq ID NO: C11 DNA Sequence
 Nucleic Acid Accession #: NM_015419.1
 Coding sequence: 1..8487

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 AATTGGGGT TTAATAGCAT ACAGGCCCTG TCAGAAACCT CATTTGCAGG ACTGACCAAG 240
 TTGGAGTAC TTAATGATCA CGGCAATGAG ATCCCAAGCA TCCCGATGG AGCTTTAAGA 300
 GACCTCAGCT CTCTTCAGGT TTTCAAGTTC AGCTACAACA AGCTGAGAGT GATCACAGGA 360
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 TTTATCCACC CTCAGCTTTT CAACGGCTTA ACGTCTCTGA GGCTACTCCA TTTGGAAGGA 480
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 AGACTCTCCA CCTAAGGCA CCTTACTTGA GCAGAGAACA TGGTTAGAAC TCTTCTGCC 600
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 ATAGCATACT CAGTGAAGT TCCCGTGAAG CTACACAGAG AGCTCATGCT CAGCAAGAC 1200
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 CATTTTACGG TGGGAATCAC AGTGACCAAG AAAGGGTCTG GCTTGCCATC CAAAGAGGGC 2040
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	TCTACTATAG	GGGAACCAGG	TGTCCCAGGC	CAATCACATC	TACAAGGACT	GACAGACAAC	3120
	ATCCACCTTG	TGAAAAGTAG	TCTAAGCACT	CAAGACACCT	TACTGATTAA	AAAGGGTATG	3180
	AAAGAGATGT	CTCAGACACT	ACAGGGAGGA	AATATGCTAG	AGGGAGACCC	CACACACTCC	3240
5	AGAAGTTCTG	AGAGTGAGGG	CCAAGAGAGC	AAATCCATCA	CTTTGCCTGA	CTCCACACTG	3300
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	ACCATGAGCA	CTCACCTTTC	TCGAAGGAGA	CCCAACGGGA	GAAGGAGATT	ACGCCCAAC	3480
	AAATTCCGCC	ACCGGCACAA	GCAAAACCCA	CCCACAACCT	TTGCCCCATC	AGAGACTTTT	3540
10	TCCTACTCAAC	CAACTCAAGC	ACCTGACATT	AAGATTTCAT	GTCAAGTGGA	GAGTTCTCTG	3600
	GTTCCTACAG	CTTGGGTGGA	TAACACAGTT	AATACCCCA	AACAGTTGGA	AATGGAGAAG	3660
	AATGCAGAAC	CCACATCCAA	GGGAACACCA	CGGAGAAAAC	ACGGGAAGAG	GCCAAACAAA	3720
	CATCGATATA	CCCTTCTTAC	AGTGAGCTCA	AGAGCGTCCG	GATCCAAGCC	CAGCCCTTCT	3780
	CCAGAAAATA	AACATAGAAA	CATTGTTACT	CCCAGTTCAG	AAACTATACT	TTTGCCCTAGA	3840
	ACTGTTTCTC	TGAAAACCTGA	GGGCCCTTAT	GATTCCCTTAG	ATTACATGAC	AACCACCAGA	3900
15	AAAATATATT	CATCTTACC	TAAAGTCCAA	GAGACACTTC	CAGTCACATA	TAAACCACA	3960
	TCAGATGGAA	AAAGAAATTAA	GGATGATGTT	GCCACAAATG	TTGACAAAAC	TAAAAGTGAC	4020
	ATTTTAGTCA	CTGGTGAATC	AAATTAATAA	GCCATACCAA	CTTCTCGCTC	CTTGGTCTCC	4080
	ACTATGGGAG	AAATTAAGGA	AGAATCCTCT	CCTGTAGGCT	TTCCAGGAAC	TCCAACCTGG	4140
20	AATCCCTCAA	GGACGGCCCA	GCCTGGGAGG	CTACAGACAG	ACATACCTGT	TACCCTTCT	4200
	GGGGAATAAT	TTACAGACCC	TCCCTTCTCT	AAAGAGCTTG	AGGATGTGGA	TTTCACTTCC	4260
	GAGTTTTTGT	CCCTTTTGAC	AGTCTCCACA	CCATTTTACC	AGGAAGAAGC	TGGTTCTTCC	4320
	ACAACTCTCT	CAAGCATAAA	AGTGGAGGTG	GCTTCAAGTC	AGGCAGAAAC	CACCACCTT	4380
	GATCAAGATC	ATCTTGAAC	CAGTGTGGCT	ATTCTCCTTT	CTGAACTAG	ACCACAGAAT	4440
25	GACACCCCTA	ACGAACCTAA	GATGAAGGAG	CCAGCATCCT	CGTCCCCATC	CACAAATCTC	4500
	ATGTCTTTGG	GACAAAACAC	CACCACTAAG	CCAGCATCTC	CCAGTCCAAG	AAATATCTCA	4560
	GCATCTAGAG	ATTCCAAGGA	AAATGTTTTT	TTGAATTATG	TGGGGAATCC	AGAAACAGAA	4620
	GCAACCCAG	TCAACAATGA	AGGAACACAG	CATATGTGAG	GGCCAAATGA	ATTATCAACA	4680
	CCCTCTTCCG	ACCGGGATGC	ATTTAACTTG	TCTACAAAGC	TGGAAATGGA	AAAGCAAGTA	4740
30	TTTGGTAGTA	GGAGTCTACC	ACGTGGGCCA	GATAGCCAAAC	GCCAGGATGG	AAGAGTTCAT	4800
	GCTTCTCATC	AACTAACACG	AGTCCCTGCC	AAACCCATCC	TACCAACAGC	AACAGTGAGG	4860
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Seq ID NO: C13 Protein Sequence
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 GCGCCCTGCG AGGCGGTGGC CATCCCTATG TGCCGGCACA TGCCCTGGAA CATCACGCGG 360
 ATGCCCAACC ACCTGCACCA CAGCACGCAG GAGAAGCCCA TCCTGGCCAT CGAGCAGTAC 420
 GAGGAGCTGG TGGACGTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTTCTG TGCCATGTAC 480
 GCGCCCATTT GCACCTTGGG GTTCCTGCAC GACCCTATCA AGCCGTGCAA GTCGGTGTGC 540
 CAACGCGCGC GCGACGACTG CGAGCCCTCT ATGAAGATGT ACAACCAACAG CTGCGCCGAA 600
 AGCCTGGCCT GCGACAGACT GCCTGTCTAT GACCGTGGCG TGTGCATTTT GCCTGAAGCC 660
 ATCGTCACGG ACCTCCCGGA GGATGTTAAG TGGATAGACA TCACACCAGA CATGATGGTA 720
 CAGGAAGAGC CTCTTGATGT TGACTGTAAG CGCCTAAGCC CCGATCGGTG CAAGTGTAAG 780
 AAGGTGAAGC CAACTTTGGC AACGTATCTC AGCAAAACT ACAGCTATGT TATTCATGCC 840
 AAAATAAAGC CTGTGCAGAG GAGTGGCTGC AATGAGGTCA CAACGGTGGT GGATGTAAAA 900
 GAGATCTTCA AGTCCCTCAT ACCATCCCT CGAACTCAAG TCCCGCTCAT TACAAATTCT 960
 TCTTGCCAGT GTCCACACAT CCTGCCCAT CAAGATGTTT TCATCATGTG TTACGAGTGG 1020
 CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
 AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG 1140
 AAGAAAACAG CCGGGCGCAC CAGTCGTAGT AATCCCCCA AACCAGAGG AAGCCTCCT 1200
 GTCCTCAAC CAGCCAGTCC CAAGAAGAAC ATTAAACTA GGAGTGCCCA GAAGAGAACA 1260
 AACCCGAAAG GAGTGTGAGC TAACTAGTTT CCAAAGCGGA GACTTCCGAC TTCCTTACAG 1320
 GATGAGGCTG GGCATGTCCT GGGACAGCCT ATGTAAGGCC ATGTGCCCTT TGCCCTAACA 1380
 ACTCACTGCA GTGCTCTTCA TAGACACATC TTGCAGCAIT TTTCTTAAG CTATGCTTCA 1440
 GTTTTTCTTT GTAAGCCATC ACAAGCCATA GTGGTAGGTT TGCCCTTTGG TACAGAAGGT 1500
 GAGTTAAAGC TGGTGGAAAA GGCTTATTGC ATTGCATTCA GAGTAACCTG TGTGCATACT 1560
 CTAGAAGAGT AGGGAATAAT ATGCTTGTGA CAATTGACG TAATATGTGC ATTGTAAAAAT 1620
 AAATGCCATA TTTCAACAA AACACGTAAT TTTTITACAG TATGTTTTAT TACCTTTTGA 1680
 TATCTGTGTG TGCAATGTTA GTGATGTTTT AAAATGTGAT GAAAAATATA TGTTTTTTAA 1740
 AAGGAACAGT AGTGGAAATGA ATGTTAAAG ATCTTTATGT GTTTATGGCT TGCAGAAGGA 1800
 TTTTGTGAT GAAAGGGGAT TTTTGAAGAA ATTAGAGAAG TAGCATATGG AAAATATATA 1860
 TGTGTTTTTT TACCAATGAC TTCAGTTTCT GTTTTAGCT AGAAACTTAA AAACAAAAAT 1920
 AATAATAAAG AAAAAATAAT AAAAAGGAGA GGCAGACAAT GTCTGGATTG CTGTTTTTTG 1980
 GTTACCTGAT TTCCATGATC ATGATGCTTC TTGTCACAC CCTCTTAAGC AGCACCAGAA 2040
 ACAGTGAGTT TGTCTGTACC ATTAGGAGTT AGGTACTAAT TAGTTGGCTA ATGCTCAAGT 2100
 ATTTTATACC CACAAGAGAG GTATGTCACT CATCTTACTT CCCAGGACAT CCACCTGAG 2160
 AATAATTGGA CAAGCTTAAA AATGGCCTTC ATGTGAGTGC CAAATTTTGT TTTTCTTCAT 2220
 TTAAATATTT TCTTTGCCCTA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG 2280
 AAAGTTGAGT TCCACCTCTG AATAGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA 2340
 AAAAAAGACT TATTTGCAGC ATTTTATCAA CAAATTTTAT AATTGTGGAC AATTGGAGGC 2400
 ATTTATTTTA AAAACAATTT TTATTGGCCT TTTGCTAACA CAGTAAGCAT GTATTTTATA 2460
 AGGCATTCAA TAAATGCACA ACGCCCAAAG GAAATAAAAT CCTATCTAAT CCTACTCTCC 2520
 ACTACACAGA GGTAAATCACT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580
 GCACCTATAA AATGATTTGA CAAATAAAA CTAGGAACCT GTATACATGT GTTTCATAAC 2640
 CTGCCCTCCT TGCTTGGCCC TTTATTGAGA TAAGTTTTCC TGTCAAGAAA GCAGAAACCA 2700
 TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760
 TATTGATATC TTAGGTGGTT TCTTCACTGA CAATACAGAA TAAACATCTC ACCGGAATTC 2820

Seq ID NO: C15 DNA Sequence
 Nucleic Acid Accession #: NM_005940
 Coding sequence: 23..1489

1 11 21 31 41 51
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 AAGCCAGCA GCGCCGCGGC GGTGCTCTCC GCGCGCTGG CTCGCGAGCG CGGCCGCGCG 60
 CGCCCTCCTG CCCCCAGATC TGCTGCTGCT GCTCCAGCG CCGCCGCTGC TGGCCCGGGC 120
 TCTGCCGCGG GACGTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180
 AGCCCTGCCC AGTAGCCCGG CACCTGCCCC TGCCACGCAG GAAGCCCCCC GGCCTGCCAG 240
 CAGCCTCAGG CTCCCCCGCT GTGGCGTGGC CGACCATCT GATGGGCTGA GTGCCCGCAA 300
 CCGACAGAAG AGGTTCTGTC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG 360
 GATCCTTCGG TTCCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420
 CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCACG AGGGCGGTGC 480
 TGACATCATG ATCGACTTCG CCAGGTACTG GCATGGGGAC GACCTGCCCT TTGATGGGCC 540
 TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC AGAGAAGGGG ATGTCCACTT 600
 CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCAAGGC ACAGACCTGC TGCAGGTGGC 660
 AGCCCATGAA TTTGGCCACG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCTGTAT 720
 GTCCGCTTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGCGCT 780
 TCACACCTTA TATGGCCAGC CTGGGCCAC TGTCACCTCC AGGACCCAG CCCTGGGCCC 840
 CCAGGTATGA ATAGACACCA ATGAGATTGC ACCGCTGGAG CCAGACGCCC GCGCAGATGC 900

CTGTGAGGCC TCCTTTGACG CGGTCTCCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC 960
 GGGCTTTGTG TGGGCGCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTTGGCCTC 1020
 TCGCCACTGG CAGGGACTGC CCAGCCCTGT GGACGCTGCC TTTCGAGGATG CCCAGGGCCA 1080
 CATTTGTGTT TTTCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCTCTGG 1140
 CCCCACACCC CTCACCGAGC TGGGCTTGGT GAGGTTCCCG GTCCATGCTG CCTTGGTCTG 1200
 GGGTCCCAGG AAGAACAAGA TTACTTTCTT CCGAGGCAGG GACTACTGGC GTTTCACCCC 1260
 CAGCACCCGG CGTGTAGACA GTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC 1320
 CTCTGAGATC GACGCTGCCT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGCCTCGGCC 1380
 CCTTACTTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCCGTCTCGT 1440
 GGGTCTTGAC TTCTTTGGCT GTGCCGAGCC TGCCAAACACT TTCTCTGAC CATGGCTTGG 1500
 ATGCCCTCAG GGGTGTCTGAC CCCTGCCAGG CCACGAATAT CAGGCTAGAG ACCCATGGCC 1560
 ATCTTTGTGG CTGTGGGCAC CAGGCATGGG ACTGAGCCCA TGTCTCTGTC AGGGGGATGG 1620
 GGTGGGGTAC AACCACCATG ACAACTGCCG GGAGGGCCAC GCAGGTCGTG GTCACCTGCC 1680
 AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740
 GGGACCCGCT ATGCAGGTCC TGGCAAACCT GGTGCGCCCTG TCTCATCCCT GTCCTCTCAGG 1800
 GTAGCACCAT GCGAGGACTG GGGGAACTGG AGTGTCTTGT CTGTATCCCT GTTGTGAGGT 1860
 TCCTTCCAGG GGTGCGCACT GAAGCAAGGG TGCTGGGGCC CCGTGGCCCTT CAGCCCTGGC 1920
 TGAGCAACTG GGTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCTCTG 1980
 ATCTGTCTGC CTCTCTGGCT ACAATCCTGG AATCTGTCTC TCCAGAATCC AGGCCAAAAA 2040
 GTTCACAGTC AATGCGGGAG GGTATTCTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100
 CAACATACCT CAATCCTGTC CCAGGCCGGA TCCTCCTGAA GCCCTTTTCG CAGCACTGCT 2160
 ATCTTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220
 TTTTAAACT GAGGATTGTC ATTAACACA GTTGTTTTCT 2260

Seq ID NO: C16 DNA Sequence
 Nucleic Acid Accession #: NM_024022
 Coding sequence: 202..1563

1 11 21 31 41 51
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 ACCGGGCACC GGACGGCTCG GGTACTTTTCG TTCTTAATTA GGTTCATGCCC GTGTGAGCCA 60
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGGGC CTACTATCTC TTCCGTGGTG 120
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180
 AGAGGTCTTG AATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTGGG CCTTGATGAT TTGAAAATAA GTCCCTGTGC ACCAGATGCA 300
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTGACTGTC 420
 TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAAGA CCAATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAAATGT TGCTGTGTC CAACTGGGTT TCCCAAGCTA TGTGAGTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCTCTG GCCACGTGTT TACCTTGCA TGCACAGCCT GTGGTCATAG AAGGGGTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCA AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGTCTGTGCA TCACGCCCTT GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTTA TGACTGTGAC CTCCTCAAGT CATGGACCAT CAGGTGGGT 1020
 CTAGTTTCCC TGTGTGACAA TCCAGCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCTGGCCA 1140
 CTCAGTTTCA ATGAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACCTCCCC 1200
 GATGGAAGAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGG TGACGCTTCC 1260
 CCTGTCTGTA ACCACGCGGC CGTCCCTTTG ATTTCCAACA AGATCTGCAA CCACAGGGAC 1320
 GTGTACGGTG GCATCATCTC CCCCTCCATG CTCTGCGCGG GCTACCTGAC GGGTGGCGTG 1380
 GACAGCTGCC AGGGGGACAG CGGGGGGGCC CTGCTGTGTC AAGAGAGGAG GCTGTGGAAG 1440
 TTAGTGGGAG CGACCACTT TGGCATCGGC TGCGCAGAGG TGAACAAGCC TGGGGTGTAC 1500
 ACCGTGTGTA CCTCTTCTCT GGACTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAAACC 1560
 TGAAGAGGAA GGGGACAGAT AGCCACCTGA GTTCTCTGAG TGAAGAAGAC AGCCCGATCC 1620
 TCCCTTGAG TCCGTGTAG GAACCTGCAC ACGAGCAGAC ACCCTTGGAG CTCTGAGTTC 1680
 CGGCACCACT AGCAGGCCCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA 1740
 GCTGCTTTTT GTTTTTTGT TTTTGTAGGT GGAGTCTCGC TCTGTGCCC AGGCTGGAGT 1800
 GCAGTGGCGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAAGC GATTCTCTTG 1860
 CCTCAGCTTC CCCAGTAGCT GGGACCACAG GTGCCGCCA CCACACCCAA CTAATTTTGT 1920
 TATTTTGTAG AGAGACAGGG TTTACCATG TTGGCCAGGC TGCTCTCAA CCCCTGACCT 1980
 CAAATGATGT GCCTGTCTCA GCCTCCACA GTGCTGGGAT TACAGGCATG GGCCACCACG 2040
 CCTAGCCTCA CGTCTCTTTC TGATCTTAC TAAGAACAAA AGAAGCAGCA ACTTGCAAGG 2100
 GCGGCTTTTC CCACTGGTCC ATCTGGTTT CTCTCCAGGG GTCTTGCAA ATTCTGTACG 2160
 AGATAAGCAG TTATGTGACC TCACGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA 2220
 CCAGCCGAGA AGTGCAGAAC TGCAGTCACT GCACGTTTTC ATCTCTAGGG ACCAGAACA 2280
 AACCACCCCT TTCTACTTCC AAGACTTATT TTCATGTG GGGAGGTTAA TCTAGGAATG 2340
 ACTCGTTTAA GGCCTATTTT CATGATTTCT TTGTAGCATT TGGTGTGTA CGTATTATTG 2400
 TCCTTTGATT CCAATAATA TGTTCCTTC CCTCAAAAAA AAAAAAAA AAAAAAAA 2460
 AAAAA 2465

Seq ID NO: C17 DNA Sequence
 Nucleic Acid Accession #: NM_003220
 Coding sequence: 63..1376

1 11 21 31 41 51
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 GAATTCGGGC TCTCTGGGTG AGAGACCGAG AGGGGCATAT CCGTTCACGC CGATCCATGA 60
 AAATGCTTTG GAAATTGACG GATAATATCA AGTACGAGGA CTGCGAGGAC CGTCACGACG 120
 GCACAGCAGA CGGACCGGCA CGGTGCCCC AGCTGGGCAC TGTAGGTCAA TCTCCCTACA 180
 CGAGCGCCCC GCCGTGTGCC CACACCCCA ATGCCGACTT CCAGCCCCA TACTTCCCC 240
 CACCTACCA GCCTATCTAC CCCAGTGC G AAGATCCTTA CTCCACGTC AACGACCCCT 300

ACAGCCTGAA CCCCTGAC GCCCAGCCGC AGCCGCAGCA CCCAGGCTGG CCCGGCCAGA 360
 GGCAGAGCCA GGAGTCTGGG CTCCTGCACA CGCACCGGGG GCTGCCTCAC CAGCTGTCCG 420
 GCCTGGATCC TCGCAGGGAC TACAGGCGGC ACGAGGACCT CTGACACGGC CCACACGCGC 480
 TCAGCTCAGG ACTCGGAGAC CTCTCGATCC ACTCCTTACC TCACGCCATC GAGGAGGTCC 540
 CGCATGTAGA AGACCCGGGT ATTAACATCC CAGATCAAAC TGTAATTAAAG AAAGGCCCGG 600
 TGTCCTCTGT CAAAGTCCAA AGCAATGCCG TCTCCGCCAT CCCTATTAAAC AAGGACAACC 660
 TCTTCGCGCG CGTGGTGAAC CCCAACGAAG TCTTCTGTTC AGTTCCGGGT CGCCTCTCGC 720
 TCCTCAGCTC CACCTCGAAG TACAAGGTCA CGGTGGCGGA AGTGACAGCG CGGCTCTCAC 780
 CACCCGAGTG TCTCAACGCG TCGTGTCTGG GCGGAGTGCT CCGGAGGGCG AAGTCTAAAA 840
 ATGGAGGAAG ATCTTTAAGA GAAAAACTGG ACAAATAGG ATTAATCTG CCTGCAGGGA 900
 GACGTAAAGC TGCCAAAGTT ACCCTGCTCA CATCACTAGT AGAGGGAGAA GCTGTCCACC 960
 TAGCCAGGGA CTTTGGGTAC GTGTGCGAAA CCGAATTTCC TGCCAAAGCA GTAGCTGAAT 1020
 TTCTCAACCG ACAACATTCC GATCCCAATG AGCAAGTGAC AAGAAAAAAC ATGCTCCTGG 1080
 CTACAAAAA GATATGCAAA GAGTTCAACG ACCTGTCTGG TCAGGACCGA TCTCCCTGG 1140
 GGAATCTACG GCCCAACCCC ATCCTGGAGC CCGGCATCCA GAGCTGCTTG ACCCACTTCA 1200
 ACCTCATCTC CACCGCTTC GGCAGCCCG CGGTGTGTGC CGCGGTACG GCCCTGCAGA 1260
 ACTATCTCAC CGAGGCCCTC AAGGCCATGG ACAAATGTA CCTCAGCAAC AACCCCAACA 1320
 GCCACACGGA CAACACGCC AAAAGCAGTG ACAAAGAGGA GAAGCACAGA AAGTGAGGCT 1380
 CTCCTCCCGC CCGCCCTTC CCACGCTCA CCAGCCCCC CGCGGCCAC CCTCCGGCGG 1440
 GTGACAGCTC CGGGATCAGC AACCTTCTCT GCTGTGCTA CTGCTGCTGC TGCTGCCGCC 1500
 GCGCCCGCG CGCTGCGCTC TGGGTCCCGG CGAGTCTCCG GGAATGCTCT CTGACTGTC 1560
 AGTGGGGCAG CCTCTCCGAC TCTGCACCCG CCTCGACCTC CCCACCCGCT CCCACACCCC 1620
 TGTGCCCCCG GAATTC 1636

Seq ID NO: C18 DNA Sequence
 Nucleic Acid Accession #: NM_002988
 Coding sequence: 71..340

1 11 21 31 41 51
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 CCGGCACGAG AGGAGTTGTG AGTTTCCAAG CCCAGCTCA CTCTGACCAC TTCTCTGCCT 60
 GCCCAGCATC ATGAAGGGCC TTGCAGCTGC CCTCCTGTCT CTGCTGTGCA CCATGGCCCT 120
 CTGCTCCTGT GCACAAGTTG GTACCAACAA AGAGCTCTGC TGCTCTGTCT ATACCTCCTG 180
 GCAGATTCCA CAAAAGTTCA TAGTTGACTA TTCTGAAACC AGCCCCAGT GCCCAAGGC 240
 AGGTGTATC CTCTTAACCA AGAGAGGCCG GCAGATCTGT GCTGACCCCA ATAAGAAGTG 300
 GGTCCAGAAA TACATCAGCG ACCTGAAGCT GAATGCCTGA GGGGCTGGA AGCTGCGAGG 360
 GTCAGGTGAA CTTGGTGGGC CCAGGAGGGA ACAGGAGCCT GAGCCAGGGC AATGGCCCTG 420
 CCACCTGGA GGCACCTCT TCTAAGAGTC CCATCTGCTA TGCCAGCCA CATTAATAA 480
 CTTTAATCTT AGTTTATGCA TCATATTTCA TTTTGAATTT GATTTCTATT GTTGAGCTGC 540
 ATTATGAAAT TAGTATTTTC TCTGACATCT CATGACATTG TCTTTATCAT CCTTCCCT 600
 TTCCCTTCAA CTCTCTGTAC ATTCAATGCA TGGATCAATC AGTGTGATTA GCTTCTCAG 660
 CAGACATTGT GCCATATGTA TCAAATGACA AATCTTTATT GAATGGTTT GCTCAGCACC 720
 ACCTTTTAAAT ATATTGGCAG TACTTATTAT ATAAAGGTA AACCAGCATT CTCACTGTGA 780
 AAAAAAAAAA AAAAAAAAAA AAA 803

Seq ID NO: C19 DNA Sequence
 Nucleic Acid Accession #: NM_004063
 Coding sequence: 121..2619

1 11 21 31 41 51
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 AGGGAGTGTT CCCGGGGGAG ATACTCCAGT CGTAGCAAGA GTCTCGACCA CTGAATGGAA 60
 GAAAAGGACT TTTAACCACC ATTTGTGAC TTACAGAAAG GAATTTGAAT AAAGAAAAC 120
 ATGATACTTC AGGCCATCT TCACTCCCTG TGTCTTCTTA TGCTTTATTT GGCAACTGGA 180
 TATGGCCAAG AGGGGAAGTT TAGTGGACCC CTGAAACCCA TGACATTTTC TATTTATGAA 240
 GGCCAGAAGC CGAGTCAAAAT TATATTCCAG TTTAAGGCCA ATCTCCTGCT TGTGACTTTT 300
 GAACATAACT GGGAGACAGA CAACATATTT GTGATAGAAC GGGAGGGACT TCTGTATTAC 360
 AACAGAGCCT TGACAGGGGA AACAGATCT ACTCACAATC TCCAGGTTGC AGCCCTGGAC 420
 GCTAATGGAA TTATAGTGA GGTCCAGTC CCTATCACC TAAGAAGTGA GGACATCAAC 480
 GACAAATGAC CCACGTTTCT CCAGTCAAAG TACGAAGGCT CAGTAAGGCA GAATCTCGC 540
 CCAGGAAAGC CCTTCTTGTA TGTCAATGCC ACAGACCTGG ATGATCCGGC CACTCCCAAT 600
 GGCCAGCTTT ATTACAGAT TGTATCCAG CTTCCCATGA TCAACAATGT CATGTACTTT 660
 CAGATCAACA AAAAAACGGG AGCCATCTCT CTTACCCGAG AGGGATCTCA GGAATTGAAT 720
 CCTGCTAAGA ATCCTTCTTA TAATCTGGTG ATCTCAGTGA AGGACATGGG AGGCCAGAGT 780
 GAGAATTCCT TCAGTGATAC CACATCTGTG GATATCATAG TGACAGAGAA TATTTGGAAA 840
 GCACCAAAAC CTGTGGAGAT GGTGGAAGC TCAACTGATC CTACCCCAT CAAAATCACT 900
 CAGGTGCGGT GGAATGATCC CGGTGCACAA TATTCCTTAG TTGACAAAGA GAAGCTGCCA 960
 AGATTCCCAT TTTCAATTGA CCAGGAAGGA GATATTTACG TGACTCAGCC CTGGGACCGA 1020
 GAAGAAAAGG ATGCATATGT TTTTATGCA GTTGCAAGG ATGAGTACGG AAAACCACTT 1080
 TCATATCCGC TGGAAATTCA TGTAAAAGTT AAAGATATTA ATGATAATCC ACCTACATGT 1140
 CCGTCACGAC TAACCGTATT TGAGGTCCAG GAGAATGAAC GACTGGGTAA CAGTATCGGG 1200
 ACCCTTACTG CACATGACAG GGATGAAGAA AATACTGCCA ACAGTTTCT AAACACAGG 1260
 ATTGTGGAGC AAATCTCCAA ACTTCCCATG GATGGACTCT TCCTAATCCA AACCTATGCT 1320
 GGAATGTTAC CTGATGCTTA AAGTCCCTTG AAGAAGCAAG ATACTCTCA GTACAACCTA 1380
 ACGATAGAGG TGTCTGACAA AGATTCCAAG ACCCTTTGTT TTGTGCAAAAT CAACGTTATT 1440
 GATATCAATG ATCAGATCCC CATCTTTGAA AAATCAGATT ATGAAAACCT GACTCTTGCT 1500
 GAAGACACAA ACATTGGGTC CACCATCTTA ACCATCCAGG CCAGTATGTC TGATGAGCCA 1560
 TTTACTGGGA GTTCTAAAT TCTGTATCAT ATCATAAAGG GAGACAGTGA GGGACGCTG 1620
 GGGGTTGACA CAGATCCCCA TACCAACACC GGATATGTCA TAATTAAAAA GCCTCTTGAT 1680
 TTTGAAACAG CAGCTGTTTC CAACATTGTG TTCAAAGCAG AAAATCCTGA GCCTCTAGTG 1740
 TTTGGTGTGA AGTACAATGC AAGTCTTTT GCCAAGTTCA CGCTTATTGT GACAGATGTG 1800
 AATGAAGCAG CTCAATTTC CCAACAGTA TTCCAAGCGA AAGTCAGTGA GGATGTAGCT 1860
 ATAGGCACTA AAGTGGGCAA TGTGACTGCC AAGGATCCAG AAGTCTGGA CATAGCTAT 1920
 TCACTGAGGG GAGACACAAG AGGTTGGCTT AAAATTGACC ACGTGACTGG TGAGATCTTT 1980

5	AGTGTGGCTC	CATTGGACAG	AGAAGCCGGA	AGTCCATATC	GGGTACAAGT	GGTGGCCACA	2040
	GAAGTAGGGG	GGTCTTCCCT	GAGCTCTGTG	TCAGAGTTCC	ACCTGATCCT	TATGGATGTG	2100
	AATGACAACC	CTCCAGGCT	AGCCAAGGAC	TACACGGGCT	TGTTCTTCTG	CCATCCCCTC	2160
	AGTGCACTTG	GAAGTCTCAT	TTTCGAGGCT	ACTGATGATG	ATCAGCACTT	ATTTCCGGGT	2220
	CCCCATTTTA	CATTTTCCCT	CGGCAGTGGG	AGCTTACAAA	ACGACTGGGA	AGTTTCCAAA	2280
	ATCAATGGTA	CTCATGCCCG	ACTGTCTACC	AGGCACACAG	AGTTTGAGGA	GAGGGAGTAT	2340
	GTGCTCTTGA	TCCGCATCAA	TGATGGGGGT	CGGCCACCCT	TGGAAGGCAT	TGTTTCTTTA	2400
10	TGGGATACCA	CTGTGGGCAT	GGCAGTGGT	ATACTGCTGA	CCACCCCTCT	GGTGATTGGT	2520
	ATAATTTTGA	CAGTTGTGTT	TATCCGCATA	AAGAAGGATA	AAGGCAAAAG	TAATGTTGAA	2580
	AGTGCTCAAG	CATCTGAAGT	CAAACCTCTG	AGAAGCTGAA	TTTGAAAAGG	AATGTTTGAA	2640
	TTTATATAGC	AAGTGCTAT	TCAGCAACAA	CCATCTCATC	CTATTACTTT	TCATCTAACG	2700
	TGCATTATAA	TTTTTAAAC	AGATATTCCC	TCTGTCCCTT	TAATATTGTC	TAAATATTTC	2760
15	TTTTTTGAGG	TGGAGTCTTG	CTCTGTGCGC	CAGGCTGGAG	TACAGTGGTG	TGATCCCAGC	2820
	TCACTGCAAC	CTCCGCTCTC	TGGGTTTACA	TGATTCTCCT	GCCTCAGCTT	CCTAAGTAGC	2880
	TGGGTTTACA	GGCACCCACC	ACCATGCCCA	GCTAATTTTT	GTATTTTAA	TAGAGACGGG	2940
	GTTCGCCCAT	TTGGCCAGGC	TGGTCTTGAA	CTCCTGACGT	CAAGTGATCT	GCCTGCCTTG	3000
	GTCTCCCAAT	ACAGGCATGA	ACCACTGCAC	CCACCTACTT	AGATATTTCA	TGTGCTATAG	3060
20	ACATTAGAGA	GATTTTTCAT	TTTTCCATGA	CATTTTTCCT	CTCTGCAAT	GGCTTAGCTA	3120
	CTTGTTTCTT	TCCCTTTTGG	GGCAAGACAG	ACTCATTAAT	TATTTCTGAT	ATTTTCTCTT	3180
	TATCAAGGAG	ATATATTCAT	GTGTCTCAT	AGAAGTCCCT	GGATTCCATT	TATGTTTTTT	3240
	CTGATTCCAT	CCTGTGTCCC	CTTCATCCTT	GACTCCTTTG	GTATTTCACT	GAATTTCAAA	3300
	CATTTGTCTG	AGAAGAAAAA	CGTGAGGACT	CAGGAAAAAT	AAATAAATAA	AAGAACAGCC	3360
25	TTTTCCCTTA	GTATTAAACG	AAATGTTTCT	GTGTCATTAA	CCATCTTTAA	TCAATGTGAC	3420
	ATGTTGCTCT	TTGGCTGAAA	TTCTTCAACT	TGGAATGAC	ACAGACCCAC	AGAAGGTGTT	3480
	CAAACACAAC	CTACTCTGCA	AACCTTGGTA	AAGGAACACG	TCAGCTGGCC	AGATTTCTCT	3540
	ACTACCTGCC	ATGCATACAT	GCTGCGCATG	TTTTCTTCAT	TCGTATGTTA	GTAAAGTTTT	3600
	GGTTATTATA	TATTTAACAT	GTGGAAGAAA	ACAAGACATG	AAAAGAGTGG	TGACAAATCA	3660
30	AGAATAAACA	CTGGTTGTAG	TCAGTTTGT	TTGTTAA			3697

Seq ID NO: C20 DNA Sequence
Nucleic Acid Accession #: NM_004443
Coding sequence: 28..3024

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40	CCGCCGCCGG	GGCTTCTGCC	GCTGCTCCCT	CCGCTGCTGC	TGCTGCCGCT	GCTGCTGCTG	120
	CCGCCGCCGT	GCGCGGCGCT	GGAGAGAGAC	CTCATGGACA	CAAAATGGGT	AACATCTGAG	180
	TTGGCGTGGA	CATCTCATCC	AGAAAGTGGG	TGGGAAGAGG	TGAGTGGCTA	CGATGAGGCC	240
	ATGAATCCCA	TCCGCACATA	CCAGGTGTGT	AATGTGCGCG	AGTCAAGCCA	GAACAACCTG	300
	CTTCGCACGG	GGTTTCACTG	GCGGCGGGAT	GTGCAGCGGG	TCTACGTGGA	GCTCAAGTTC	360
45	ACTGTGCGTG	ACTGCAACAG	CATCCCCAAC	ATCCCCGGCT	CCTGCAAGGA	GACCTTCAAC	420
	CTCTTCTACT	ACGAGGCTGA	CAGCGATGTG	GCCTCAGCCT	CCTCCCCCTT	CTGGATGGAG	480
	AACCCCTACG	TGAAGTGGGA	CACCATTGCA	CCCGATGAGA	GCTTCTCGCG	GCTGGATGCC	540
	GGCCGTGTCA	ACACCAAGGT	GCGCAGCTTT	GGGCCACTTT	CCAAGGCTGG	CTTCTACCTG	600
	GCCTTCCAGG	ACCAGGGCGC	CTGCATGTGC	CTCATCTCCG	TGCGCGCCTT	CTACAAGAG	660
50	TGTGCAATCA	CCACCGCAGG	CTTCGCACTC	TTCCCCGAGA	CCCTCACTGG	GGCGGAGCCC	720
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	CTCAAGCTCT	ACTGCAACGG	CGATGGGGAG	TGGATGGTGC	CTGTGGGTGC	CTGCACCTGT	840
	GCCACCGGCC	ATGAGCCAGC	TGCCAAGGAG	TCCCATGTCC	GCCCCGTGTC	CCCTGGGAGC	900
	TACAAGGCGA	AGCAGGCTGA	GGGGCCCTGC	CTCCCATGTC	CCCCAACACG	CCGTACACAC	960
55	TCCCCAGCCG	CCAGCATCTG	CACCTGCCAC	AATAACTTCT	ACCGTGACAG	CTCGGACTCT	1020
	GCGGACAGTG	CCTGTACCAC	CGTGCCATCT	CCACCCGAG	GTGTGATCTC	CAATGTGAAT	1080
	GAAACCTCAC	TGATCTCTGA	GTGGAGTGGG	CCCCGGGACC	TGGGTGGCCG	GGATGACCTC	1140
	CTGTACAAAT	TCATCTGCAA	GAAGTGCCAT	GGGGCTGGAG	GGGCCTCAGC	CTGCTCACGC	1200
	TGTGATGACA	ACGTGGAGTT	TGTGCTCGG	CAGCTGGGCC	TGACGGAGCG	CCGGGTCCAC	1260
60	ATCAGCCATC	TGCTGGGCCA	CACGCGTAC	ACCTTTGAGG	TGCAGGCGGT	CAACGGTGTG	1320
	TCGGGCAAGA	GCCCTCTGCC	GCCTCGTTAT	GCGGCCGTGA	ATATCACCAC	AAACCAAGCT	1380
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65	GGGCTTCCGG	CTGACGCCCC	CTATGTGGTC	CAGGTCCGTG	CCCGCACAGT	AGCTGGCTAT	1620
	GGGCAGTACA	GCCGCCCTGC	CGAGTTTGGG	ACCACAAGTG	AGAGAGGCTC	TGGGGCCCGC	1680
	CAGCTCCAGG	AGCAGCTTCC	CCTCATCGTG	GGTCCGCTA	CAGCTGGGCT	TGTCTTCTGT	1740
	GTGGCTGTGC	TGCTCATCGC	TATCGTCTGC	CTCAGGAAGC	AGCGACACGG	CTCTGATTCG	1800
	GAGTACACGG	AGAAGCTGCA	GCAGTACATT	GCTCCTGGAA	TGAAGGTTTA	TATTGACCTT	1860
70	TTTACCTACG	AGGACCTTAA	TGAGGCTGTT	CGGGAGTTTG	CCAAGGAGAT	CGACGTGTCC	1920
	TGCGTCAAGA	TCGAGGAGGT	GATCGGAGCT	GGGGAATTTG	GGGAAGTGTG	CCGTGGTCTG	1980
	CTGAAACAGC	CTGGCCGCGG	AGAGGTGTTT	GTGGCCATCA	AGACGCTGAA	GGTGGGCTAC	2040
	ACCGAGAGGC	AGCGGCGGGA	CTTCTTAAGC	GAGGCCCTCA	TCATGGGTCA	GTTTGATCAC	2100
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75	GAGTTCTATG	AAAACCTGCG	CCTGGACTCC	TTCTCTCGGC	TCAACGATGG	GCAGTCTACG	2220
	GTCTATCCAGC	TGGTGGGCAT	GTTGCGGGGC	ATTGCTGCCG	GCATGAAGTA	CCTGTCCGAG	2280
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	TGCAAAAGTCT	CAGACTTTGG	CCTCTCCGCG	TTCTTGAGAG	ATGACCCCTC	CGATCCTACC	2400
	TACACCAATT	CCCTGGGCGG	GAAGATCCCC	ATCCGCTGGA	CTGCCCCAGA	GGCCATAGCC	2460
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	GAGCAGGATT	ACCGGCTGCC	ACCACCCATG	GACTGTCCCA	CAGCACTGCA	CCAGCTCATG	2640
	CTGGACTGCT	GGGTGCGGGC	CCGGAACCTC	AGGCCCAAT	TCTCCCAGAT	TGTCAATACC	2700
	CTGACACAGC	TCATCCGCAA	TGCTGCCAGC	CTCAAGGTCA	TTGCCAGCGC	TCAGTCTGGC	2760
	ATGTCACAGC	CCCTCCTGGA	CCGCACGGTC	CCAGATTACA	CAACCTTCAC	GACAGTTGGT	2820

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 15 AGTTGCCCTT TGCCCCCAG AGACTGACTC TCAGAGCCAG AGATGGGATG TGTGAGTGTG 3660
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20 Seq ID NO: C21 DNA Sequence
 Nucleic Acid Accession #: NM_001804
 Coding sequence: 82..879

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 CCCCCTCCAG ACTTTAGCCC GGTGCGGGCG CCCCCTGGGC CCGGCCCGGG CCTCCTGGCG 420
 CAGCCCTCGG GGGGCCCCGG CACACCGTCC TCGCCCCGAG CGCAGAGGCC GACGCCCTAC 480
 35 GAGTGGATGC GCGCGAGCGT GGCGGCCGGA GGCGGCGGTG GCAGCGGTAA GACTCGGACC 540
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 AAGAAGAAAC AGCAGCAGCA ACAGCCCCCA CAGCCGCGGA TGGCCCAAGGA CATCACGGCC 780
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 55 TTTTCTCTCT CTTTTCAAA 1699

Seq ID NO: C22 DNA Sequence
 Nucleic Acid Accession #: NM_021978
 Coding sequence: 36..2603

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 65 TGAATGGCTT GGAGGAAGGC GTGGAGTTCC TGCCAGTCAA CAACGTCAAG AAGGTGGAAG 180
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 TGCTGGGGAT CGGCTTCTTG GTGTGGCATT TGCAGTACCG GGACGTGGCT GTCCAGAAGG 300
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 70 GCGGAGTCCC ATTCTTGGGC CCCTACCACA AGGAGTCGGC TGTGACGGCC TTCAGCGAGG 480
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GAGCTTCGGA GCTCTCTCAG TGAAGTGGT GGGGCTGCCG GATCTGGGCT GTGGGGCCCT 3000
TGGGCCACGC TTTTGAAGAA GCCCAGGCTC GGAGGACCCCT GGAAACACGA CGGGTCTGAG 3060
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AACATTTTAT TTCTTTTAA AAAAAAAA 3149

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Seq ID NO: C23 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2268

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Seq ID NO: C24 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2424

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	CTGGACATCA	GCCCCGAGAG	GGTCAGAGTG	GGAGCATTTCC	AGTTCAGTTC	CACCTCCTCAT	300
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	GGGTTCGCTG	GAGGCAGAAA	TGCTTCTGTG	CCCAGATCC	TCATCATCGT	CACTGATGGG	480
	AAGTCCCAAG	GGGATGTGGC	ACTGCCATCC	AAGCAGCTGA	AGGAAAGGGG	TGTCACGTGT	540
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10	AGAGGGCAGC	ACGTGCTGTT	GGCTGAGCAG	GTGGAGGATG	CCACCAACGG	CCTCTTCAGC	660
	ACCTCAGCA	GCTCGGCCAT	CTGCTCCAGC	GCCACGCCAG	ACTGCAGGGT	CGAGGCTCAC	720
	CCCTGTGAGC	ACAGGACGCT	GGAGATGGTC	CGGGAGTTCC	CTGGCAATGC	CCCATGCTGG	780
	AGAGGATCGC	GGCGGACCCCT	TGCGGTGCTG	GCTGCACACT	GTCCTTCTTA	CAGCTGGAAG	840
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15	TCGCAGCCCT	GCCAGAATGG	AGGCACATGT	GTTCCAGAAG	GACTGGACGG	CTACCAGTGC	960
	CTCTGCCCCG	TGGCCTTTTG	AGGGGAGGCT	AACTGTGCCC	TGAAGCTGAG	CCTGGAATGC	1020
	AGGGTCGACC	TCTCTTTCCT	GCTGGACAGC	TCTGCGGGCA	CCACTCTGGA	CGGCTTCTCT	1080
	CGGGCCAAAG	TCTTCGTBAA	GCGGTTTGTG	CGGGCCGTGC	TGAGCGAGGA	CTCTCGGGCC	1140
	CGAGTGGGTG	TGGCCACATA	CAGCAGGGAG	CTGCTGGTGG	CGGTGCTGT	GGGGGAGTAC	1200
20	CAGGATGTGC	CTGACCTGGT	CTGGAGCCTC	GATGGCATTG	CCTTCCGTGG	TGGCCCCACC	1260
	CTGACGGGCA	GTGCTTGGCG	GACAGCGGCA	GAGCGTGGCT	TGCGGAGCGC	CACCAGGACA	1320
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	CAGCGGCCAG	GGTGCCGGAC	ACAAGCCCTG	GACCTCGTCT	TCATGTTGGA	CACCTCTGCC	1620
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	ACTGCTTCG	GGGTGGACAC	CAAAACCACC	CGGGCTGCGA	TGCTGCGGGC	CATTAGCCAG	1800
30	GCCCCCTACC	TAGGTGGGGT	GGGCTCAGCC	GGCACCCGCC	TGCTGCACAT	CTATGACAAA	1860
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	CCCCGGGATT	CCCTGATCCA	CGTGGCAGCT	TACGCCGACC	TGCGGTACCA	CCAGGACGTG	2100
35	CTCATTGAGT	CCCTGTGTTG	AGAAAGCCAAG	CAGCCAGTCA	ACCTCTGCAA	ACCCAGCCCG	2160
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	GGCTGGGAGG	GCCCCACTG	CGAGAAACGT	GAGTGGAGCT	CTTGCTCTGT	ATGTGTGAGC	2280
	CAGGATGGA	TTCTTGAGAC	GCCCCGAGG	CACATGGCTC	CCGTGCAGGA	GGGCAGCAGC	2340
	CGTACCCCTC	CCAGCAACTA	CAGAGAAGGC	CTGGGCACCT	AAATGGTGCC	TACCTTCTGG	2400
40	AATGTCTGTG	CCCCAGGTCC	TTAG				2424

Seq ID NO: C25 DNA Sequence

Nucleic Acid Accession #: XM_097386.3

Coding sequence: 142..795

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	TCCCGTGAC	CAGGGTCTGC	AGCAGCCAAT	GGGGCCTGGC	TGCTGTCTGC	ATCTGGCGCG	240
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	GGGTGAGGG	CTGGGTCTGT	TCCCTCGGGC	TGCGTGTGTG	TGTCGGGAAT	CCTGCGTGTG	360
	GTGTCTGTGG	GCGATCCGGC	CTCCCGCGCG	TGGGTGGACC	TGGATTCTAA	CTCAGAGGAC	420
55	TTGAGCCTGC	TGTTAACTCC	GATGATTGTA	GGGACAGGCG	GGGTGGGTGG	GGGGTGGGCG	480
	CGAGGCTGGG	TCCCGGCCCA	GGAGAAGGAA	GTCTGTGAAG	GCAGTGGCCA	TGCTGGCCGT	540
	GGAATATGGG	GGCGGTTGCA	GAGGCTCTAT	GGGGCCCCGT	CCTGGATACT	CGGCAGGAAG	600
	CCGTGTCTGC	AGAGGCTCCT	CCCTGCCTCA	GGTGGCCCCG	TTCAACCCCA	GCGGTGCCCA	660
	TCTCCTGCCA	CCGCTCTGTC	GTGGGGGTTT	AAATTCTGTT	TGGCTTTCTG	GGGTGCAGCT	720
60	CAGCACCCCC	CCTTATGAG	ACTGGGAGGG	GGTGGGGCAG	TCCCTCAGC	CACGAGGACC	780
	CTGGATGGGT	TCTAGTTTCA	TTGGGACCGT	GGGGCCTGGC	TGCGTACTGA	GTGGGTGCCC	840
	CACAGTCAAG	GCCAACGGGG	GCTCCCCCTG	CTCTGAGATG	TTGGGAGAAA	GGCGGCTTCT	900
	GGAACCTTCC	GTGGGACCCG	TAAATGGCTG	TCCAGAAAGG	CGGGAGGGTG	GGCACGGGGC	960
	ACGGGGGGCG	GCTGGGGTCG	TTGTTAAGGG	TCACGCATCT	GTACAGTTGA	ATTTCTTTTC	1020
65	TCTTATCATG	TTTTACCCAC	CTTGTCCCTT	TTTTCCCCAA	TTGTGCTTTT	GCAATTTTTT	1080
	CCTTGGCAAA	TGTAACCTCA	GCCTTTCATT	CATGACGTGT	GAAATTTTCA	TTTCTCTGGA	1140
	GTTTGTGAGA	CGCGTGGGGA	ACCACGCTTG	AAACTCAGGT	AATAGGAGGA	AAAAAAAAAA	1200
	AACTTAAAAA	AATTTTAAAA	AAACATAAAA	CTACTCTCTA	CCTCTGGCTG	GGCCGAGCCT	1260
	GTCTGCGCCT	GGCGCGGCA	GGGTGGCCTG	TAACAATTTT	AGTTTTTCGA	GAACATTCAG	1320
70	GTATTAAAAA	GAAAAA					1337

Seq ID NO: C26 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 95..2128

75	1	11	21	31	41	51	
	GGGGTAGTTT	GTAGGGACGC	AGCTCTCCAC	GTGCGCGACT	GCGAGGCTGG	ACGCTACGGG	60
	CTCCTGAAAA	GGAGAGACAC	CAGCATTTGC	CACATGCTGT	TCATCCACTG	ACTTTACATT	120
80	TGCTTCTTGG	GAGCTTGTGG	TCCGCGTTGA	CCATCCCAAT	GAAGAGCAGC	AGAAAGACGT	180
	CACACTGAGA	GTATCTGGAG	ACCTTCATGT	TGGAGGAGTG	ATGCTCAAGT	TAGTAGAACA	240
	GATCAATATA	TCCCAAGACT	GGTCAGACTT	TGCTCTTTGG	TGGGAACAGA	AGCATTGCTG	300
	GCTTCTGAAA	ACCCACTGGA	CCCTGGACAA	ATATGGGGTC	CAGGCAGATG	CAAGCTTCT	360
	CTTCAACCCCT	CAGCATAAAA	TGCTGCGCCT	TCGTCTGCCG	AATTTGAAGA	TGGTGAGGTT	420
	GCGAGTCAGC	TTCTCAGCTG	TGGTTTTTAA	AGCTGTCACT	GATATCTGCA	AAATCCTGAA	480

5	TATTAGAAGA	TCAGAAGAGC	TTTCTTGT	AAAGCCGTCT	GGTGACTATT	TTAAGAAGAA	540
	GAAGAAAAAA	GACAAAAATA	ATAAGGAACC	CATAATTGAA	GATATTTCTAA	ACCTGGAGAG	600
	TTCTCCAACA	GCTTCAGGTT	CATCAGTAAG	TCTTGGTTTA	TACAGTAAAA	CCATGACCCC	660
	TATATATGAC	CCCATCAATG	GAACACCAGC	ATCATCCACC	ATGACTTGGT	TCACTGACAG	720
	CCCTTTGACG	GAACAAAAC	GCAGCATCCT	CGCATTGAGC	CAACCCCCC	AGTCCCCAGA	780
	AGCACTTGCG	GATATGTACC	AGCCTCGGTC	TCTGGTTGAT	AAAGCCAAGC	TCAATGCAGG	840
	TTGGCTAGAC	TCCTCAGGCT	CCCTTATGGA	ACAAGGCATC	CAAGAGGATG	AGCAGCTGCT	900
	CTTACGATTT	AAATATTATT	CTTTCTTCGA	CTTGAATCCT	AAATATGATG	CTGTCCGAAT	960
10	AAACCAACTC	TATGAGCAAG	CCAGGTGGGC	CATTCTCTTA	GAAGAAATTG	ATTGCACAGA	1020
	GGAAGAAATG	TTGATCTTTG	CAGCTCTACA	GTACCACATT	AGCAAACTGT	CGTTGTCTGC	1080
	TGAAACACAG	GATTTTGCAG	GCGAGTCCGA	GGTTGATGAA	ATAGAAGCGG	CGCTTCTTAA	1140
	TTTGGGAAGTA	ACCCTAGAAG	GTGGAAAAAG	GGACAGCCTT	TTGGAGGACA	TTACTGATAT	1200
	CCCTAAACTT	GCAGATAATC	TCAAATTATT	TAGGCCCAAG	AAGTTACTAC	CAAAAGCTTT	1260
15	CAAACAATAT	TGGTTTATCT	TTAAAGACAC	ATCCATAGCA	TACTTTAAAA	ATAAGGAACT	1320
	TGAACAAGGA	GAACCACTAG	AAAAACTAAA	TCTTAGAGGC	TGCGAAGTTG	TGCCCGATGT	1380
	AAATGTAGCA	GGAAGAAAAT	TTGGAATCAA	GTTACTAATC	CCTGTTGCCG	ATGGTATGAA	1440
	TGAAATGTAT	TTGAGATGTG	ACCATGAGAA	TCAATACGCC	CAATGGATGG	CTGCTGCAT	1500
	GTTGGCATCG	AAGGGCAAAA	CCATGGCAGA	CAGCTCTAC	CAGCCAGAGG	TCCTCAACAT	1560
20	CCTTTCAATTT	CTGAGGATGA	AAAACAGGAA	CTCTGCATCT	CAGGTGGCTT	CCAGTCTCGA	1620
	AAACATGGAT	ATGAACCCAG	AATGTTTTGT	GTCAACACGG	TGTGCAAAAA	GACACAAATC	1680
	CAACACAGCTG	GCCGCCCGGA	TCCTGGAGGC	GCACCAGAAC	TTGGCCCGAG	TGCCCTTGGT	1740
	CGAAGCCAAG	CTGCGGTTCA	TCCAGGCGTG	GCAGTCACTG	CCTGAGTTTG	GCCTCACCTA	1800
	CTACCTTGTC	AGATTTAAAG	GAAGCAAAAA	AGATGACATT	CTGGGAGTTT	CATATAACAG	1860
25	GTTGATTAAA	ATTGATGCGA	CCACCGGGAT	TCCAGTGACA	ACATGGAGAT	TCACAAATAT	1920
	CAACACAGTGG	AATGTAAACT	GGGAAACCCG	GCAGGTGGTC	ATCGAGTTTG	ACCAAAACGT	1980
	CTTTACTGCT	TTACCTGCCC	TGAGTGACGA	TTGCAAGATT	GTGCAAGAGT	ACATTGGCGG	2040
	CTACATTTTC	TTGTCCACCC	GCTCCAAGGA	CCAGAATGAA	ACACTCGATG	AGGACTTGT	2100
	CCACAAATTTG	ACCGGCGGTC	AGGATTGAAA	CAAGCACCGG	TGCTCGGCTC	ACACCAACAA	2160
30	GGCAAGCCAA	AGCGCGCCCT	CCCCAGAGGG	ATCCCTAACG	TGCCCGAGAT	GTAGATTCTG	2220
	GACTAACAGA	CAACATACAT	TCACCGCTGG	TCACCCAGAT	CCTCATTCAA	ACCCACTGCT	2280
	GGCACATCCC	TTTCTTACT	TTGCCCTGTG	CTACCAGCCA	CGGAAGGAGC	CTCTCTTGTT	2340
	TTTTCTATAA	AATGGTAGG	CAGGAGAAAA	GCAGGTGCCC	TAAGATTGCT	CTAAGGCCCA	2400
	GCATGTGGTT	ACAGTTCTCT	GACTTGACGA	ACCTGCCAGG	TGTATGGCTA	CAAGTTATCC	2460
35	TCGTGCTGAT	CTGTCTCATT	ACTAAGTCAA	TGGAGAAGAC	AGAAAGGTAT	AAATCACGTG	2520
	TAGCAAGAAC	AACCTTTATT	TCACAACTC	AGGTATGAAA	CGAAACGCCT	GTCTTTCATG	2580
	GAAGTCTTTT	TAGCTCCTGT	CTTTTCAAAA	TGGCAGAGGG	AGTTCTTACA	CACACTTTTT	2640
	CCCTGGAGGC	CAAGGTCCTAG	GGGTAGAAAG	GGGAGGGGTG	GGGCTACCAG	GTAGCAGTTG	2700
	ACAACCCAAG	GTGAGAGGAG	TGGCCCTCAG	TGTCATCTGT	CCACAGTGAT	ACCTGCCAAG	2760
40	ATGACCACTG	ACCCACATCT	GGTCTTAGTC	ATTGGTCTCC	TCAGATTTCT	GGGGCCACCT	2820
	GCAAGCCCCA	TTCCATTCTC	ACAGATCTCT	CAGCCACCTG	TAAGTCTTTT	GTGAAGATGT	2880
	GGGTGACACA	GGGGGACAGG	AAAACCCATT	TCTCAACCCA	GATCCATGTC	TCCACTGCTT	2940
	CTACTCTGGG	TTGGGATTCA	GGAAGACAGG	CACAGTCCCT	TCTGTTTATA	GAAACACCTG	3000
	CCAGTGTCAA	GGATTCCAGT	CAGGTGTCTA	TCCCAACTGG	TCAGGGAGAG	AAGGGCAGAC	3060
45	CCATTCTCAA	AGACCACCAT	GTCCAAAGGT	TGACAGCTCC	CCACTGGCTG	CCCCCACAGG	3120
	GGCTTTAGGC	TGGTCTGGGT	CATGGGGAAG	CGTCCCTCTT	ATCGCTGGTC	TGTGTTCTCC	3180
	TGGATTGGGT	ATCTATGTTG	GTACGACTCC	TGGCCTTTTA	TCTAAAGGAC	TTTGGCTTTT	3240
	GTAAATCACA	AGCCAATAAT	AGACTTTTTT	CTCCCCCTCT	GTTTTTTGCT	GTGTCTCTC	3300
	TGCCTTGAGA	CTGCCCTGAG	ACAGTGCTTG	CCTTGAGAGA	GTGAGCCAAT	TAACAGCTGC	3360
50	CTGAATTGTC	ATTTTCCATT	TTGGTTTGT	AGAGGTGGGA	GGGGTGGGTT	TTGAGAAGGT	3420
	CAAAAGCAAT	ACCAGAACTA	AAGGGAAATA	TCAGACAATA	TTTTATTATT	TTTTCATAGA	3480
	TGTTCTGCCA	CACAAAGAAC	TTGGGGTGTA	AGGATAAGGC	AAAAGCTCCA	ATCCCATTTT	3540
	TCAGTTCTTC	TAGGATGCAC	CCCTCAGGGA	GCCTGGCCAG	AGTTCAGAGG	CCCGTGAGCG	3600
	TCAGCTGTTG	CTTTATTTTC	CATCAAAGCC	CTCTGAGAAG	TGAGACCTCA	GCAATTCCGG	3660
55	GAGCCACATA	GAGACAGACT	TGGCAAGGGA	CCCCCTGGTT	CTGAGCCAGT	AGCTGCCATC	3720
	TGGAAATTCC	TCCTTTAGCC	TCCTCTAGA	GGTGAATGTG	AATGAAGCCT	CCCAAGCACC	3780
	CGCTGAATTT	CTGAGGCTTT	GCTTAAAGCT	CAGAAGTGGT	TTAGGCATTT	GGAAAACTCG	3840
	GTTCACATCA	TAAAGAACTT	GATTTGAAAT	GTTTTCTATA	GAAACAAGTG	CTAAGTGATC	3900
	CGTATTATAC	TTGATGTTGG	TCATTTCTCA	GTCTTATTTT	TCAGTTCTAT	TATTTTAGAA	3960
60	CCTAGTCAGT	TCCTTAAAGT	TATAACTGGT	CCTACATTAA	AATAATGCTT	CTCGATGTCA	4020
	GATTTTACCT	GTTTGTCTGT	GAGAACATCT	CTGCCTAATT	TACCAAGGCC	AGACCTTCAG	4080
	TTCAACATGC	TTTCTAGCTT	TTTCATAGTT	GTCTGACATT	TCCATGAAAA	CAAAAGGAACC	4140
	AACTTTGTTT	TAAACAAACT	TTGTTTGGTT	ACAGTTTTC	GGGGAGCGTT	TCTTCCATGA	4200
	CACACAGCAA	CATCCCCAAG	AAATAAACAA	GTGTGACAAA	AAAAAATAAA	AACAAACCTA	4260
65	AATGCTACTG	TTCCAAAGAG	CAACTTGATG	GTTTTTTTAA	ATACTGAGTG	CAAAAGGTCA	4320
	CCCAAAATCC	TATGATGAAA	TTTAAATTA	ATGGGCACCT	TTCAACATCA	TTTGCTTCCT	4380
	TATCTACAGT	TGATTGAGAA	ATCTGCATTT	TTTATTCTTT	TATATGACTT	TTAAGTAAAA	4440
	GATTTTATATG	GATTTGAAAA	AAAAAATAAA	A			4471

Seq ID NO: C27 Protein Sequence
Protein Accession #: NP_005161.1

75	1	11	21	31	41	51	
	MDGGTLPRSA	PPAPPVPGVC	AARRRPASPE	LLRCSRRRRP	ATAETGGGAA	AVARRNERER	60
	NRVKLVNLGF	QALRQVPHFG	GASKKLSKVE	TLRSAYEYIR	ALQRLLAIED	AVRNALAGGL	120
	RPQAVRPSAP	RGPPTTFPVA	ASPSRASSSP	GRGGSSEPGS	PRSAYSDDSD	GCEGALSPAE	180
	RELLDFSSWL	GGY					193

Seq ID NO: C28 DNA Sequence
Nucleic Acid Accession #: NM_017763
Coding sequence: 169..2520

80	1	11	21	31	41	51	

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	AAGCATAAAT	GTCTTTTCC	TCCATTTGTC	TGGATCTGAG	AACTTGCATT	TGGTATTAGC	120
	TAGTGAAGC	AGTATGTATG	GTTGAAGTGC	ATTGCTGCAG	CTGGTAGCAT	GAGTGGTGGC	180
5	CACCAGTCG	AGCTGGCTGC	CCTCTGGCCC	TGGCTGCTGA	TGGCTACCCCT	GCAGGCAGGC	240
	TTTGGACGCA	CAGGACTGGT	ACTGGCAGCA	GCGGTGGAGT	CTGAAAGATC	AGCAGAACAG	300
	AAAGCTGTTA	TCAGAGTGAT	CCCTTTGAAA	ATGGACCCCA	CAGGAAACT	GAATCTCACT	360
	TTGGAAGGTG	TGTTTGCTGG	TGTTGCTGAA	ATAACTCCAG	CAGAAGGAAA	ATTAATGCAG	420
	TCCCACCCAC	TGTACCTGTG	CAATGCCAGT	GATGACGACA	ATCTGGAGCC	TGGATTCACT	480
10	AGCATCGTCA	AGCTGGAGAG	TCCTCGACGG	GCCCCCGGCC	CCTGCCTGTC	ACTGGCTAGC	540
	AAGGCTCGGA	TGGCGGGTGA	GCGAGGAGCC	AGTGCTGTCC	TCTTTGACAT	CACCTGAGGAT	600
	CGAGCTGCTG	CTGAGCAGCT	GCAGCAGCCG	CTGGGGCTGA	CCTGGCCAGT	GGTGTGTATC	660
	TGGGGTAATG	ACGCTGAGAA	GCTGATGGAG	TTTGTGTACA	AGAACCAAAA	GGCCCATGTG	720
	AGGATTGAGC	TGAAGGAGCC	CCCGCCCTGG	CCAGATTATG	ATGTGTGGAT	CCTAATGACA	780
15	GTGGTGGGCA	CCATCTTTGT	GATCATCTGT	GCTTCGGTGC	TGCGCATCCG	GTGCCGCCCC	840
	CGCCACAGCA	GGCCGGATCC	GCTTCAGCAG	AGAACAGCCT	GGGCCATCAG	CCAGCTGGCC	900
	ACCAGGAGGT	ACCAGGCCAG	CTGCAGGCAG	GCCCGGGGTG	AGTGGCCAGA	CTCAGGGAGC	960
	AGCTGCAGCT	CAGCCCCGTG	GTGTGCCATC	TGCTGGAGG	AGTTCTCTGA	GGGGCAGGAG	1020
	CTACGGGTCA	TTTCTGCTCT	CCATGAGTTC	CATCGTAACT	GTGTGGACCC	CTGGTTACAT	1080
20	CAGCATCGGA	CTTGCCCCCT	CTGCGTGTTC	AACATCACAG	AGGGAGATTG	ATTTTCCAG	1140
	TCCCTGGGAC	CCTCTCGATC	TTACCAAGAA	CCAGGTCGAA	GACTCCACCT	CATTGCGCAG	1200
	CATCCCGGCC	ATGCCCACTA	CCACCTCCCT	GCTGCCTACC	TGTTGGGCC	TTCCCGGAGT	1260
	GCATCTGGCTC	GGCCCCCAG	ACCTGGTCCC	TTCTTGCCAT	CCCAGGAGCC	AGGCATGGGC	1320
	CCTCGGCATC	ACCGCTTCCC	CAGAGCTGCA	CATCCCCGGG	CTCCAGGAGA	GCAGCAGGCG	1380
25	CTGGCAGGAG	CCCAGCACCC	CTATGCACAA	GGCTGGGGAA	TGAGCCACCT	CCAATCCACC	1440
	TCACAGCACCC	CTGTGCTGTG	CCCAGTGCCC	CTACGCCGGG	CCAGGCCCCC	TGACAGCAGT	1500
	GGATCTGGAG	AAAGCTATTG	CACGAAACGC	AGTGGGTACC	TGGCAGATGG	GCCAGCCAGT	1560
	GACTCCAGCT	CAGGGCCCTG	TCATGGCTCT	TCCAGTGACT	CTGTGGTCAA	CTGCACGGAC	1620
	ATCAGCCTAC	AGGGGGTCCA	TGGCAGCAGT	TCTACTTTCT	GCAGCTCCCT	AAGCAGTGAC	1680
30	TTTGAACCCC	TAGTGTACTG	CAGCCCTAAA	GGGGATCCCC	AGCGAGTGA	CATGCAGCCT	1740
	AGTGTGACCT	CTCGGCCCTG	TTCTTTGGAC	TCGGTGGTGC	CCACAGGGGA	AACCCAGGTT	1800
	TCCAGCCATG	TCCATACCA	CCGCCACCAG	CACCACCCT	ACAAAAAGCG	GTTCAGTGG	1860
	CATGGCAGGA	AGCCTGGCCC	AGAAACCGGA	GTCCCCCAGT	CCAGGCCTCC	TATTCTCGG	1920
	ACACAGCCCC	AGCCAGAGCC	ACCTTCTCCT	GATCAGCAAG	TCACCGGATC	CAACTCAGCA	1980
35	GGCCCTTCGG	GGCGGCTCTC	TAACCCACAG	TGCCCCAGGG	CCCTCCCTGA	GCCAGCCCCT	2040
	GGCCAGTTTG	AGCCCTCCAG	CATCTGCCCC	AGTACCAGCA	GTCTGTTCAA	CTTGCAAAAA	2100
	TCCAGCCTCT	CTGCCCGACA	CCCACAGAGG	AAAAGGCGGG	GGGGTCCCTC	CGAGCCACC	2160
	CCTGGCTCTC	GGCCCCCAGG	TGCAACTGTG	CACCCAGCTT	GCCAGATTTC	TCCCCATTAC	2220
	ACCCCCAGTG	TGGCATATCC	TTGGTCCCCA	GAGGCACACC	CCTTGATCTG	TGGACCTCCA	2280
40	GGCCTGGACA	AGAGGCTGCT	ACCAGAAACC	CCAGGCCCTT	GTTACTCAA	TTACAGCCA	2340
	GTGTGGTTGT	GCCTGACTCT	TCGCCAGCCC	CTGGAACCC	ATCCACCTGG	GGAGGGGCT	2400
	TCTGAATGGA	GTCTGACAC	CGCAGAGGGC	AGGCCATGCC	CTTATCCGCA	CTGCCAGGTG	2460
	CTGTCCGGCC	AGCCTGGCTC	AGAGGAGGAA	CTCGAGGAGC	TGTGTGAACA	GGCTGTGTGA	2520
	GATGTTTCAGG	CCTAGCTCCA	ACCAAGAGTG	TGCTCCAGAT	GTGTTTGGGC	CCTACCTGGC	2580
45	ACAGAGTCCT	GCTCCTGGGA	AAGGAAAGGA	CCACAGCAAA	CACCATTCTT	TTTGCCGTAC	2640
	TTCTTAGAAG	CACCTGGAAG	GGACTGGTGA	TGGTGGAGGG	TGAGAGGGTG	CCGTTTCTCT	2700
	CTCCAGCTCC	AGACCTTGTC	TGCAGAAAC	ATCTGCAGTG	CAGCAATCC	ATGTCCAGCC	2760
	AGGCAACCA	CTGCTGCCCT	TGGCGTGTGT	GGGCTGGATC	CCTTGAAGGC	TGAGTTTTTG	2820
	AGGGCAGAAA	CTAGCTATG	GGTAGCCAGG	TGTTACAAAG	GTGCTGCTCC	TTCTCCAACC	2880
50	CCTACTTGGT	TTCCCTTACC	CCAAGCTCA	TGTTTATACC	AGCCAGTGGG	TTCCAGCAGAA	2940
	CGCATGACAC	CTTATCACCT	CCCTCCTTGG	GTGAGCTCTG	AACACCAGCT	TTGGCCCTTC	3000
	CACAGTAAGG	GTGCTACATC	AGGGGCAACC	CTGGCTCTAT	CATTTTCTCT	TTTTGCCAAA	3060
	AGGACAGATA	GCATAGGTGA	GCCTGAGCA	CTAAAAGGAG	GGGTCCCTGA	AGCTTTCCCA	3120
	CTATAGTGTG	GAGTTCTGTC	CCTGAGGTGG	GTACAGCAGC	CTTGGTTCTT	CTGGGGGTTG	3180
55	AGAATAAGAA	TAGTGGGGAG	GGAAAACTC	CTCCTTGAAG	ATTCTCTGTC	TCAGAGTCCC	3240
	AGAGAGGTAG	AAAGGAGGAA	TTTCTGCTGG	ACTTTATCTG	GGCAGAGGAA	GGATGGAATG	3300
	AAAGTAGAAA	AGGCAGAAAT	ACAGCTGAGC	GGGGACAACA	AAGAGTTCTT	CTCTGGGAAA	3360
	AGTTTTGTCT	TAGAGCAAGG	ATGGAAAATG	GGGACAACAA	AGGAAAAGCA	AAGTGTGACC	3420
	CTTGGGTTTG	CACAGCCCA	AGGCCAGCT	CCCCAGTATA	AGCCATACAG	GCCAGGGACC	3480
60	CACAGGAGAG	TGGATTAGAG	CACAAGTCTG	GCCTCACTGA	GTGGACAAGA	GCTGATGGGC	3540
	CTCATCAGGG	TGACATTCAC	CCCAGGGCAG	CCTGACCACT	CTTGGCCCTT	CAGGCATTAT	3600
	CCCATTTGGA	ATGTGAATGT	GGTGGCAAG	TGGGCAGAGG	ACCCACCTGT	GGAACCTTTT	3660
	TCCTCAGTT	AGTGGGGAGA	CTAGCACCTA	GGTACCCACA	TGGGTATTTA	TATCTGAACC	3720
	AGACAGACGC	TTGAATCAGG	CACATGTGTA	AGAAATATAT	TTATTGTGCTA	ATATATTTAT	3780
65	CCACAAAAA	AAAAA	AA				3802

Seq ID NO: C29 Protein Sequence
Protein Accession #: NP_004280.2

70	1	11	21	31	41	51	
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	TLFPTNLTF	LSPVDNHRN	LTSQDLYDL	DINIFDEINL	MSLATEDNFD	PIDVSQFLDE	120
	PDSDSLGLSL	SSHNNTSVIK	SNSSHSVCD	GAIGYCTDHE	SSSHHDLGA	VGGYYPEPSK	180
75	LCHLDQSDSD	PHGDLTFQHV	FNHNTYHLQP	TAPESTSEPF	PWPGKSQKIR	SRYLEDTDRN	240
	LSRDEQRAKA	LHLPFVSDEI	VGMPVDSFNS	MLSRYYLTDL	QVSLIRDIRR	RGKNKVAAGN	300
	CRKKRLDII	NLEDDVCNLQ	AKKETLKREQ	AQCNAKINIM	KQKLHDLYHD	IFSRRLRDDQ	360
	RPVNPNIHAL	QCTHDGSILI	VPKELVASGH	KKETQKGRK			400

80 Seq ID NO: C30 DNA Sequence
Nucleic Acid Accession #: NM_004442
Coding sequence: 19..2982

1 11 21 31 41 51

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 TGAGAAAGTGT CTGTTTCAATA CCTTCACCAA TTTTGTATGA GGTGTGTTGT TCTTTTCTTG 5160
 TAAACTTAAT GAAATAAAGC ATGAAGACAA GATTAGAAGA AAAAGAATGA AAAGGAACAA 5220
 ACAAAGCGTC CAAGAAATAT GGGACTATGT GACAAGAACA AACTTACGTT TGACTGGTGT 5280
 GCTGAAAATG ACAGGGAGAA TGAAACCAAG TTGGAACAA CTCTTCAGGA TATTATCCAG 5340
 GAGAACTTCT CCAACCTAGC AAGACAGACC AACGTTCAAA TTCAGGAAAT ACAGAGAAAC 5400
 CCCAAAGATA TTCTCGAGA AGAGCAACCC GAAGACACAT AATTGTGAGA TTCACCAAGG 5460
 TTGAAATGAA GGAATAAATG CTAAGGGCAG CCAGAGAGAA AGGTCAGGTT ACTCACAATA 5520
 GGAAGCCCAT CAGACTAACA GCAGATCTCT CTGCAGAAAC CCTACAACCT AGAAGAGAGT 5580
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 GAGATTTTGT CACCACCAGG CCTGCCCTAC AAGACATCCT GAAGGAAGCA CTAAATATGG 5760
 AAAAGAAAAA CTGGTGCCAG CCACTGCAAA AAATACCAAA TTGTAGAGAC CATTGACACT 5820
 ATGAAGAAAC CGTGTCAACT AATGGGCAAA ATAACCAGCT AGTATCATAA TGACAGGATC 5880
 AGATTACAC ATACCAATAT TAACCTTATA TCTAAATGGG CTAAATCCCC CAATTAAAG 5940
 ACGCAGACTG GCAAAATGGT TAAAGAGTCA AGACTCATTT GTGTGCCGTA TTCAGGAGAC 6000
 CCATCTCACG TGCAAAGACA CACATAGGCT CAGAGTAAAA GGGATACAGG GGAATTC 6057

Seq ID NO: C31 DNA Sequence
 Nucleic Acid Accession #: NM_031942.1
 Coding sequence: 145..1260

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 CCCGAGCCCC GCCCTCCCGG GCCCGGGTCG GCGCGCCCGC CTGCCCAGCC GCGCTGCTGC 60
 TGCTCTCTCT GCTGTGGGAC CGCTGACCGC GCGGCTGCTC CGCTCTCCCC GCTCCAAGCG 120
 CCATCTGGGG CACCCGCCAC CAGCATGGAC GCTCGCCGCG TGCCGAGAGG AGATCTCAGA 180
 GTAAAGAGAA ACTTAAAGAA ATTCAATAT GTGAAGTTGA TTTCCATGGA AACCTCGTCA 240
 TCCTCTGATG ACAGTTGTGA CAGCTTTGCT TCTGATAATT TTGCAAAAC GAGGCTGCAG 300
 TCAGTTCCGG AAGGCTGTAG GACCCGCGAG CAGTGCAGGC ACTCTGGACC TCTCAGGGTG 360
 GCGATGAAGT TTCCAGCGCG GAGTACCAGG GGAGCAACCA ACAAAAAGC AGAGTCCCGC 420
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 AATTTTTTGG AGAAAAGGGC TTTAAATATA AAGCAAAACA AAGCAATGCT TGCAAAACTC 540
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 TTGATATTAA AAACATAGCT GTGGTTCTTT GCAGTTTCTT GTAAATTTAT AAACCAAGCA 2160
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Seq ID NO: C32 DNA Sequence
 Nucleic Acid Accession #: NM_012445.1
 Coding sequence: 276..1271

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 CCCTGGGCAA GGCCTCTGCG GCTCTCTTCC TGGCCACTCT CGGCGCGGCC GGCAGGCTC 360
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Seq ID NO: C33 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1314

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CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCAGTGGCAG TCCGCTCTCT CAAGGACCGA TCCACACTGC AGGTGTCTGA CTCGGCCACA 360
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Seq ID NO: C34 DNA Sequence

Nucleic Acid Accession #: NM_003045.1

Coding sequence: 148..2037

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CAGATGCTGC GCGGAAGGT GGTGGACTGT AGCCGGGAGG AGACGCGGCT GTCTCGCTGC 240
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GTCTGGCTG GAGCTGTGGC CCGTGAGAA GCAGGCCCTG CCATTGTCTC CTCTTCTCTG 360
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Seq ID NO: C35 DNA Sequence
 Nucleic Acid Accession #: NM_002776.1
 Coding sequence: 82..912

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Seq ID NO: C36 DNA Sequence
 Nucleic Acid Accession #: XM_095088
 Coding sequence: 1..4074

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Seq ID NO: C37 DNA Sequence
 Nucleic Acid Accession #: NM_032044
 Coding sequence: 182..658

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 45 CTTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCCTGGA TGGTTTACC ACAAGTCCAA 300
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Seq ID NO: C38 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 52..3042

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 65 GCTCACCAG GAAAAATATG CAATCGTCCC ATTGATATAC AGGCCACTAC AATGGATGGA 60
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 70 GACCGGGGCA GAGCCTGCCG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180
 CCCAACTCA CAGTCACCAT TGACACCAAT GTGAACAGCA CCATTTCTGAA CTTGGAGGAT 240
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 75 GCGGAGGTTG GGCTTCTGAG CCGGAACATC ATAGTGATGG GGGAGATGGA GGACAAATGC 480
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 AAGTTTGCTC TGGGATTTAA GGCAGCACAC TTGGAGGGCA CGGAGCTGAA GCATATGGGA 600
 CAGCAGCTGG TGGTTCAGTA CCCGATTTCAT TTCCACCTGG CCGGTGATGT AGACGAAAGG 660
 GGAGGTTATG ACCCACCAC ATACATCAGG GACCTCTCCA TCCATCATAC ATTCTCTCGC 720
 80 TGCGTACAG TCCATGGCTC CAATGGCTTG TTGATCAAGG ACGTTGTGGG CTATAACTCT 780
 TTGGGCCACT GCTTCTTAC GGAAGATGGG CCGGAGGAAC GCAACACTTT TGACCACCTG 840
 CTTGGCCTCC TTGTCAAGTC TGGAACCTTC CTCCCTCGG ACCGTGACAG CAAGATGTGC 900
 AAGATGATCA CAGGAGACTC CTACCCAGGG TACATCCCCA AGCCCAGGCA AGACTGCAAT 960
 GCTGTGTCCA CCTTCTGGAT GGCCAAATCC AACACAACCC TCATCAACTG TGCCGCTGCA 1020
 GGATCTGAGG AAACCTGGATT TTGTTTATT TTTCAACAGG TACCAACGGG CCCCTCCGTG 1080

5	GGAATGTACT	CCCCAGGTTA	TTCAGAGCAC	ATTCCACTGG	GAAAATTCTA	TAACAACCGA	1140
	GCACATTCCA	ACTACCGGGC	TGGCATGATC	ATAGACAACG	GAGTCAAAAC	CACCGAGGCC	1200
	TCTGCCAAGG	ACAAGCGGGC	GTTCTCTCTA	ATCATCTCTG	CCAGATACAG	CCCTCACCAG	1260
	GACGCCGACC	CGCTGAAGCC	CCGGGAGCCG	GCCATCATCA	GACACTTCAT	TGCCTACAAG	1320
	AACCGAGACC	ACGGGGCGTG	GCTGCGCGGC	GGGGATGTGT	GGCTGGACAG	CTGCCGGTTT	1380
	GCTGACAATG	GCATTGGCCT	GACCTTGGCC	AGTGGTGGAA	CCTTCCCCTA	TGACGACGGC	1440
	TCCAAGCAAG	AGATAAAGAA	CAGCTTGTTC	GTTGGCGAGA	GTGGCAACGT	GGGGACGGAA	1500
	ATGATGGACA	ATAGGATCTG	GGGCCCTGGC	GGCTTGGACC	ATAGCGGAAG	GACCCCTCCT	1560
10	ATAGGCCAGA	ATTTTCCAAT	TAGAGGAATT	CAGTTATATG	ATGGCCCCAT	CAACATCCAA	1620
	AACTGCACCT	TCCGAAGATT	TGTGGCCCTG	GAGGGCCGGC	ACACCAGCGC	CCTGGCCTTC	1680
	CGCCTGAATA	ATGCCTGGCA	GAGCTGCCCC	CATAACAACG	TGACCCGCAT	TGCCTTTGAG	1740
	GACGTTCCGA	TTACTTCCAG	AGTGTTCTTC	GGAGAGCCTG	GGCCCTGGTT	CAACCAGCTG	1800
	GACATGGATG	GGGATAAGAC	ATCTGTGTTC	CATGACGTCG	ACGGCTCCGT	GTCCGAGTAC	1860
15	CCTGGCTCCT	ACCTCACGAA	GAATGACAAC	TGGCTGTGTC	GGCACCAGAG	CTGCATCAAT	1920
	GTTCCCGACT	GGAGAGGGGC	CATTTGCACT	GGGTGCTATG	CACAGATGTA	CATTCAAGCC	1980
	TACAAGACCA	GTAACTTCGG	AATGAAGATC	ATCAAGAATG	ACTTCCCCAG	CCACCTCTTT	2040
	TACCTGGAGG	GGGCGCTCAC	CAGGAGCACC	CATTACCAGC	AATACCAACC	GGTTGTCAAC	2100
	CTGCAGAAGG	GCTACACCAT	CCACTGGGAC	CAGACGGCCC	CCGCCGAATC	GGCCATCTGG	2160
20	CTCATCAACT	TCAACAAGGG	CGACTGGATC	CGAGTGGGGC	TCTGCTACCC	GCGAGGCACC	2220
	ACATTTCTCA	TCCTCTCGGA	TGTTCACAAT	CGCCTGTCTG	AGCAAAACGTC	CAAGACGGGC	2280
	GTCTTCTGTA	GGACCTTGCA	GATGGACAAA	GTGGAGCAGA	GCTACCTTGG	CAGGAGCCAC	2340
	TACTACTGGG	ACGAGGACTC	AGGGCTGTTG	TTCTTGAAGC	TGAAGCTCA	GAACGAGAGA	2400
	GAGAAGTTTG	CTTTCTGCTC	CATGAAAGGC	TGTGAGAGGA	TAAAGATTAA	AGCTCTGATT	2460
25	CCAAAGAACG	CAGGCGTCAG	TGACTGCACA	GCCACAGCTT	ACCCCAAGTT	CACCGAGAGG	2520
	GCTGTCTGAT	ACGTGCCGAT	GCCCAAGAAG	CTCTTTGGTT	CTCAGCTGAA	AACAAAGGAC	2580
	CATTTCCTGG	AGGTGAAGAT	GGAGAGTTCC	AAGCAGCACT	TCTTCCACCT	CTGGAACGAC	2640
	TTCCGCTTACA	TTGAAGTGGG	TGGGAAGAAG	TACCCAGATT	CGGAGGATGG	CATCCAGGTG	2700
	GTGGTGATTG	ACGGGAACCA	AGGGCGCGTG	GTGAGCCACA	CGAGCTTCAG	GAACCTCCATT	2760
30	CTGCAAGGCA	TACCATGGCA	GCTTTTCAAC	TATGTGGCGA	CCATCCCTGA	CAATTCCATA	2820
	GTGCTTATGG	CATCAAGGGG	AAGATACGTC	TCCAGAGGCC	CATGGACCAG	AGTGCTGGAA	2880
	AAGCTTGGGG	CAGACAGGGG	TCTCAAGTTG	AAAGAGCAAA	TGGCATTCGT	TGGCTTCAAA	2940
	GGCAGCTTCC	GGCCCATCTG	GGTGACACTG	GACACTGAGG	ATCACAAAGC	CAAAATCTTC	3000
	CAAGTTGTGC	CCATCCCTGT	GGTGAAGAAG	AAGAAGTTGT	GAGGACAGCT	GCCGCCCGGT	3060
35	GCCACCTCGT	GGTAGACTAT	GACGGTGACT	CTTGGCAGCA	GACCAGTGGG	GGATGGCTGG	3120
	GTCCCCCAGC	CCCTGCCAGC	AGCTGCCTGG	GAAGGCCGTG	TTTCAGCCCT	GATGGGCCAA	3180
	GGGAAGGCTA	TGAGAGACCC	TGGTGCTGCC	ACCTGCCCTT	ACTCAAGTGT	CTACCTGGAG	3240
	CCCTTGGGGC	CCCTTGGGGC	AATGCTGGAA	ACATTCACTT	TCCTGCAGCC	TCTTGGGTGC	3300
	TTCTCTCCTA	TCTGTGCCTC	TTCAGTGGGG	GTTTGGGGAC	CATATCAGGA	GACCTGGGTT	3360
40	GTGCTGACAG	CAAGATCCCA	CTTTGGCAGG	AGCCCTGACC	CAGCTAGGAG	GTAGTCTGGA	3420
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	GAGAAAGAGC	CTTGGCCTTA	AGGAAATCTT	TACTCCTGTA	AGCAAGAGCC	AACCTCACAG	3540
	GATTAGGAGC	TGGGGTAGAA	CTGGCTATCC	TTGGGGAAGA	GGCAAGCCCT	GCCTCTGGCC	3600
	GTGTCACCTT	TTCAGGAGAC	TTTGAGTGGC	AGGTTTGGAC	TTGGACTAGA	TGACTCTCAA	3660
45	AGGCCCTTTT	AGTTCTGAGA	TTCCAGAAAT	CTGCTGCATT	TCACATGGTA	CCTGGAACCC	3720
	AACAGTTTAT	GGATATCCAC	TGATATCCAT	GATGCTGGGT	GCCCCAGCGC	ACACGGGATG	3780
	GAGAGGTGAG	AACATAATGCC	TAGCTTGAGG	GGTCTGCAGT	CCAGTAGGGC	AGGCAGTCAG	3840
	GTCATGTGTC	ACTGCAATGC	CAGGTGGAGA	AATCACAGAG	AGGTAAATATG	GAGGCCAGTG	3900
	CCATTTCAGA	GGGGAGGCTC	AGGAAGGCTT	CTTGCTTACA	GGAATGAAGG	CTGGGGGCAT	3960
50	TTTGCTGGGG	GGAGATGAGG	CAGCCTCTGG	AATGGCTCAG	GGATTTCAGCC	CTCCCTGCCG	4020
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	ATGATGGAGA	AGTGTGGTCA	GAGGGGAGCA	ATGGGCTTTG	CTGCTTATGA	GCACAGAGGA	4140
	ATTCAGTCCC	CAGGCAGCCC	TGCCTCTGAC	TCCAAGAGGG	TGAAGTCCAC	AGAAGTGAGC	4200
	TCCTGCTCTA	GGGCTCTATT	TGCTCTTCAT	CCAGGGAATC	GAGCACAGGG	GGCCTCCAGG	4260
55	AGACCTTAGA	TGIGCTCTGA	CTCCCTCGGC	CTGGGATTTC	AGAGCTGGAA	ATATAGAAAA	4320
	TATCTAGCCC	AAAGCCTTCA	TTTTAACAGA	TGGGGAAAGT	GAGCCCCCAA	GATGGGAAAG	4380
	AACCAACACG	CTAAGGGAGG	GCCTGGGGAG	CCCCACCCTA	GCCCTTGCTG	CCACACCACA	4440
	TTGCCTCAAC	AACCGGCCCC	AGAGTGCCCC	GGCACTCCTG	AGGTAGCTTC	TGGAAATGGG	4500
	GACAAGTCCC	CTCGAAGGAA	AGGAATGAC	TAGAGTAGAA	TGACAGCTAG	CAGATCTCTT	4560
60	CCCTCCTGCT	CCCAGCGCAC	ACAAACCCGC	CCTCCCTCTG	GTGTTGGCGG	TCCCTGTGGC	4620
	CTTCACTTTG	TTCATACCTT	GTCAGCCGAG	CCTGGGTGCA	CAGTAGCTGC	AACTCCCCAT	4680
	TGGTGCTACC	TGGCTCTCCT	GTCTCTGCAG	CTCTACAGGT	GAGGCCAGGC	AGAGGGAGTA	4740
	GGGCTCGCCA	TGTTTCTGGT	GAGCCAAATT	GGCTGATCTT	GGGTGTCTGA	ACAGCTATTG	4800
	GGTCCACCCC	AGTCCCTTTC	AGCTGCTGCT	TAATGCCCTG	CTCTCTCCCT	GGCCCACTTT	4860
65	ATAGAGAGCC	CAAAGAGCTC	CTGTAAGAGG	GAGAACTCTA	TCTGTGGTTT	ATAATCTTGC	4920
	ACGAGGCACC	AGAGTCTCCC	TGGGTCTTGT	GATGAACCTA	ATTTATCCCC	TTTCTTGCCC	4980
	CAACCACAAA	CTCTTCTCCT	CAAAGAGGGC	CTGCCTGGCT	CCCTCCACCC	AACTGCACCC	5040
	ATGAGACTCG	GTCGAAGAGT	CCATTCCCCA	GGTGGGAGCC	AACTGTACAG	GAGGTCTTTC	5100
	CCACCACAAA	TCTTTCACTG	GCTGGGAGGT	GACCATAGGG	CTCTGCTTTT	AAAGATATGG	5160
70	CTGCTTCAAA	GGCCAGAGTC	ACAGGAAGGA	CTTCTTCCAG	GGAGATTAGT	GGTGATGGAG	5220
	AGGAGAGTTA	AAATGACCTC	ATGTCCTTCT	TGTCCACGGT	TTTGTGAGT	TTTCACTCTT	5280
	CTAATGTCAAG	GGTCTCACAC	TGTGAACCA	TTAGGATGTG	ATCACTTTCA	GGTGGCCAGG	5340
	AATGTGAAT	GTCTTGGGCT	CAGTTCACTT	AAAAAAGATA	TCTATTTGAA	AGTTCTCAGA	5400
	GTTGTACATA	TGTTTCAACG	TACAGGATCT	GTACATAAAA	GTTTCTTTCC	TAAACCATTC	5460
75	ACCAAGAGCC	AATATCTAGG	CATTTTCTTG	GTAGCACAAA	TTTTCTTATT	GCTTAGAAAA	5520
	TGTGCTCCTC	TGTTATTTCT	GTTTGTAAAG	CTTAAGTGAG	TGAGGTCTTT	AAGGAAAGCA	5580
	ACGCTCCTCT	GAAATGCTTG	TCTTTTTTCT	GTTGCCGAAA	TAGCTGGTCC	TTTTTCGGGA	5640
	GTTAGATGTA	TAGAGTGTTT	GTATGTAAAC	ATTTCTTGTA	GGCATCACCA	TGAACAAAGA	5700
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80	AATTGTCTTA	AATGTCAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA		5808

Seq ID NO: C39 DNA Sequence
Nucleic Acid Accession #: NM_014373
Coding sequence: 322.1338

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 5 ATGTCTCCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180
 AAATAACATA ATTGAAGGCA GTAAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA 240
 GACCCACTGG AGAGGACAGA AAATGAAGCA GTGTTTTATC ATGTGTATTT CAGCAGGTCT 300
 TCTTGAATTA TAACTAAAAA TATGACTGCT CTCTCTTCAG AGAACTGCTC TTTTCAGTAC 360
 10 CAGTTACGTC AAACAAACCA GCCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT 420
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 TTTATGGAAT ATTTTTCAT TTTACTAGCA TTCGTGATC TTTTACTTTT GGTAAACATT 540
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 ATCTGCCCTAT TTTTCCCTTT ACTTATGGCT TTTTGCATTA TCCAGTTTTC 660
 15 CTGACAGCTT GTATAGATTA TTGCTGAAT TTCTCTAAAA CAACCAAGCT TTCATTAAAG 720
 TGTCAAAAAA TATTTTATTT CTTTACAGTA ATTTTAAATT GGATTTTCACT CCTTGCTTAT 780
 GTTTTGGGAG ACCAGCCAT CTACCAAGC CTGAAGGCAC AGAATGCTTA TTCTCGTCAC 840
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 GTTTTATTTT AAAACAAA TAATTCCAAG AAGTTTATAT AGTTATTTCAG GGACACTATA 1560
 30 TTACAAATAT TACTTTGTTA TTAACACAAA AAGTGATAAG AGTTAACTAT TGGCTATACT 1620
 GATGTTTGTG TTACTCAAAA AAACACTACTG ATGCAAACTG TTATGTAAAT CTGAGATTTT 1680
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 AAAAAAAA 1749

Seq ID NO: C40 DNA Sequence
 Nucleic Acid Accession #: BC012089
 Coding sequence: 1..2571

1 11 21 31 41 51
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 45 CAGAAGGCAT ATGAATCCAA AATTGATTAT GACAAGATTG TCTACTATGA AGCAGGGATT 300
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 50 AGCATTTGCA TCTTCTATGG TTTTGTGGCA AATCACCAGG TAAGAACCAG GATCAAAAGG 540
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 GAGCAAAATCA AATATATATT GGCCCACTAC AACACTACCA AGGACAAGCG GTTCACAGAT 660
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 ATCCCTGTTC TTGATGAGAT TAAAGTCCAT GCAACAGCGA TCAAGGAGAC CAAAGAGGCG 780
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 55 AGTCTGACCA GCGTGAACAC TAGCCTGCGG TCATCTCTCA ATGACCCTCT GTGCTTGGTG 900
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 60 GGTTCAGATA TOGACAATGT AACTCAGCGT CTTCCTATTC AGGATATACT CTCAGCATT 1200
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 70 CATACTGGAA GCATAAGCAG TGAATTGGAA AGTCTGAAGG TAAATCTTAA TATCTTCTG 1800
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 80 CCCTGAATT TGTTTTGGTT TGGCATAGGA AAAGCTACTG TATTTTACT TCCGGCTCTA 2400
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Seq ID NO: C41 DNA Sequence

Nucleic Acid Accession #: NM_033049
Coding sequence: 28..1566

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	GAAACTGCCA	CTAGTGGTCC	TACAGTAGCT	GCAGCTGATA	CCACTGAAAC	TAATTTCCCT	180
10	GAAACTGCTA	GCACCACAGC	AAATACACCT	TCTTTCCCAA	CAGCTACTTC	ACCTGCTCCC	240
	CCCATAATTA	GTACACATAG	TTCTCCCA	ATTCTACAC	CTGCTCCCC	CATAATTAGT	300
	ACACATAGTT	CCTCCACAAT	TCCTATACCT	ACTGCTGCAG	ACAGTGAGTC	AACCACAAAT	360
	GTAAATTCAT	TAGCTACCTC	TGACATAATC	ACCGCTTCAT	CTCCAAATGA	TGGATTAAATC	420
	ACAAATGGTTC	CTTCTGAAAC	ACAAAGTAAC	AATGAAATGT	CCCCCACCAC	AGAAGACAAT	480
15	CAATCATCAG	GGCCTCCCAC	TGGCACCGCT	TTATTGGAGA	CCAGCACCTC	AAACAGCACA	540
	GGTCCCGACA	ATCCTTGCCA	AGATGATCCC	TGTGCAGATA	ATTCTGTATG	TGTTAAGCTG	600
	CATAATACAA	GTTTTGCTCT	GTGTTTAGAA	GGGTATTACT	ACAACTCTTC	TACATGTAAG	660
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	GAGAAACATT	CCATGGCCTA	TCAAGACTTG	CATAGTGAAA	TTACTAGCTT	GTTTAAAGAT	780
20	GTATTGGACA	CATCTGTTTA	TGGACAGACT	GTAATTCCTA	CTGTAAGCAC	ATCTCTGTCA	840
	CCAAGATCTG	AAATGCGTGC	TGATGACAAG	TTGTGTAATG	TAAACAATAGT	AACAATTTTG	900
	GCAGAAACCA	CAAGTGACAA	TGAGAAGACT	GTGACTGAGA	AAATTAATAA	AGCAATTAGA	960
	AGTAGCTCAA	GCAACTTTCT	AAACTATGAT	TTGACCCCTC	GGTGTGATTA	TTATGGCTGT	1020
	AACAGACTGT	CGGATGACTG	CCTCAATGGT	TTAGCATGCG	ATTGCAAAATC	TGACCTGCAA	1080
	AGGCCTAAAC	CACAGAGCCC	TTTCTGCGTT	GCTTCCAGTC	TCAAGTGTCC	TGATGCTGTC	1140
25	AACGCACAGC	ACAAGCAATG	CTTAATAAAG	AAGAGTGGTG	GGGCCCTTGA	GTGTGCGTGC	1200
	GTGCCCGGCT	ACCAGGAAGA	TGCTAATGGG	AACTGCCAAA	AGTGTGCATT	TGGCTACAGT	1260
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	AAGCATATTG	AAGAAGAGAA	CTTGATTGAC	GAAGACTTTC	AAAATCTAAA	ACTGCGGTGC	1440
30	ACAGGCTTCA	CCAATCTTGG	AGCAGAAGGG	AGCGTCTTTC	CTAAGGTCAG	GATAACGGCC	1500
	TCCAGAGACA	GCCAGATGCA	AAATCCCTAT	TCAAGACACA	GCAGCATGCC	CCGCCCTGAC	1560
	TATTAGAATC	ATAAGAATGT	GGAAACCGCC	ATGGCCCCCA	ACCAATGTAC	AAGCTATTAT	1620
	TTAGAGTGTT	TAGAAAGACT	GATGGAGAAG	TGAGCACCAG	TAAAGATCTG	GCCTCCGGGG	1680
	TTTTTCTTCC	ATCTGACATC	TGCCAGCCTC	TCTGAATGGA	AGTTGTGAAT	GTTTGCAACG	1740
35	AATCCAGCTG	ACTTGTCTAA	TAAGAATCTA	TGACATTAAA	TGTAGTAGAT	GCTATTAGCG	1800
	CTTGTCAAGG	AGGTGGTTTT	CTTCAATCAG	TACAAAGTAC	TGAGACAATG	GTTAGGGTTG	1860
	TTTTCTTAAT	CTTTTCTCTG	GTAGGGCAAC	AAGAACCATT	TCCAATCTAG	AGGAAGCTC	1920
	CCCAGCATTG	CTTGCTCCTG	GGCAAACATT	GCTCTTGAGT	TAAGTGACCT	AATTCCCCTG	1980
	GGAGACATAC	GCATCAACTG	TGGAGGTCCG	AGGGGATGAG	AAGGGATACC	CACCACCTTT	2040
40	CAAGGCTCAC	AAGCTCACTC	TCTGACAAGT	CAGAATAGGG	ACACTGCTTC	TATCCCTCCA	2100
	ATGGAGAGAT	TCTGGCAACC	TTTGAACAGC	CCAGAGCTTG	CAACCTAGCC	TACCCCAAGA	2160
	AGACTGGAAA	GAGACATATC	TCTCAGCTTT	TTCAGGAGGC	GTGCCCTGGG	ATCCAGGAAC	2220
	TTTTTGATGC	TAATTAGTAAG	GCCTGGACTA	AAAATGTCCA	CTATGGGGTG	CACCTCACAG	2280
45	TTTTTGAATG	GCTAGGAGGC	AGAAGGGGCA	GAGAGTAAAA	AAATGACCTT	GGTAGAAGGA	2340
	AGAGAGGCAA	AGGAACTGGG	GTGGGGAGGA	TCAATTAGAG	AGGAGGCACC	TGGGATCCAC	2400
	CTTCTTCTTT	AGGTCCCTTC	CTCCATCAGC	AAAGGAGCAC	TTCTCTAATC	ATGCCCTCCC	2460
	GAAGACTGGC	TGGGAGAAGG	TTTAAAAACA	AAAAATCCAG	GAGTAAGAGC	CTTAGGTCAG	2520
	TTTGAAATTT	GAGACAAACT	GTCTGGCAAA	GGGTGCGAGA	GGGAGCTTGT	GCTCAGGAGT	2580
50	CCAGCCGTCC	AGCCTCGGGG	TGTAGGTTTC	TGAGGTGTGC	CATTGGGGCC	TCAGCCTTCT	2640
	CTGGTGACAG	AGGCTCAGCT	GTGGCCACCA	ACACACAACC	ACACACACAC	AACCACACAC	2700
	ACAAATGGGG	GCAACCACAT	CCAGTACAAG	CTTTTACAAA	TGTTATTAGT	GTCTCTTTTT	2760
	ATTTCTAATG	CCTTGCTCTC	TTAAAAGTTA	TTTATTGTTT	TATTATTATT	TGTTCTTGAC	2820
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55	AAAAAAA						2887

Seq ID NO: C42 DNA Sequence
Nucleic Acid Accession #: NM_001432.1
Coding sequence: 167..676

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65	TCCGACGCCG	CCCTCCGCCA	AGCCCCAGCG	CCCGCTCCCA	TCGCCGATGA	CCGCCGGGAG	180
	GAGGATGGAG	ATGCTCTGTG	CCGGCAGGGT	CCCTGCGCTG	CTGCTCTGCC	TGGGTTTCCA	240
	TCTTCTACAG	GCAGTCTCTA	GTACAACGTG	GATTCCATCA	TGTATCCCAG	GAGAGTCCAG	300
	TGATAACTGC	ACAGCTTTAG	TTCAGACAGA	AGACAATCCA	CGTGTGGCTC	AAGTGTCAT	360
	AACAAAGTGT	AGCTCTGACA	TGAATGGCTA	TTGTTTGCAT	GGACAGTGCA	TCTATCTGGT	420
70	GGACATGAGT	CAAACTACT	GCAGGTGTGA	AGTGGGTTAT	ACTGGTGTCC	GATGTGAACA	480
	CTTCTTTTGA	ACCGTCCACC	AACCTTTAAG	CAAAGAGTAT	GTGGCTTTGA	CCGTGATTCT	540
	TATTATTTTG	TTTCTTATCA	CAGTCGTCCG	TTCCACATAT	TATTTCTGCA	GATGGTACAG	600
	AAATCGAAAA	AGTAAAGAAC	CAAGAAGGA	ATATGAGAGA	GTTACCTCAG	GGGATCCAGA	660
	GTTGCCGCAA	GTCTGAATAT	GAGAGAGTTA	CCTCAGGGGA	TCCAGAGTTG	CCGCAAGTCT	720
75	GAATGGCGCG	ATCAAACTTA	TGGGCAGGGA	TAACAGTGTG	CTGGTTAAT	ATTAATATTC	780
	CATTTTATTA	ATAATATTTA	TGTTGGGTCA	AGTGTTAGGT	CAATAACACT	GTATTTTAAT	840
	GTACTTGAAA	AATGTTTTTA	TTTTTGTTTT	ATTTTGTGACA	GACTATTGTC	TAATGTATAA	900
	TGTGCAGAAA	ATATTTAATA	TCAAAAGAAA	ATTGATATTT	TTATACAAGT	AATTTCCCTGA	960
	GCTAAATGCT	TCATTGAAAG	CTTCAAAGTT	TATATGCCTG	GTGCACAGTG	CTTAGAAGTA	1020
80	AGCAATTCCC	AGGTCTATAG	TCAAGAATTG	TTAGCAAAATG	ACAGATTCTT	GTAAGCCTAT	1080
	ATATATAGTC	AATATCGATT	AGTAAGTATG	TTTTTTATGT	TCCTCAAATC	AGTGATAATT	1140
	GGTTTGACTG	TACCATGGTT	TGATATGTAG	TTGGCACCAT	GGTATCATAT	ATTAACAAAC	1200
	TAATGCAATT	AGAAATTTGG	AGAAGCAAAT	ATAGGTCCTG	TGTTAAACAC	TACACATTGT	1260
	AAACAAGCTA	ACCTTGGGGA	GTCTATGGTC	TCTTCACTCA	GGTCTCAGCT	ATAATTCTGT	1320
	TATATGAGGG	GCAGTGGACA	GTTCCCTATG	CCAACCTCAG	ACTCCTACAG	GTACTAGTCA	1380

5	CTCATCTACC	AGATTCTGCC	TATGTAAAAT	GAATTGAAAA	ACAATTTTCT	GTAATCTTTT	1440
	ATTTAAGTAG	TGGGCATTTC	ATAGCTTCAC	AATGTTCCCT	TTTTGTATAT	TACAACATTT	1500
	ATGTGAGGTA	ATTATTGCTC	AACAGACAAT	TAGAAAAAAG	TCCACACTTG	AAGCCTAAAT	1560
	TTGTGCTTTT	TAAGAAATATT	TTTAGACTAT	TTCTTTTAT	AGGGGCTTTG	CTGAATTTCTA	1620
	ACATTAAATC	ACAGCCCAAA	ATTTGATGGA	CTAATTATTA	TTTTAAAAATA	TATGAAGACA	1680
	ATAATCTTAC	ATGTTGTCTT	AAGATGGAAA	TACAGTTATT	TCATCTTTTA	TTCAAGGAAG	1740
	TTTTAACTTT	AATACAGCTC	AGTAAATGGC	TTCTTCTAGA	ATGTAAAGTT	ATGTATTTAA	1800
	AGTTGTATCT	TGACACAGGA	AATGGGAAAA	AACCTAAAAA	TTAATATGGT	GTATTTTTCC	1860
10	AAATGAAAAA	TCTCAATTGA	AAGCTTTTAA	AATGTAGAAA	CTTAAACACA	CCTTCTCTGT	1920
	GAGGCTGAGA	TGAAAACTAG	GGCTCATTIT	CCTGACATTT	GTTTATTTTT	TGGAAGAGAC	1980
	AAAGATTTCT	TCTGCACCTC	GAGCCCATAG	GTCTCAGAGA	GTTAATAGGA	GTATTTTTGG	2040
	GCTATTGCAT	AAGGAGCCAC	TGCTGCCACC	ACTTTTGGAT	TTTATGGGAG	GCTCCTTCAT	2100
	CGAATGCTAA	ACCTTTGAGT	AGAGTCTCCC	TGGATCACAT	ACCAGGTCAG	GGAGGATCTG	2160
15	TTCTTCTCT	ACGTTTATCC	TGGCATGTGC	TAGGGTAAAC	GAAGGCATAA	TAAGCCATGG	2220
	CTGACCTCTG	GAGCACCAGG	TGCCAGGACT	TGCTTCCATG	TGTATCCATG	CATTATATAC	2280
	CCTGGTGCAA	TCACACGACT	GTCACTTAAA	GTCTGGGCC	TGGCCCTTAC	TATTAGGAAA	2340
	ATAAACAGAC	AAAAACAAGT	AAATATATAT	GGTCTTATAC	ATATTGTATA	TATATTCATA	2400
	TACAAACATG	TATGTATACA	TGACCTTAAT	GGATCATAGA	ATTGCACTCA	TTTGGTGCTC	2460
20	TGCTAACCAT	TTATATAAAA	CTTAAAAACA	AGAGAAAAAG	AAAAATCAAT	AGATCTAAAC	2520
	AGTTATTTCT	GTTCCTTATT	TAATATAGCT	GAAGTCAAAA	TATGTAAAGAA	CACATTTTAA	2580
	ATACTCTACT	TACAGTTGGC	CCTCTGTGGT	TAGTTCCACA	TCTGTGGATT	CAACCAAGTT	2640
	AGGACGGAAA	ATGCTTAAAA	AATAATACAA	CAACAACAAA	AAATACATTA	TAACAACATAT	2700
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25	GTGGCAGCAT	CTCGGCTCAC	TGCAACCTCA	CCTCCCGGTT	TCAAGAGATC	CTCCTGCCCT	2820
	AGCCCTCCTGA	GCAGCTGGGA	CTACAGGCGC	ATGCCACCAT	GCCCAGCTAA	TTTTTGTATT	2880
	TTTAGTAGAG	GCGGGGTTTC	ACCATGTTGG	CCAGGATGGT	CTCAATCTCC	TAACCTTGAG	2940
	ATCCACCCTC	CACAGCCTCC	CAAAGTCTG	GGATTACAGG	CGTGAGCCAC	CGCAGGTAGC	3000
	ATTTACATTA	GGTATTACAA	GTAATGTAAA	GATGATTTAA	GTATACAGGA	GGATGTGAAT	3060
30	AGGTTATATG	CAAGCACTAT	GCCCTTTTAT	ATAAGTGACT	TGAACATCTG	TGCCCGATT	3120
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	ATTTATTAAC	GCTTACTAGA	TGTGAGGAGA	GTCTGAATAT	TTTCAGTGAT	CTTGGCTGTT	3240
	TCAAAAAAAT	CTATTGACTT	TTCAATAAAT	CAGCTGCAAT	CCATTATTAT	CATTTACAAA	3300
	AGATTATTG	TAAGCCTCTC	AATCTTGGTT	TTTCAGTTGA	TCTTAAGCAT	GTCAATTCAT	3360
35	AAAAACAAGT	CATTTTGTGA	TTTTTCATCT	TTAAGAATGC	TTAAAAAAGC	TAATCCCTAA	3420
	AATAGTTAGA	TCTTTGTAAA	TGCATATTAA	ATAATAAAGT	ATGACCACCA	TTACTTTTTTA	3480
	TGGGTGAAAA	TAAGACAAAA	ATAATAGTTT	TAGTGAGGAT	GGTGCTGAGT	AAACATAAAA	3540
	ACTGATTTGC	TCTCAGCTGA	TGTGCTCTGT	ACACAGTGGG	AAGATTTTAG	TTCAACATTA	3600
	GTCTAACTCC	CCCA'TTTTAC	AGATTCTCA	CTATATATAT	TTCTAGAAGG	GGCTATGCAT	3660
40	ATTCATGTGA	TTGAGAACCA	AAGCAACCAC	AAATGCATAA	ATGCATAATT	TATGGTCTTC	3720
	AACCAAGGCC	ACATAATAAC	CCAGTTAACT	TACTCTTTAA	CCAGGAATAT	TAAGTTCTAT	3780
	AACTAGTACT	CAAGGTTTAA	CCTTAAAAAT	AAGATTTCCT	TAACTTAAAC	CTTAAAAATTG	3840
	ATATTATATT	AAACATACAT	AATACAATGT	AACTCCAAGT	TTCTCTGAA	TATTTTGTGC	3900
	TCTAATCTCT	CTGCCGAAAG	TCAAAGTGAT	GGGAGAATTG	GTATACTGGT	ATGACTACGT	3960
45	CTTAAGTCAG	ATTTTATTTT	ATGAGTCTTT	GAGACTAAAT	TCAATCACC	CCAGGTATCA	4020
	AATCAACTTT	TATGCAGCAA	ATATATGATT	CTAGTGTCTG	ACTTTTGTGA	AATTCAGTAA	4080
	TGCAGTTTTT	AAAAACCTGT	ATCTGACCCA	CTTTGTAAAT	TTTGCTCCAA	TATCCATTCT	4140
	GTAGACTTTT	GAAAAAAAAG	TTTTTAATTT	GATGCCCAAT	ATATTCTGAC	CGTTAAAAAA	4200
	TTCTTGTTCA	TATGGGAGAA	GGGGGAGTAA	TGACTTGTAC	AAACAGTATT	TCTGGTGTAT	4260
50	ATTTTAAATGT	TTTTAAAAAG	AGTAATTTCA	TTTAAATATC	TGTTATTCAA	ATTTGATGAT	4320
	GTAAATGTGA	TTTTCATGTA	TTTTCTTTT	ATTTTGCAC	CTGTAATTGC	ACTTTTAAAG	4380
	TTTGAAGAGC	CATTTTGGTA	AACGGTTTTT	ATTAAAGATG	CTATGGAACA	TAAAGTTGTA	4440
	TTGCATGCAA	TTTAAAGTAA	CTTATTGAC	TATGAATATT	ATCGGATTAC	TGAATTGTAT	4500
	CAATTGTGTT	GTGTTCAATT	TCAGCTTTGA	TAATTGTGTA	CCTTAAGATA	TGAAGGAGA	4560
55	AAATAGATAA	TTTACAAGAT	ATTATTAATT	TTTATTATAT	TTCTTGGGA	ATTGAAAAAA	4620
	ATTGAATAAA	ATAAAAATGC	ATTGAACATC	TTGCATTCAA	AATCTTCACT	GAC	4673

Seq ID NO: C43 DNA Sequence
Nucleic Acid Accession #: AF011468.1
Coding sequence: 257..1468

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	CAAGTCCCTT	GTCCGTTCTT	CCGTCCCTGA	GTGTCTTGG	CGCTGCCTTG	TGCCCGCCCA	180
	GCGCCTTTGC	ATCCGCTCCT	GGGCACCGAG	GCGCCCTGTA	GGATACTGCT	TGTTACTTAT	240
	TACAGCTAGA	GGCATCATGG	ACCGATCTAA	AGAAAACTGC	ATTTACAGGAC	CTGTTAAGGC	300
70	TACAGCTCCA	GTTCGAGGTT	CAAAAAGTGT	TCTCGTGACT	CAGCAAATTC	CTTGTCAGAA	360
	TCCATTACCT	GTAATAAGTG	GCCAGGCTCA	GCGGGTCTTG	TGTCCTTCAA	ATTCTTCCCA	420
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	GCAGAAGCAA	TTGCAGGCAA	CCAGTGTACC	TCATCCTGTC	TCCAGGCCAC	TGAATAACAC	540
	CCAAAAAGAGC	AAGCAGCCCC	TGCCATCGGC	ACCTGAAAAAT	AATCCTGAGG	AGGAACTGGC	600
75	ATCAAAACAG	AAAAATGAAG	AATCAAAAAA	GAGGCGAGTG	GCTTTGGAAG	ACTTTGAAAT	660
	TGGTCGCCCT	CTGGGTAAAG	GAAAGTTTGG	TAATGTTTAT	TTGGCAAGAG	AAAAGCAAAG	720
	CAAGTTTATT	CTGGCTCTTA	AAGTGTATT	TAAAGCTCAG	CTGGAGAAAG	CCGGAGTGGA	780
	GCATCAGCTC	AGAAGAGAAAG	TAGAAATACA	GTCCACCTT	CGGCATCCCTA	ATATTCTTAG	840
	ACTGTATGGT	TATTTCCATG	ATGCTACCGAG	AGTCTACCTA	ATTCTGGAAT	ATGCACCCT	900
80	TGGAACAGTT	TATAGAGAAC	TTCAAGAACT	TTCAAAGTTT	GATGAGCAGA	GAACTGCTAC	960
	TTATATAACA	GAATTGGCAA	ATGCCCTGTC	TTACTGTCTAT	TCGAAGAGAG	TTATTTCATAG	1020
	AGACATTAAG	CCAGAGAAGT	TACTTCTTGG	ATCAGCTGGA	GAGCTTAAAA	TTGCAGATTT	1080
	TGGGTGGTCA	GTACATGGCTC	CATCTTCCAG	GAGGACCACT	CTCTGTGGCA	CCCTGGACTA	1140
	CCTGCCCCCT	GAAATGATTG	AAGGTGCGAT	GCATGATGAG	AAGGTGGATC	TCTGGAGCCT	1200
	TGGAGTTCTT	TGCTATGAAT	TTTATGTTGG	GAAGCCTCCT	TTTGAGGCAA	ACACATACCA	1260

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Seq ID NO: C44 DNA Sequence
 Nucleic Acid Accession #: NM_013372
 Coding sequence: 63..617

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Seq ID NO: C45 DNA Sequence
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 CATCTGAGC CTTCTGTAG GGCTCACCTG GGGCTTTGGA ATAGGAACAA TAGTGGACAG 2640
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 CTTATGCTTT GGAATACTCT TGGACAGTAA GCTGCGACAA CTTCTGTTC ACAAGTTGTC 2760
 TGCCTTAAGT TCTTGGAAAG AAACAGAAAA GCAAACTCA TCAGATTAT CTGCCAAACC 2820
 CAAATTTCTA AAGCCTTTCA ACCCACTGCA AAACAAAGGC CATATGCAAT TTTCTCATAC 2880
 TGGAGATTCC TCCGACAACA TCATGCTAAC TCAGTTTGTG TCAAAATGAAT AAGGCAAGGA 2940
 ATCATAAAT CAAGAAAAA TTTCCAGAAC AACTTGACAT TTAGAGACAA ATGTCAATGA 3000
 AGAAATTATG CTCAGTATTG GATCGGGTTT TCTGATTTAG GGGTCTGGGA ATAAACAAG 3060
 AATGTCTCAG TGCTTCA 3078

Seq ID NO: C46 DNA Sequence
 Nucleic Acid Accession #: NM_000584.1
 Coding sequence: 75..374

1 11 21 31 41 51
 AGCAGAGCAC ACAAGCTTCT AGGACAAGAG CCAGGAAGAA ACCACCGGAA GGAACCATCT 60
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 CTGCAGCTCT GTGTGAAGGT GCAGTTTTCG CAAGGAGTGC TAAAGAAGCT AGATGTCACT 180
 GCATAAAGAC ATACTCCAAA CCTTTCACC CCAATTTTAT CAAAGAAGCT AGAGTGATTG 240
 AGAGTGGACC ACACCTGCCT AACACAGAAA TTATTGTAAA GCTTCTGTAT GGAAGAGAGC 300
 TCTGTCTGGA CCCCAAGAAA AACTGGGTGC AGAGGGTGTG GGAGAAGTTT TTGAAGAGGG 360
 CTGAGAAATC ATAAAAAAT TCATTCTCTG TGGTATCCAA GAATCAGTGA AGATGCCAGT 420
 GAAACTTCAA GCAATCTTAC TTCAACACT CATGTATTGT GTGGGTCTGT TGTAGGGTTG 480
 CCAGATGCAA TACAAGATTC CTGGTTAAAT TTGAATTTCA GTAAACAATG AATAGTTTTT 540
 CATGTACCA TGAATATACC AGAACAATCT TATATGTAAA GTATTATTTA TTTGAATCTA 600

CAAAAACAA CAAATAATTT TTAATATATA GGATTTTCCT AGATATTGCA CGGGAGAATA 660
 TACAAATAGC AAAATTGAGC CAAGGGCCAA GAGAATATCC GAACCTTAAT TTCAGGAATT 720
 GAATGGGTTT GCTAGAATGT GATATTTGAA GCATCACATA AAAATGATGG GACATAAAT 780
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 TGTTTATAT GTACAAATAG ATTCTTATAA TATTATTAA ATGACTGCAT TTTTAAATAC 1500
 AAGGCTTTAT ATTTTAACT TTAAGATGTT TTTATGTGCT CTCCAATTT TTTTACTGT 1560
 TTCTGATTGT ATGGAATAT AAAAGTAAAT ATGAAACATT TAAATATATA TTTGTGTGCA 1620
 AAGTAAAAA AAAAAAAA 1639

Seq ID NO: C47 DNA Sequence
 Nucleic Acid Accession #: NM_005603.1
 Coding sequence: 1..3756

1 11 21 31 41 51
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 GAATGTACAT GGCAAGTCAA AGCAACAGAT CGCAAGTACC ACGAACCAACC TCACCTTTATG 240
 AACACAAAAA TCTTGTGTAT TAAGGAGAGT AAATATGCGA ATAATGCAAT TAAACATAC 300
 AAGTACAACG CATTTACCTT TATACCAATG AATCTGTTTG AGCAGTTTAA GAGAGCAGCC 360
 AATTATATAT TCCTGGCTCT TCTTATCTTA CAGGCAGTTC CTCAAATCTC TACCCTGGCT 420
 TGGTACACCA CACTAGTGCC CCTGCTTGTG GTGCTGGGCG TCACCTGCAAT CAAAGACCTG 480
 GTGGACGATG TGGCTCGCCA TAAATGGAT AAGGAAATCA ACAATAGGAC GTGTGAAGTC 540
 ATTAAGGATG GCAGGTTCAA AGTTGCTAAG TGGAAAGAAA TTCAAGTTGG AGACGTCATT 600
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 CCCTCTACCC GTGGATTCTT CATTCTCTGG GGCTATATCA TTGTTCTCAA CACCATGGTA 1200
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 CAGGATGGAG AGGCACCTTC CGACTACCA TCTTTTGCCG TCACCAATGC CTCTGCTCTT 3240
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GTTGCCATTC GATTCTGTG AATGACCATC TGGCCATCAG AAAGTGATAA GATCCAGAAG 3540
 CATCGCAAGC GGTGGAAGGC GGAGGAGCAG TGGCAGCGAC GGCAGCAGGT GTTCCGCCGG 3600
 GGCGTGTCAA CGCGGCGCTC GGCTACGCC TTCTCGCACC AGCGGGGCTA CGCGGACCTC 3660
 ATCTCCTCCG GCGCAGCAT CGCAAGAAG CGCTCGCCG TGTATGCCAT CGTGGCGGAT 3720
 GGCACCGCG AGTACAGCG CACCGGGGAC AGCTGA 3756

Seq ID NO: C48 DNA Sequence
 Nucleic Acid Accession #: XM_044533
 Coding sequence: 238..2751

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 GGAGGCGGGG GCCCCCGGG CGACTCGGGG GCGGACCGCG GGGCGGAGCT GCGGCCGCTG 180
 AGTCCGGCCG AGCCACTGA GCCGAGCCG CGGGACACCG TCGCTCTGCT TCTCGAATG 240
 CTGCGCACCG CGATGGGCCT GAGGAGCTGG CTGCGCGCCC CATGGGGCGC GCTGCCGCT 300
 CGGCCACCGC TGCTGTGCT CTGCTGCTG CTGCTCTGCT TGCGAGCGCC GCCTCCGACC 360
 TGGCGCTCA GCCCCGCGAT CAGCCTGCCT CTGGGCTCTG AAGAGCGGCC ATTCCTCAGA 420
 TTCGAAGCTG AACACATCTC CAACTACACA GCCCTTCTGC TGAGCAGGGA TGGCAGGACC 480
 CTGTACGTGG GTGCTCGAGA GGCCCTCTTT GCACCTAGTA GCAACCTCAG CTTCCTGCCA 540
 GCGGGGAGT ACCAGGAGCT GCTTTGGGGT GCAGACGCG AGAAGAAACA GCAGTGCAGC 600
 TTCAAGGGCA AGGACCCACA GCGCGACTGT CAAAACATACA TCAAGATCCT CTGCGCGCTC 660
 AGCGGCGAGT ACCTGTTCAC CTGTGGCACA GCAGCCTTCA GCCCATGTG TACCTACATC 720
 AACATGGAGA ACTTCAACCCT GGCAAGGGAC GAGAAGGGGA ATGTCTCTCT GGAAGATGGC 780
 AAGGGCCGTT GTCCCTTCGA CCGAATTTT AAGTCCACTG CCTGGTGGT TGTATGGCGAG 840
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Seq ID NO: C49 DNA Sequence
 Nucleic Acid Accession #: NM_007019.1
 Coding sequence: 41..580

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Seq ID NO: C50 DNA Sequence
Nucleic Acid Accession #: NM_014584.1
Coding sequence: 227..1633

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AAAATCGTGC CCTCTTTACA TATGTCCTAT CAGGTATAAC ATGTTGAAAT GTCACATTAG 3180
TAGTAAAGTG GGGTTTATTT ATATAGTGGT TAAGAAATGT CAGTTTACAC TGCTGTATAC 3240
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Seq ID NO: C51 DNA Sequence
Nucleic Acid Accession #: NM_002888.1
Coding sequence: 37..723

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 CCTCAGGATG CTGGGGTCCC GCGCAGGCTC CTGCAGCAGA AGGCGCGCGC GGCCTTTCAC 240
 TTCTTCAACT TCCGGTCCGG CTCGCCAGC GCGCTGCGAG TGCTGGCCGA GGTGCAGGAG 300
 GGCCGCGCGT GGATTAATCC AAAAGAGGGA TGTAAGTTC ACCTGGTCTT CAGCACAGAG 360
 CGCTACAACC CAGAGTCTTT ACTTCAGGAA GGTGAGGGAC GTTTGGGGAA ATGTTCTGCT 420
 CGAGTGTGTT TCAAGAATCA GAAACCCAGA CCAACCATCA ATGTAACCTG TACACGGCTC 480
 ATCGAGAAAA AGAAAGACA ACAAGAGGAT TACCTGCTTT ACAAGCAAAT GAAGCAACTG 540
 AAAAACCCCT TGGAAATAGT CAGCATACCT GATAATCATG GACATATTGA TCCCTCTCTG 600
 AGACTCATCT GGGATTGGC TTTCCTTGGG AGCTCTTACG TGATGTGGGA AATGACAACA 660
 CAGGTGTAC ACTACTACTT GGCACAGCTC ACTAGTGTGA GGCAGTGGGT AAGAAAAACC 720
 TGAAATTAAT CTGTGCCCAC AAGAGTTACA ATCAAAGTGG TCTCCTTAGA CTGAATTCAT 780
 GTGAACTTCT AATTTCATAT CAAGAGTTGT AATCACATTT ATTTCAATAA ATATGTGAGT 840
 TCCTGC 846

Seq ID NO: C52 DNA Sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94..378

1 11 21 31 41 51
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 TTCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT 300
 AAAGGACAAC GATGCTTAAA TCCCAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTTT 360
 GAAAGAAAAG ATTTTAAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 AGACTTTTCT ATGGTTTGTG GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAGG ACCAAAAACA GAAATACAGT CTTCTGAAT GAATGACAAT CAGAATTCCA 600
 CTGCCCAAAG GAGTCCAGCA ATTAATATGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTACCATC CGAGTTTACA AAGTGCTTTC ACCTTCTTAC TGTTGTATT ATACATTCAT 720
 GCATTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTACTAT 780
 GAGAACATT CTGCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TTCCCTCAAAC ATTTTTTCAT GCAAAATACAC ACTTCTTTCC 960
 CCAAAATACA TGTAGCACAT CAATATGTAG GGAAACATTC TTATGCATCA TTTGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 TGGGATACAT GCACACAGTGC ACATATTTCA TAACCAAAT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 TGTACTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTGGAC ACATTTGAAA 1260
 TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAATG TATACCTAGC 1320
 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 TTGTTTCATG CTATATACTG TAAATTTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440
 GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTTCTTTT TTAACAAAAA AAA 1493

Seq ID NO: C53 DNA Sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..609

1 11 21 31 41 51
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 ATGCTGCGGC AGGTGCTTCG CAGAGGGCTC CAGTCGTTCT GCCACAGGCT GGGTTTGTGC 60
 GTGAGCCGGC ACCCGTCTT TTTCTCACC GTGCCGCGAG TCCTGACAAT CACCTTCGGC 120
 CTCAGCGCGC TCAACCGCTT CCAGCCCGAG GCGCAGCTGG AGCGCCTGGT CGCTCCCGAC 180
 CACAGCCTGG CCAAGATCGA GCGCAGCCTG GCCAGCAGCC TTTTCCCGCT GGACCACTGC 240
 AAAAGCCAGC TCTATTGCGA CTTACACACC CCTGGGAGGT ATGGCAGGGT GATCCTCCTC 300
 TCCCAACCG GGGACCAAT TTTGCTCCAG GCTGAGGGGA TCCTGCAGAC CCACCGAGCC 360
 GTGCTGGAAG TGAAGGTGAA CCACAAGGGC TATAATTATA CTTTTTCCCA TCTGTGTGTG 420
 TTGAGAAATC AGGATAAGAA ATGCGTGCTG GATGATATTA TTTCACTGCT AGAGGATCTC 480
 AGGCAGGCTC CCGTCTCCAA TAAGACAACA GCCAGGTGTC AAGTGAGGTA TCCCAACACT 540
 AAATTAAGG TATGCTCCTT CTGCATGCTT CTGCCAATTA AAGAGGCAGC ACTTCATTTT 600
 TTGCCCTAA 609

Seq ID NO: C54 DNA Sequence
 Nucleic Acid Accession #: NM_002438.1
 Coding sequence: 104..4474

1 11 21 31 41 51
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 GCCTCTCTGT CCATCAGGAG AAGGAAAGGA TAAACCTGG GCCATGAGGC TACCCCTGCT 120
 CCTGGTTTTT GCCTCTGTCA TTCGGGTGTC TGTTCTCCTA CTGGACACCA GGCAATTTTT 180
 AATCTATAAT GAAGATCACA AGCGCTGCGT GGATGCAGTG AGTCCAGTG CCGTCCAAC 240
 CGCAGCTTGC AACAGGATG CCGAATCACA GAAATTCCGA TGGGTGTCCG AATCTCAGAT 300
 TATGAGTGTG GCATTTAAAT TATGCCTGGG AGTGCCATCA AAAACAGACT GGGTTGCTAT 360
 CACTCTCTAT GCCTGTGACT CAAAAAGTGA ATTTTCAAGAA TGGGAGTGCA AAAATGACAC 420
 ACTTTTGGGG ATCAAAGGAG AAGATTTATT TTTTAACTAC GGCAACAGAC AAGAAAAGAA 480
 TATATGCTC TACAAGGATG CGGGTTTATG GAGCAGGTGG AAGATCTATG GAACACAGA 540
 CAATCTGTGC TCACAGAGTT ATGAAGCCAT GTATACGCTA CTAGGCAATG CCAATGGAGC 600
 AACCTGTGCA TTCCCGTTCA AGTTTGAAGA CAAGTGGTAC GCAGATTGCA CGAGTGTGCG 660
 GCGGTGCGAT GGATGGCTCT GGTGCGGAAC CACTACTGAC TATGACACAG ACAAGCTATT 720

5	TGGATATTGT	CCATTGAAAT	TTGAGGGCAG	TGAAAGCTTA	TGGAATAAAG	ACCCGCTGAC	780
	CAGCGTTTCC	TACCAGATAA	ACTCCAATC	CGCTTTAACG	TGGCACCAAG	CGAGGAAAAG	840
	CTGCCAACAA	CAGAACGCTG	AGCTCCTGAG	CATCACAGAG	ATACATGAGC	AAACATACCT	900
	GACAGGATTA	ACCAGTTCCT	TGACCTCAGG	ACTCTGGATT	GGACTTAACA	GTCTGAGCTT	960
	CAACAGCGGT	TGGCAGTGGG	GTGACCGCAG	TCCTTTCCGA	TATTTGAACT	GGTTACCAGG	1020
	AAGTCCATCA	GCTGAACCTG	GAAAAAGCTG	TGTGTCACTA	AATCCTGGAA	AAAATGCTAA	1080
	ATGGGAAAAAT	CTGGAATGTG	TTCAGAAACT	GGGCTATATT	TGCAAAAAGG	GCAACACCAC	1140
	TTTAAATTCT	TTTGTATTTC	CCTCAGAAAG	TGATGTGCCT	ACTCACTGTC	CTAGTCAGTG	1200
10	GTGGCCGTAT	GCCGGTCAC	GTTACAAGAT	TCACAGAGAT	GAGAAAAAAA	TCCAGAGGGA	1260
	TGCTCTGACC	ACCTGCAGGA	AGGAAGCGG	TGACCTCACA	AGTATCCACA	CCATCGAGGA	1320
	ATTGGACTTT	ATTATCTCCC	AGCTAGGATA	TGAGCCAAAT	GACGAATTGT	GGATCGGCTT	1380
	AAATGACATT	AAGATTCAAA	TGTACTTTGA	GTGGAGTGAT	GGGACCCCTG	TAACGTTTAC	1440
	CAAATGGCTT	CGTGGAGAAC	CAAGCCATGA	AAACAACAGA	CAGGAGGATT	GTGTGGTGAT	1500
15	GAAAGGCAAG	GATGGGTACT	GGGCAGATCG	GGGCTGTGAG	TGGCCTCTTG	GCTACACTCTG	1560
	CAAGATGAAA	TCACGAAGCC	AAGGTCGAGA	AATAGTGGAA	GTGCAAAAAG	GCTGCAGGAA	1620
	AGGCTGGAAA	AAACATCACT	TTTACTGCTA	TATGATTGGA	CATACGCTTT	CAACATTTCG	1680
	AGAAGCAAA	CAACCTCTGT	ATAATGAGAA	TGCTTATTTA	ACAACATATT	AAGACAGATA	1740
	TGAACAAGCC	TTCTCTGACT	GTTTCGTGG	CTTAAGGCCT	GAAAAATATT	TCTGGACAGG	1800
20	ACTTTCAGAT	ATACAAACCA	AAGGGACTTT	TCAGTGGACC	ATCGAGGAAG	AGGTTTCGGT	1860
	CACCCACTGG	AATTCAGATA	TGCCAGGGCG	AAAGCCAGGG	TGTGTTGCCA	TGAGAACCCG	1920
	GATTGCAGGG	GGCTTATGGG	ATGTTTGA	ATGTGATGAA	AAGGCAAAAT	TTGTGTGCAA	1980
	GCACTGGGCA	GAAGGAGTAA	CCCACCCACC	GAAGCCACG	ACGACTCCCG	AACCCAAATG	2040
	TCCGAGGAT	TGGGGCGCCA	GCAGTAGAAC	AAGCTTGTGT	TTCAAGCTGT	ATGCAAAAAG	2100
25	AAAACATGAG	AAGAAAAAGT	GGTTTGAATC	TCGAGATTTT	TGTCGAGCTC	TGGGTGGAGA	2160
	CTTAGCTAGC	ATCAATAACA	AAGAGGAACA	GCAAAACAATA	TGGCGATTAA	TAACAGCTAG	2220
	TGGAAGCTAC	CACAAACTGT	TTTGGTTGGG	ATTGACATAT	GGGAAGCCCT	CAGAAGGTTT	2280
	TACTTGGAGT	GATGGTTCTC	CTGTTTCATA	TGAAAACTGG	GCTTATGGAG	AACCTAATAA	2340
	TTATCAAAAT	GTTGAATACT	GTGGTGAGCT	GAAAGGTGAC	CCTACTATGT	CTTGGAAATGA	2400
30	TATTAATTGT	GAACACTCTA	ACAACCTGGT	TTGCCAGATA	CAAAAAGGAC	AAACACCAAA	2460
	ACCTGAGCCA	ACACAGCTCT	CTCAAGACAA	TCCACCAAGT	ACTGAAGATG	GGTGGGTTAT	2520
	TTACAAAGAC	TACCAGTATT	ATTTACGCAA	AGAGAAGGAA	ACCATTGGACA	ATGCGCGAGC	2580
	GTTTTGCAAG	AGGAATTTTG	GTGATCTTGT	TTCTATTCAA	AGTGAAAGTG	AAAAGAAGTT	2640
	TCATGGAATA	TATGTAACAA	GAAATGATGC	ACAGTCTGCA	TATTTTATTG	GTTTATTGAT	2700
35	CAGCTTGGAT	AAAAAGTTTG	CTTGGATGGA	TGGAAGCAAA	GTGGATTACG	TGCTCTGGGC	2760
	CACAGGTGAA	CCCAATTTTG	CAAATGAAGA	TGAAAACTGT	GTGACCATGT	ATTCAAATTC	2820
	AGGGTTTTTG	AATGACATTA	ACTGTGGCTA	TCCAAACGCC	TTCAATTTGCC	AGCGACATAA	2880
	CAGTAGTATC	AATGCTACCA	CAGTTATGCC	TACCATGCCC	TCGGTCCCAT	CAGGGTGCAA	2940
	GGAAGGTTGG	AATTTCTACA	GCAACAGTG	TTTCAAATC	TTTGGATTTA	TGGAAGAAGA	3000
40	AAGAAAAAAT	TGGCAAGAGG	CACGAAAAGC	TTGTATAGGC	TTTGGAGGGA	ATCTGGTCTC	3060
	CATACAAAAT	GAAAAAGAGC	AAGCATTTCT	TACCTATCAC	ATGAAGGACT	CCACTTTCAG	3120
	TGCTTGAGCT	GGGCTGAATG	ATGTCAATTC	AGAACACACG	TTCTTTTGGG	CGGATGGACG	3180
	AGGAGTCCAT	TACACAACCT	GGGGGAAAGG	TTACCCCTGG	GGAAGAGAGG	GCAGTCTTTC	3240
	TTATGAAGAT	GCTGACTGTG	TTGTTATTAT	TGGAGGTGCA	TCAATGAAG	CAGGAAAATG	3300
45	GATGGATGAT	ACCTGCGACA	GTAACGAGG	CTACATATGC	CAGACACGAT	CCGACCCCTC	3360
	CTTGACTAAT	CCTCCAGCAA	CGATTCAAAC	AGATGGCTTT	GTTAAATATG	GCAAAAAGCAG	3420
	CTATTCACTC	ATGAGACAAA	AATTTCAATG	GCATGAAGCG	GAGACATACT	CGAAGCTTCA	3480
	CAATTCCCTT	ATAGCCAGCA	TTCTGGATCC	CTACAGTAAT	GCATTTGCGT	GGCTGCAGAT	3540
	GGAAACATCT	AATGAACGTG	TGTGGATCGC	CCTGAACAGT	AACCTTGACTG	ATAATCAATA	3600
50	CACCTGGACT	GATAAGTGGG	GGGTGAGGTA	CACATACTGG	GCTGCTGATG	AGCCCCAAT	3660
	GAAATCAGCA	TGTGTTTATC	TGGATCTTGA	TGGCTACTGG	AAGACAGCAC	ATTGCAATGA	3720
	AAGTTTTTAC	TTTCTCTGTA	AAAGATCAGA	TGAAATCCCT	GCTACTGAAC	CCCCACAAC	3780
	GCCTGGCAGA	TGCCCGGAGT	CAGATCACAC	AGCATGGATT	CCTTTCATG	GTCACTGTTA	3840
	CTATATTGAG	TCCTCATATA	CAAGAACTG	GGGCCAAGCT	TCTCTGGAAT	GTCTTCGAAT	3900
55	GGGTTCTCTT	CTGGTTTCCA	TTGAAAGTGC	TGCAGAATCC	AGTTTTCTGT	CATATCGGGT	3960
	TGAGCCACTT	AAAAGTAAAA	CCRAATTTTG	GATAGGATTG	TTCAGAAATG	TTGAAGGGAC	4020
	GTGGCTGTGG	ATAAATAACA	GTCGGTCTC	CTTTGTCAAC	TGGAACACAG	GAGATCCCTC	4080
	TGGTGAACGG	AATGATTGTG	TAGCTTTACA	TGCGTCTTCT	GGGTTTTGGA	GTAATATTCA	4140
60	CTGTTCTTCC	TACAAAGGAT	ATATTTGTAA	AAGACCAAAA	ATTATTGATG	CTAAACCTAC	4200
	TCATGAATTA	CTTACAACAA	AAGCTGACAC	AAGGAAGATG	GACCTTCTTA	AACCGTCTTC	4260
	CAACGTGGCC	GGAGTAGTCA	TCATTGTGAT	CCTCCTGATT	TTAACGGGTG	CTGGCCTTGC	4320
	CGCCTATTTC	TTTTATAAGA	AAAGACGTGT	GCACCTACCT	CAAGAGGGCG	CCTTTGAAAA	4380
	CACCTCTGAT	TTTAACAGTC	AGTCAAGCCC	AGGAACCTAGT	GATATGAAAG	ATCTCGTGGG	4440
65	CAATATTGAA	CAGAATGAAC	ACTCGGTCAT	CTAGTACCTC	AATGCGATTG	TGAGATATT	4500
	GAATTTTATA	AAATTGTAA	TGAAATTTAA	AATTTTTAGT	TCAATGTGAT	TGTTTTCTTT	4560
	AAAATGAGTA	CTGAATTGTA	CTGGTCTGTC	CTTTTTCTCT	TTGCCTAATT	GAAGAAATAA	4620
	TTGCTTGT	TTAGCCTGG	CAAGATATTT	TCATAAAAGA	GGGATAACAA	TGCTGATTAC	4680
	TACCTTTTAA	AATATTTTAC	ATAAATGCAC	AGCACCACAG	CACCACATCT	AAGCATTAGT	4740
70	GATGGGTAGC	TGATGTGAGC	TTTATGTGGA	TTTAAAGCAC	TCTAGAAACA	ATGAAGCTTC	4800
	TTGGCATATT	TTAAGGAGCT	CCCAAAATGT	GTTACCTATT	AAATTGTAA	TCAGCAAGTA	4860
	GAAGACCATT	TGAAAAGTCA	GGTACAAAT	TCCTCAAGTG	GCATAAAAAT	GTAAGTCAAGT	4920
	TTCTCTTTTA	CCAGTTTTTA	TTTCCACTCC	AATATTATTAG	AACCTTATT	GTACATGTGC	4980
	AGAAGAAATA	GGCAGCTGAG	AATCTTGT	CCCCAAGAG	AGTTTTACAG	GCTGAGTGT	5040
	GCAAAATGTG	TCTTTGTCT	GTTATATGTA	TATCAGGAAT	ACAAGGATGT	GAAATAAAAC	5100
75	TGTAATTTG	CATAACTGGA	TGTACTAGA	TAATGTGAAA	TAAACATTAA	AGACAAGGTC	5160
	TATTTTTAAT	AAAAAAAATA	AAAAA				5185

Seq ID NO: C55 DNA Sequence
Nucleic Acid Accession #: NM_024574.2
Coding sequence: 424..2130

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	CCCGCCGCCC	AGCCCCGCA	CGCTCCCTGC	AGTTTAAAG	GACCTCCCG	CGCTTCTCGG	120

5	CGCTGCCCCG	GGATTCCCCA	GCCCCGCGCG	GCTCCCTACT	CCACTTCGCA	GCAACTTCGG	180
	CGACCGCGCG	CCGCCCCGCC	TCGCCCGCCT	TTGAAAGTTG	CTGTGCCGAC	CGCAAAGTTG	240
	GGACACTTCA	GCGGATTGAA	TTTTTCTCTT	TTATCTGCCT	CCGTCCCCGC	CCTCCAGGCT	300
	TCTCGTTCCT	GGATATTGGT	GCTTAGCATC	TTGGCAGGGT	CCGGGGACGT	GGACTATTTC	360
	GCACACCACA	CCACGGGGAG	GGATTTTTTT	CTATTTTCCC	TACGAAAAAC	AGATCTTTTT	420
	AAGGATGGTG	CTGCTCCACT	GGTGCTCTGT	GTGGCTCCTG	TTTCCACTCA	GCTCAAGGAC	480
	CCAGAAGTTA	CCCACCGGG	ATGAGGAAC	TTTTCAGATG	CAGATCCGGG	ACAAGGCATT	540
	TTTTCATGAT	TCGTAGTAA	TTCCAGATGG	AGCTGAAATT	AGCAGTTATC	TCTTTAGAGA	600
10	TACACCTAAA	AGGTATTTCT	TTGTGGTTGA	AGAAGACAAT	ACTCCATTAT	CAGTCACAGT	660
	GACGCCCTGT	GATGCGCCTT	TGGAGTGGAA	GCTGAGCCTC	CAGGAGCTGC	CAGAGGACAG	720
	GAGCGGGGAA	GGCTCAGGTG	ATCTGGAACC	TCTTGAGCAG	CAGAAGCAGC	AGATCATTAA	780
	TGAGGAAGGC	ACTGAGTTAT	TCTCCTACAA	AGGCAATGAT	GTGAGTATT	TTATATCGTC	840
	TAGTTCCCCA	TCCGGTTTAT	ATCAGTTGGA	TCTTCTTTCA	ACAGAGAAAG	ACACACATT	900
	CAAAGTATAT	GCCACCACAA	CTCCAGAATC	TGATCAGCCA	TACCTGAGT	TACCTATGA	960
15	CCCAAGAGTA	GATGTGACCT	CACTGGGGCG	CACCACGGTC	ACTTTGGCCT	GGAAACCAAG	1020
	CCCCACTGCC	TCTTTGCTGA	AACAACCCAT	TCAGTACTGT	GTGGTCATCA	ACAAAGAGCA	1080
	CAATTTCAAA	AGTCTCTGTG	CAGTGGGAAG	AAAACTGAGT	GCAGATGATG	CTTTTATGAT	1140
	GGCACCGAAA	CTCGGTCTGG	ACTTCAGCCC	CTTTGACTTT	GCCCACTTTG	GATTTCTTTC	1200
	TGATAATTCA	GGTAAAGAAC	GCAGTTTCCA	GGCAAAGCCT	TCTCCAAAAC	TGGGGCGTCA	1260
20	TGTCTACTCC	AGGCCCAAGG	TTGATATTCA	AAAAATCTGC	ATAGGAAAAC	AGAACATCTT	1320
	CACCGTCTCT	GATCTGAAAC	CCGACACGCA	GTACTACTTT	GACGTATTTG	TGGTCAACAT	1380
	CAACAGCAAC	ATGAGCAGCG	CTTATGTAGG	TACCTTTGCC	AGGACCAAGG	AAGAAGCCAA	1440
	ACAGAAGACA	GTCCAGCTCA	AAGATGGGAA	GATAACAGAT	GTATTTGTTA	AAAGGAAGGG	1500
25	AGCAAAGTTT	CTACGGTTTG	CTCCAGTCTC	TTCTCACCAA	AAAGTCACCT	TCTTTATTCA	1560
	CTCTTGTCTG	GATGCTGTCC	AAATCCAAGT	GAGAAGAGAT	GGGAAACTTC	TCTGTCTCA	1620
	GAATGTGGAA	GGCATTTCAGC	AGTTTCAGCT	TAGAGGAAAA	CCTAAAGCTA	AATACCTCGT	1680
	TCGACTGAAA	GGAAACAAGA	AAGGAGCATC	TATGTTGAAA	ATTCTAGCTA	CCACAAGGCC	1740
	TACTAAGCAG	TCATTTCCCT	CTCTTCCTGA	AGACACAAGA	ATCAAAGCCT	TTGACAAGCT	1800
30	CCGTACTCTG	TCTTCGGCCA	CCGTGGCCTG	GCTAGGCACT	CAGGAAAGGA	ACAAAGTTTG	1860
	CATCTACAAA	AAAGAGTGG	ATGATAACTA	CAATGAAGAC	CAGAGAAAAA	GAGAGCAAAA	1920
	CCAATGTCTA	GGACCAGATA	TAAGGAAGAA	GTCAAGAAAG	GTCCCTCTGA	AATATTTCCT	1980
	CAGTCAAAAC	CTGCAGAAAG	CAGTGACCAC	AGAAACAATT	AAAGGTCTTC	AGCCTGGCAA	2040
	ATCTTACCTG	CTGGATGTTT	ATGTCATAGG	ACATGGGGGG	CACCTCTGTA	AGTATCAGAG	2100
35	TAAGGTTGTG	AAAACTAGAA	AGTTCTGTGA	GTTACCTTCT	TATAGAGATA	TATTATGTAG	2160
	AACTCCAGGA	GGGACATTAA	ATCATTCTAA	GTATAAATCG	ACTACTCCCA	CAGTTGAGAG	2220
	AAGTTGTGAC	CTGTACTTGT	ACTATGGAAG	GAAGGATATC	AACGTGTGTA	TATTGATGTT	2280
	TATATAAGTA	ACTCTTGAAG	GAGACTTGT	CTAGCGTGCC	CCATGGTACC	TAGTGTGTGT	2340
	CTGATGCCGG	TTGGTGTCAA	AGATAGAGGG	CTTCTTGAAG	GAACTTGCCA	TTCTTGTGCT	2400
40	TGACCACTGC	ATGAACCTGT	TCTAAATTAT	TTTATTACCT	AAAAATTAA	AATATGCCAT	2460
	TCATTGCACA	CACCCACAAA	TGCAAAATCAT	TCCTCTCTAT	AGATGCTAGG	ATATATATAA	2520
	ATTATTTTAT	AAATCTCTGT	TTTAAATGTC	AGTGTCTCTA	TGATTGTAAA	CTATTAAATT	2580
	CTTTTCTCTAT	TAAAGTACAG	ATCTAATCTA	AGTATTATTA	AGTTGATAGC	CCTCTAGTCA	2640
	GTTATATTGC	TATTGTAAAT	TCTTGTGTTG	TGAGTAAAT	GTTTAAATAC	TATATGTATC	2700
45	TCATGTACAA	AGTTGACATA	CATTATATTC	ATGTACATAA	AATTAAGAG	ATTAGATTAT	2760
	ATACTGTTAA	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA	2808

Seq ID NO: C56 DNA Sequence
Nucleic Acid Accession #: BC034229.1
Coding sequence: 373..1422

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	CTTCCTCAGC	CTGCTCAATG	TGAAGCCCTT	GATCATGATT	CACCTCCACT	TAATAAATAA	120
	AGTGTTTTACA	AATCAGAATA	ACTTTTAGAC	AATATTAAAG	TGGTAATCAT	GAACAGAAAA	180
	GATTTTGTAG	TTCTTCCATG	GGGAAAACCT	GGAAATTCTG	TAAAGCTAAA	ATATAGCAAT	240
	GTAATAATTA	AAACAAAAGT	CTAAGATTG	AAGAGATAAT	TTGCTTCAGG	ATTTTGTAGG	300
60	AAGGCAAAAT	CTAACTTTAA	AAACCAGATT	TCGGAGAAAT	ACAAAAGAAA	TAGAAATGCT	360
	CAGAAGCTGC	GAATGGAGAA	AGTACAGTTA	GAGTTTGAGA	ACCAAGAGAT	GGAGAAGAAA	420
	CTGCAAGAAT	TCCGATCCAC	AAGAAACAAA	GAAAAGGAAG	ATAGAGAGTC	AAGCGAGTAT	480
	TACTGGAAAT	CTGGAAAAGT	GGGCAAAATT	GTCAATCAAT	CATATATGAT	GTCACAAAAT	540
	AAAGGAAATG	TTGTTAAGTT	TTCTGCTGGA	AAAGTGAAAT	TAAAATTGCT	GAAGGAACAG	600
65	ATTCAAGAGC	CAGTGAAACC	AACAGTTAAT	TATAAAATGG	CAAATTCTTC	AGAATGTGAA	660
	AAACCAAGA	TAAATGGGAA	AGTTTGTGGA	CAGTGTGAGA	ACAAAGCTGC	TCTACTGGTA	720
	TGCCCTGAAT	GTGGAGAAGA	TTATTGTTCA	GGATGCTTTG	CTAATGTTCA	CCAGAAAGGG	780
	GCACTAAAGC	TCCACAGAAG	AACTCTTTTG	CAGGCAAGAT	CTCAAATATT	ATTCAATGTA	840
	TTGGATGTTG	CCCATCAGTT	TATAAAGGAT	GTTAATCCAG	ATGAACCCAA	AGAGGAGAAT	900
70	AAITCTACAA	AGGAAACCA	TAAAATTCAA	CATAAACCCA	AATCTGTACT	TCTCCAGAGG	960
	AGCAGCTCTG	AGGTAGAAAT	TACAACGATG	AAAAGAGCAC	AACGTACAAA	ACCAAGAAAG	1020
	AGTCTGTTGT	GTGAAGGGTC	ATTTCGATGA	GAAGCTTCTG	CACAGTCTTC	TCAGGAAGTG	1080
	TTAAGTCAAT	GGAGAACCGG	AAATCATGAT	GACAACAAGA	AACAGATTTT	ACATGCAGCA	1140
	GTAAAAGACT	CATTGGAAGA	ATGCGAAGTA	CAGACTAATC	TGAAAAATTG	GAGAGAACCA	1200
75	CTTAATATTG	AACTTAAAGA	AGACATTCTA	TCCTATATGG	AAAAATTATG	GCTTAAAAAA	1260
	CACAGGAGAA	CTCCACAAGA	GCAACTTTTT	AAATGCTACC	AGATACGTTT	CCCATCCAC	1320
	ATGAACACCAC	TGGTGTGCA	CAGTGTCTC	AAAATGAAAA	CGATGAAGAT	AGTGATGGTG	1380
	AGGAGACCAA	AGTACAACAC	ACAGCTCTTT	TATTGCCAGT	AGAAACATTA	AACATAGAGA	1440
	GACCTGAACC	ATCTCTGAAG	ATAGTCGAAC	TGGATGATAC	TTATGAGAG	GAATTTGAAG	1500
80	AAGCAGAAAA	TATTGTGCTT	TACAAAGTTA	AATTAGCTGA	TGCAGACAGT	CAACGAAGTT	1560
	GTGCTTTTCA	TGATTGTGAG	AAGAATAGCT	TTCCATATGA	AAATGGCATC	CATCAACATC	1620
	ATGTTTTTCA	TAAGGGAAAG	AGAGACTTCT	TAAATCTTTG	TCTGAGAAAC	AGCTCTACTT	1680
	ATTATAAAGA	TAATTCAAAA	GGAGAAACTT	CAACACAGAA	TTTTGACAAC	ATCGTGGATC	1740
	CTGATGTGTA	TTCTTCTGAC	ATTGAAAAAA	TTGAGGAAAG	CACCTCCTTT	GAAAGAAATT	1800
	TAAAGGAGAA	AAATATAGGT	TTAGAAAGTA	ATCAAAAGTC	TGATGATTCC	TGTGTATCAC	1860

TTGAAAGCAA GGACACTTTG CTAGGTAGAG ATTTAGAAAA AGCTCCCATT GAGGAGAAAT 1920
 TATCTCAAGA CATCAAAGAA TCCTTGGAAT TGAGCAATCT GTATAAGAGG CCAAGCTTTG 1980
 AAGAATCAAA AACTACAAAG TCATCACTGT TGTTACAAGA AATAGCCTGC AGAAGTAAAGC 2040
 CTATAACAAA ACAAATATCAA GGACTTGAGA GATTCTTTAT TTTTGATACA AATGAAAGAC 2100
 TCAACTTACT TCCTTCTCAT CGTTTAGAAT GCAACAATTC CAGTACTAGG ATTACACTTG 2160
 CAGGTCAGAA ATCAGAGAGA CCTTCAACAG CAAATTTTCC ACTTTCCAAC TCTGTTAAAG 2220
 AAAGCTCCAG TTGCCTTTCA TCCTCTCATC CTCGATCAAG AAGTGCAGCT GCTCAATCAT 2280
 CATCTAGAGC TGCTTCTGAA ATTTAGAGAA TTGAATATAT TGATATTACT GACCAGAATG 2340
 AGCTTTCGTA AGATGACACT ACTGATCAAC ATACTTTAGA CAATTTGGAA AAAGAATTAC 2400
 AAGTGTGAG ATCTCTTGCA GATACTTCAG AAAAGCTTTA CAGCTTAACC TCAGAAGAGT 2460
 TCCCAGATT CAGCAGCCAA TCAGTAATA TAAGTCAGAT TTCCACAGAT TTCTTAAGA 2520
 CCTCACATGT GAGGGGTCCC TGTGGAGTTG AGGAATTGAG CTGTTCTGGA AGAGATACCA 2580
 AAATTCAGTC TTGCTGTCA CTTTCTGAGA GCAGTACAGA TGAGGAGGAG GAAGATTTTC 2640
 TCAACAAGCA ACATGTCATC ACACCTACCGT GGTCAAAGAG TACTTAAAGA TTATTGTGTC 2700
 ATTACTGTTT CCATTTTGTA CCCAGAGTAA AGCAACAAC TGAGAAAAGT AACCAAGTGA 2760
 TTACCTATCC AAGTGCTGGA GATTTTGATT ACTAATGTCT TTGATGTTTC AAGGCTACAA 2820
 ACTAATAAAA GTAAAAATTAT AAGTTCAAAA AAATTTTTAA AAAAAAAT AAAAAA 2876

Seq ID NO: C57 DNA Sequence
 Nucleic Acid Accession #: NM_024687.1
 Coding sequence: 138..1706

1 11 21 31 41 51
 AAAAAATGA TGACAAACAG AAACAGAAAT TACATGCAGC AGTAAAAGAC TCATTGGAAG 60
 AATGCGAAGT ACAGACTAAT CTGAAAATTT GGAGAGAACCT ACTTAATATT GAACTTAAAG 120
 AAGACATTCT ATCCTATATG GAAAAATTAT GGCTTAAAAA ACACAGGAGA ACTCCAAG 180
 AGCAACTTTT TAAATGCTA TCAGATACGT TCCCACATCC ACATGAAACC ACTGGTGATG 240
 CACAGTGTTT TCAAAATGAA AACGATGAAG ATAGTGATGG TGAGGAGACC AAAGTACAAC 300
 ACACAGCTCT TTTATTGCCA GTAGAAACAT TAAACATAGA GAGACCTGAA CCATCTCTGA 360
 AGATAGTCGA ACTGGATGAT ACTTATGAAG AGGAATTTGA AGAAGCAGAA AATATTGTGC 420
 CTTACAAAGT TAAATTAGCT GATGCAGACA GTCAACGAAG TTGTGCTTTT CATGATTGTC 480
 AGAAGAATAG CTTTCCATAT GAAAATGGCA TCCATCAACA TCATGTTTTC GATAAGGGAA 540
 AGAGAGACTT CTTAAATCTT TGTCTGAGAA ACAGCTCTAC TTATTATAAA GATAATTCAA 600
 AAGGAGAAAC TTCAAACACA GATTTTGACA ACATCGTGGA TCCTGATGTG TATTCTTCTG 660
 ACATTGAAAA AATTGAGGAA AGCACCCTCT TTGAAAGAAA TTTAAAGGAG AAAAATATAG 720
 GTTTAGAAAG TAATCAAAAG TCTGATGATT CCTGTGTATC ACTTGAAAGC AAGGACACTT 780
 TGCTAGGTAG AGATTTAGAA AAAGCTCCCA TTGAGGAGAA ATTATCTCAA GACATCAAAG 840
 AATCCTTGGA ATTGAGCAAT CTGTATAAGA GGCCAAAGCT TGAAGAATCA AAAACTACAA 900
 AGTCATCACT GTTGTACAA GAAATAGCCT GCAGAAGTAA GCCTATAACA AAACAATATC 960
 AAGGACTTGA GAGATTCTTT ATTTTGTATA CAAATGAAAG ACTCAACTTA CTTCTTCTC 1020
 ATCGTTTAGA ATGCAACAAT TCCAGTACTA GGATTACACT TGCAGAAGAC AGAGAATGGA 1080
 TTCCAGACCA TAGCTTAAGT GAATATGCTG ATAATGCAAT TGTCTGGGT GTTCTGCAGG 1140
 GTGCTCAGAG TCCATCATCA AGTAGAAAAAC AGCAAAAGAT GGGTCAGAAA TCACAGAGAC 1200
 CTTCAACAGC AAATTTTCCA CTTTCCAAC CTGTTAAAGA AAGCTCCAGT TGCCTTTCAT 1260
 CCTCTCATCC TCGATCAAGA AGTGCAGCTG CTCATCATC ATCTAGAGCT GCTTCTGAAA 1320
 TTTCAGAAAT TGAATATATT GATATTACTG ACCAGAATGA GCTTTCCTTA GATGACACTA 1380
 CTGATCAACA TACTTTAGAC AATTTGGAAA AAGAATTACA AGTGCTGAGA TCTCTTGACG 1440
 ATACTTCAGA AAAGCTTTAC AGCTTAACCT CAGAAGAGTT CCCAGATTTT AGCAGCCAAT 1500
 CACTGAATAT AAGTCAGATT TCCACAGATT TCCTTAAGAC CTCACATGTG AGGGGTCCCT 1560
 GTGGAGTTGA GGAATTGAGC TGTTCTGGAA GAGATACCAA AATTCACTCT TTGCTGTGAC 1620
 TTTCTGAGAG CAGTACAGAT GAGGAGGAGG AAGATTTTCT CAACAAGCAA CATGTCATCA 1680
 CACTACCGTG GTCAAAGAGT ACTTAAAGAT TATTTGTTC TACTGTTTC CATTTTGTAC 1740
 CCAGAGTAAA GCAAAACACT GAGAAAAGTA ACCAAGTGAT TACCTATCCA AGTGTGGAG 1800
 ATTTTGATTA CTAATGTCTT TGATGTTTCA AGGCTACAAA CTAATAAAG TAAATTTATA 1860
 AGTTCAAAA AAAAAAATA AAAA 1884

Seq ID NO: C58 DNA Sequence
 Nucleic Acid Accession #: NM_005408.1
 Coding sequence: 76..372

1 11 21 31 41 51
 AAAAGGCCGG CGGAACAGCC AGAGGAGCAG AGAGGCAAAG AAACATTGTG AAATCTCCAA 60
 CTCTTAACTT TCAACATGAA AGTCTCTGCA GTGCTTCTGT GCCTGCTGCT CATGACAGCA 120
 GCTTTCAACC CCCAGGGACT TGCTCAGCCA GATGCATCA ACGTCCCATC TACTTGCTGC 180
 TTCACATTTA GCAGTAAGAA GATCTCCTTG CAGAGGCTGA AGAGCTATGT GATCACCACC 240
 AGCAGGTGTC CCCAGAAGGC TGTCTCTTCT AGAACCAAC TGGGCAAGGA GATCTGTGCT 300
 GACCCAAAGG AGAAGTGGGT CCAGAATTAT ATGAAACACC TGGGCCGGAA AGCTCACACC 360
 CTGAAGACTT GAACTCTGCT ACCCCTACTG AAATCAAGCT GGAGTACGTG AAATGACTTT 420
 TCCATTCTCC TCTGGCTTCC TCTTCTATGC TTTGGAATAC TTCTACCATA ATTTTCAAAT 480
 AGGATGCAAT CGGTTTGTG ATTCAAATG TACTATGTGT TAAGTAATAT TGCTATTAT 540
 TTGACTTGTT GCTGGTTTGG AGTTTATTG AGTATTGCTG ATCTTTTCTA AAGCAAGGCC 600
 TTGAGCAAAG AGTTGCTGT CTCTAAGCCC CCTTCCCTTC CACTATGAGC TGCTGGCAGT 660
 GGGTTTGTAT TCGGTTCCCA GGGGTTGAGA GCATGCCTGT GGGAGTCATG GACATGAAGG 720
 GATGCTGCAA TGTAGGAAGG AGAGCTCTTT GTGAATGTGA GGTGTGCTA AATATGTTAT 780
 TGTGAAAGA TGAATGCAAT AGTAGGACTG CTGACATTTT GCAGAAAATA CATTTTATT 840
 AAAATCTCCA AAAAAAATA 860

Seq ID NO: C59 DNA Sequence
 Nucleic Acid Accession #: AK097746.1
 Coding sequence: 185..2224

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5	CTTTCATGAC	AGTAACAAAT	CCAAGATTTT	GGAAAAAGCGC	CTACGATATT	TAAATGACCA	60
	CTTCACATAC	AACCTATATG	GTAATATATG	CCGATCACTA	TTTGAGAAGG	ACAAGCTGTT	120
	ATTTTCCTTT	TTATTATGTG	CCAATCTTCT	TCTGGCAAGG	AAAGAGATTG	AATACCAGGA	180
	ACTGATGTTT	CTTTTAACTG	GAGGAGTAAG	TCTTAAAAGT	GCTGAGAAAA	ATCCTGATCC	240
	AACCTGGCTA	CAGGACAAAA	GCTGGGAGGA	AATCTGTGCG	GCAAGTGAAT	TTCTGCCTT	300
10	CAGAGGACTC	AGGCAACATT	TTTGTGAACA	TATATATGAA	TGGCGAGAAA	TCTATGACAG	360
	TAAAGAGCCA	CATAATGCTA	AATTTCACG	ACCAATGGAT	AAGAACCTAA	ATGAACTACA	420
	GAAAATAATA	ATTCTTCGGT	GTTTAAGACC	TGATAAGATA	ACCCCAGCTA	TAACAAACTA	480
	TGTAACCTGAC	AACTAGGGA	AAAAGTTTGT	AGAGCCTCCA	CCATTGTGAT	TGACAAAGAG	540
	TTACTTGGAT	TCAAATTGCA	CCATTCCCTT	AATTTTGTGT	CTATCTCCAG	GAGCAGATCC	600
15	TATGGCCAGC	CTGCTGAAAT	TTGCAAAATG	TAAATCTATG	TCTGGAAATA	AGTTTCAAGC	660
	TATTTCACTG	GGACAGGGAC	AAGGACCGAT	TGCAGCAAAA	ATGATTAAAG	CAGCAATTGA	720
	AGAAGGAAC	TGGGTGTGCC	TACAGAATTG	CCATCTTGCA	GTGTCTCGGA	TGCCCATGTT	780
	GGAAAAAATA	TGTGAAGATT	TTACCTCTGA	AACCTGTAA	TCATCTTTTA	GGCTTTGGCT	840
	GACAAGCTAT	CCATCTTCAA	AATTCCAGT	AACAATTCTA	CAGAATGGAG	TAAAAATGAC	900
20	TAATGAACCT	CCCACGGGTC	TTCGGCTGAA	TCTCCTTCAA	TCATATCTCA	CTGATCCAGT	960
	TTCTGATCCT	GAGTTTTCCT	AGGGATGCCG	TGGAAGAGGA	CTGTTATTTA	TCAATGAATA	1020
	TGATACAATT	CCATTGTGAAG	CTATATCTTA	CCTGACTGGG	GAGTGTAATT	ATGGAGGAAG	1080
	AGTGACAGAC	GATTGGGACA	GACGCTTCT	ATTAACCATG	CTGGCTGACT	TTTATAATCT	1140
	GTACATAGTT	GAACCCCTC	ATTATAAGTT	TTCCTCCAGT	GGAAACTATT	TTGCACCTCC	1200
25	TAAAGGCAC	TATGAGGACT	ACATTGAATT	CATTAAAGAA	CTTCCATTTA	CTCAACACCC	1260
	TGAGATATTT	GGATTACATG	AAAAAGTTGA	CATCTCCAAG	GATCTTCAAC	AAACAAAAAC	1320
	CTCTTTTGAG	TCCTTGCTCC	TCACCCAGGG	AGGCTCCAAA	CAGACAGGAG	CCTCAGGAAG	1380
	TACTGATCAG	ATTCTGTTAG	AAATTACCAA	AGATATCCTC	AACAAGCTCC	CTAGTGATT	1440
	CGACATTGAA	ATGGCACTAC	GGAAAGTATC	TGTGAGATAT	GGAAGAAAGCA	TGAATACTGT	1500
30	GTTAGTACAA	GAAATGGAAA	GATTTAACAA	TTTAATTATA	ACTATACGTA	ACACTCTACG	1560
	GGACCTTGAA	AAAGCTATTA	AGGGTGTGGT	TGTGATGGAT	TCTGCATTGG	AGGCACTCTC	1620
	CAGTAGCTTA	CTTGTGTGAA	AGGTTCCAGA	AATATGGGCC	AAACGTTTCA	ACCCAAGCCT	1680
	TAAGCCCTTG	GGAAAGTTACA	TCACAGATTT	CCTAGCCCGG	TTGAACTTTT	TACAGGACTG	1740
	GTATAATTCA	GGAAACCTT	GTGTGTTTTG	GCTGTGAGT	TTCTTTTTCA	CTCAGGCCCT	1800
35	TTTAAGCTGA	GCTATGCGA	ATTATGCCAG	AAAATATACC	ACCCCTATTG	ATTTGCTAGG	1860
	ATATGAATTT	GAGGTATATC	CATCTGATAC	ATCTGACACA	TCACCAGAAG	ATGGTGTTTA	1920
	TATCCACGGA	CTGTATCTCG	ATGGCGCACG	CTGGGACCGA	GAAAGTGGAT	TGCTTGCTGA	1980
	ACAATATCCC	AAACTTCTGT	TTGACCTGAT	GCCCATCATA	TGGATAAAAC	CAACTCAAAA	2040
	ATCTCGGATT	ATAAAGTCGG	ATGCCCTATG	CTGTCCCTTC	TACAAGACAA	GTGAACGTAA	2100
40	AGGAACCTTT	TTCCACTACG	GACATTCTAC	TAACTTTGTC	ATTGCAATGT	TGTTAAAAAC	2160
	AGACCAACCT	ACTCGGCACT	GGATCAAGCG	CGGGGTTGCT	TTGCTTTGTC	AGTTGGATGA	2220
	CTAAATTGGA	CAAATTTATA	AAACATCCAA	AAGTTT			2256

Seq ID NO: C60 DNA Sequence
Nucleic Acid Accession #: J02761.1
Coding sequence: 14..1159

45	1	11	21	31	41	51	
	GAATTCGGGT	GCCATGGCTG	AGTCACACCT	GCTGCAGTGG	CTGCTGCTGC	TGCTGCCCCAC	60
50	GCCTCTGTGG	CCAGGCACTG	CTGCCCTGGAC	CACCTCATCC	TTGGCCTGTG	CCGAGGGCCC	120
	TGAGTTCTCG	TGCCAAAGCC	TGGAGCAAGC	ATTGCACTGC	AGAGCCCTAG	GGCATTGCCT	180
	ACAGGAAGTC	TGGGGACATG	TGGGAGCCGA	TGACCTATGC	CAAGAGTGTG	AGGACATCGT	240
	CCACATCCTT	AACAAGATGG	CCAAGGAGGC	CATTTTCCAG	GACACGATGA	GGAAAGTTCT	300
55	GGAGCAGGAG	TGCAACGCTG	TCCCTTGAAG	GCTGCTCATG	CCCCAGTGCA	ACCAAGTGCT	360
	TGACGACTAC	TTCCCTCTGG	TCATCGACTA	CTTCCGAAC	CAGACTGACT	CAACCGGCAT	420
	CTGTATGCAC	CTGGGCTGTG	GCAATCCCG	GCAGCCAGAG	CCAGAGCAGG	AGCCAGGGAT	480
	GTACAGCCCC	CTGCCCAAC	CTCTGCGGGA	CCCTCTGCCA	GACCTCTGCT	TGGACAAAGCT	540
	CGTCTCTCCT	GTGCTGCCCC	GGGCCCTCCA	GGCGAGGCC	GGGCCCTACA	CACAGGATCT	600
60	CTCGAGCAG	CAATTCCCCA	TTCTCTCTCC	CTATTGCTGG	CTCTGCAGGG	CTCTGATCAA	660
	GCGGATCCAA	GCCATGATTG	CCAAGGGTGC	GCTAGCTGTG	GCAGTGCCCC	AGGTGTGCCG	720
	CGTGGTACCT	CTGGTGGCCG	GCGGCATCTG	CCAGTGCCTG	GCTGAGCGCT	ACTCCGTCAT	780
	CCTGCTCGAG	ACGCTGCTGG	GCCGCATGCT	GCCCCAGCTG	GTCTGCCGCC	TCGTCCTCCG	840
	GTGCTCCATG	GATGACAGCG	CTGGCCCAAG	GTGCGCGACA	GGAGAATGGC	TGCCGCGAGA	900
65	CTCTGAGTGC	CACCTCTGCA	TGTCCGTGAC	CACCCAGGCC	GGGAACAGCA	GCGAGCAGGC	960
	CATACCACAG	GCAATGTCTC	AGGCCTGTGT	TGGCTCCTGG	CTGGACAGGG	AAAAGTGCAA	1020
	GCAATTTGTG	GAGCAGCAC	CGCCCCAGCT	GCTGACCCTG	GTGCCAGGG	GCTGGGATGC	1080
	CCACACCACT	TGCCAGGCC	TGGGGGTGTG	TGGGACCATG	TCCAGCCCTC	TCCAGTGTAT	1140
	CCACAGCCCC	GACCTTTGAT	GAGAACTCAG	CTGTCCAGCT	GCAAGGAAA	AGCCAAAGTA	1200
70	GACGGGCTCT	GGGACCATGG	TGACCAGGCT	CTTCCCTTGC	TCCCTGGCCC	TCGCCAGCTG	1260
	CCAGGCTGAA	AAGAAGCCTC	AGCTCCACAC	CCGCCCTCCT	CACCTCCCTT	CCTCGGCAGT	1320
	CACCTTCACT	GTTGGACAC	GGGCCCCAG	CCCTGTGTCG	GCCTTGTCTG	TCTCAGCTCA	1380
	ACCACAGTCT	GACACCAGAG	CCCACTTCCA	TCCTCTCTGG	TGTGAGGCAC	AGCGAGGGCA	1440
	GCACTCTGGAG	GAGCTCTGCA	GCCTCCACAC	CTACCACGAC	CTCCACAGGC	TGGGCTCAGG	1500
75	AAAAACCAAG	CACCTGCTTTA	CAGGACAGGG	GGTTGAAGCT	GAGCCCCGCC	TCACACCCAC	1560
	CCCATGACAC	TCAAAGATTG	GATTTTACAG	CTACTTGCAA	TTCAAATTC	AGAAGAATAA	1620
	AAAAATGGGA	CATACAGAA	TCTAAAGAT	AGACATCAGA	AATTGTTAAG	TTAAGCTTTT	1680
	TCAAAAAATC	AGCAATTCCC	CAGCGTAGTC	AAGGGTGGAC	ACTGCACGCT	CTGGCATGAT	1740
	GGGATGGCGA	CCGGGCAAGC	TTTCTTCTC	GAGATGCTCT	GCTGCTTGAG	AGCTATTGCT	1800
80	TTGTTAAGAT	ATAAAAGGG	GTTTCTTTT	GTCTTCTGT	AAGGTGGACT	TCCAGATTTT	1860
	GATTGAAAGT	CCTAGGGTGA	TTCTATTTCT	GCTGTGATTT	ATCTGCTGAA	AGCTCAGCTG	1920
	GGGTTGTGTC	AGCTAGGGAC	CCATTCCTGT	GTAATACAAT	GTCTGCACCA	ATGCTAATAA	1980
	AGTCTTATTC	TCTTTTAAAA	AAAAAAAACG	GAATTC			2026

Seq ID NO: C61 DNA Sequence

Nucleic Acid Accession #: NM_139172.1
Coding sequence: 19..552

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      GGGGCTCTGGG GAGGTGACAT GTTGGGCTGT GGGATCCCAG CGCTGGGCCT GCTCCTGCTG 60
      CTGCAGGGCT CCGCAGACCG AAATGGAATC CAGGGATTCT TCTACCCATG GAGCTGTGAG 120
      GGTGACATAT GGGACCGGGA GAGCTGTGGG GGCCAGGCGG CCATCGATAG CCCCAACCTC 180
      TGCTGCGCTC TCCCGTGTCT CTACCGCAAT GGGGTCTGCT ACCACCAGCG TCCAGACGAA 240
10     AACGTGCGGA GGAAGCACAT GTGGGCGCTG GTCTGGACGT GCAGCGGCCT CCTCCTCTCTG 300
      AGCTGCAGCA TCTGCTTGTG CTGTGGGGCC AAGCGCCGGG ACGTGCTGCA TATGCCCGGT 360
      TTCTGGCGG GTCCGTGTGA CATGTCCAAG TCCGTCTCGC TGCTCTCCAA GCACCGAGGG 420
      ACCAAGAAGA CGCCGTCCAC GGGCAGCGTG CCAGTCGCCC TGTCCAAAGA GTCCAGGGAT 480
      GTGGAGGAG GCACCGAGGG GGAAGGGACG GAGGAGGGTG AGGAGACAGA GGGCAGAGAA 540
15     GAGGAGGATT AGGGGAGTCC CCGGGGACT GCTCAATACA GATACGGTGG ACG 593

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Seq ID NO: C62 DNA Sequence
Nucleic Acid Accession #: NM_054023.2
Coding sequence: 98..379

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20     1      11      21      31      41      51
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      GGGGACACTT TGTATGGCAA GTGGAACCAC TGGCTTGGTG GATTTTGCTA GATTTTCTG 60
      ATTTTAAAC TCCTGAAAAA TATCCCAGAT AACTGTCATG AAGCTGGTAA CTATCTTCCT 120
      GCTGGTGACC ATCAGCCTTT GTAGTTACTC TGCTACTGCC TTCCTCATCA ACAAGTGCC 180
      CCTTCTGTT GACAAGTTGG CACCTTTACC TCTGGACAA ATTCTTCCCT TTATGGATCC 240
      ATTAAAGCTT CTCTGAAAAA CTCTGGGCAT TTCTGTTGAG CACCTTGTGG AGGGGCTAAG 300
      GAAGTGTGTA AATGAGCTGG GACCAGAGGC TTCTGAAGCT GTGAAGAAAC TGCTGGAGGC 360
      GCTATCACAC TTGGTGTGAC ATCAAGATAA AGAGCGGAGG TGGATGGGGA TGGAAAGATGA 420
30     TGCTCCTATC CTCCCTGCTC GAAACCTGTT CTACCAATTA TAGATCAAAT GCCCTAAAAAT 480
      GTAGTGACCC GTGAAAAGGA CAAATAAAGC AATGAATACT AAAAAAAAAA AAAAAAAAAA 540
      AAAAAAAAAA 550

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Seq ID NO: C63 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..2874

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35     1      11      21      31      41      51
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      TGGATGTCCA GAGGAGCATA TCAGCGGAGG AACACACGGG CAGCTGGACG TCCAGAGGAA 120
      TGCACTGACA GAAACTGGCA TGCTGGCAGA ACACGTGGAA TTTGGCTGGG GCAGTGGAG 180
      GAGAGATGTT CAGATGTGTT CGGAGTTTCT TTCTTCTGGT GGGTTCGTGG TCTCGCTGGC 240
      TCAGGAGCGA AGCTGCAGAC CTTCACGCCA GCCCAGGAAG GGGCTCCAC AGTGCAGCGG 300
      CAGGCTGAAG CGCTCCTCAA GTGCCGCGAG AGTGGGCGTC CAGGCAGAGG AGGCGCCGAG 360
      ACCGAGCGAG CGAGGGATGC CAGCATGCTG TCACCTCTCA GTGCTGCCAT GCGAAACTAC 420
      CCACAGTCCT CTACCATCCC TCCAAGAAGA TCCTACTCTC CAACCGAAAT TGCTCACAAG 480
      AGTTACTCCT GCAGCCTTCC AGACATGAAA ATCTCCATGG CAGAATCTGG CCCCTCCTTG 540
      GATAGCCTTG ACATTCTGGA GGATGGCGAG TCTGGGTAC CATTTCTTGT GACTCATTG 600
      TACTTTCTGG GGGTTGTGAC CACTGGGATG GAACAAC TAGTATTTGAAAC AGGACCAAAC 660
      ATATTTGATT TGCAATTTA TGTGAAGGAT GAGGTTGGTG TCACAGACCT GCAAGTCTCTG 720
      ACTGTCAGG TAACAGATGT GAACGAGCCA CCTCAGTTTC AAGGCAACTT GGCAGAAGAT 780
      CATCTCCGTG CAGACGAGCT ACATTTCAT GCTCATAGTC ACACGTACGT GAGGGTAGTG 840
      GCTACTGCAT TGGCCAGGCA CAGGCTTAGA TCTAGCATTG GTTCCCCCTT CTGGGACACC 900
      TTCTGTGTTG TGGTGGGCTC GCAGTATTTT CTGATTTCTC CCCCAGAGAG CTTCAAGATG 960
      TCTGTCTAAT GCACCTCTTT CTCCACAACA GAATTGGACT TTGAAGCAGG ACACAGAAGT 1020
      TTCCATCTCA TCGTGGAGGT GAGGGACAGT GGAGGCTCCA AAGCCTCCAC AGAGCTCCAG 1080
      GTGAACATCG TGAACCTCAA CGACGAAGTC CCTCGCTTTA CCAGCCCGAC ACGAGTGATC 1140
      ACAGTCTCTG AGGAATCTAG TCCAGGAACC ATCGTGGCCA ATATCACAGC GGAGGATCCT 1200
      GATGTGAAG GTTTTCCGAG CCACCTCCTC TACAGCATT CCACTGTAG CAAATATTTT 1260
      ATGATAAATC AGTTGACTGG TACAATCCAA GTGGCCCAA GGATAGACCG AGATGCAGGT 1320
      GAATTGAGAC AAAATCCAC CATTTCCCTG GAAGTTCTAG TGAAGGACAG ACCATATGGG 1380
      GGTGAGGAGA ATCGCATCCA GATAACCTTC ATTGTGGAAG ACGTCAACGA CAATCCTGCC 1440
      ACATGCCAAA AGTTCACCTT CAGATCCAGT CTCCACCTG CTCTGTGCTC CAAGACGCTG 1500
      ACCTGGATGG ATACCGTATT AGACTGTTTT CATGCTGCTG ATAAAGATAT ACCTGTGACT 1560
      GGGCGATTTA CAAAAGAAAG AGGTTTAATT GGACTTACAG TTCCACATGG CTGGGGAAGC 1620
      CTCACAATCA TGGCAGAAAG CAAGGAGGAG CAAGTACAT CTTACATGGA TGGCAGCAGG 1680
      CAAAGAGATA GAGCTTGTGT AGGGAAACTC CTCCTTATAA AGCCATCAGA TCTCATGAGA 1740
      CTTAGTCACT ATCAGCAGAA CAACTCAGGA AAGACTTGCC CCCATGATT CATTTCCTCC 1800
      TACCAGGTCC CTCCCAACA ATGTAGGAAT TCAAGAATCC AGGCCACCAA CAACGAAGAC 1860
      ACAAGCTCTG TCACCTGTAC TGTGAACATC CTTGAAGAAA ATGATGAAAA GCCAATTGT 1920
      ACTCCAACT CTTATTTCTT GGCCTCCCA GTGGATCTGA AAGTTGGCAC AAATATTCTG 1980
      AATTTCAAGC TGACATGTAC CGACCTTGAT TCCAGCCCA GATCTTCCG TTATTCCATT 2040
      GGCCCGAGTA ACGTCAACAA TCATTTCACC TTCTCTCCCA ATGCTGGTTC CAATGTACA 2100
      CGCTGCTGC TTACATCTCG CTTTGACTAT GCTGGTGGGT TTGATAAGAT CTGGGACTAC 2160
      AAGCTACTGT TTAAGTAAAC TGATGACAAC TTGATGCTG ACAGGAAGAA AGCGGAGGCT 2220
      CTTGTTGAGA CAGGAACAGT GACACTGAGT ATTAAGTCA TTCCCAACCC AACCACTATC 2280
      ATCACCACGA CCCCAGGCC CAGGTCACCC TATCAGGTCC TGAGGAAAAA CGTTTACTCT 2340
      CCATCTGAT GGTACGTGCC GTTTGTATC ACTTTGGGCT CCATATTGCT TCTGGGTCTC 2400
      CTCGTGTACC TGGTCTCTCT ATTGGCCAAA GCCATCCCA GACACTGCC CTGCAAGACT 2460
      GGGAGAAACA AGGAACCTCT GACAAAGAAA GGAGAAACGA AGACTGCAGA GAGAGACGTC 2520
      GTGGTGGAAA CTATCCAGAT GAACACTATC TTTGATGGAG AAGCCATAGA TCCAGAGCCT 2580
      GAGCAAGCTT CACTCGAGCT CTATGCCCTG CTGCCAGCT GCTGCGACCC TAGTCCAGTA 2640
      ACCCTAAGAA AGGTCAGGT GTGTGGGAG AGTGAAGAGA CCGGTCACTG TTCGGGCCAC 2700

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ATCACACTTC CCGGCAAGAT TCCAGTCGAT GACCCCAAGGA AACAGGAAAC AGGCCTGCAG 2760
 GGTGATTTCG AGGTCTGGAC TCTATGCCCC GCTGTGAAGG TGGTTGTAGG CAGCCCTCAA 2820
 GCTGAACGGT GCATTCGATT GGCTCTCAGT CTGAAAAAGT ACAGTTCTGA TTAA 2874

5

Seq ID NO: C64 DNA Sequence
 Nucleic Acid Accession #: XM_168571.1
 Coding sequence: 155..988

10 1 11 21 31 41 51
 | | | | | |
 TACACAGTCC TGGAGGAACT GAGTCCAGGA ACCATCGTGG CCAATATCAC AGCGGAGGAT 60
 CCTGATGATG AAGGTTTTTC CAGCCACCTC CTCTACAGCA TTACCACTGT TAGCAAATAT 120
 TTCATGATAA ATCAGTTGAC TGGTACAATC CAAGTGGCCC AAAGGATAGA CCGAGATGCA 180
 GGTGAATTGA GACAAAATCC CACCATTTCC CTGGAAGTTC TAGTGAAGGA CAGACCATAT 240
 15 GGGGGTCAGG AGAATCGCAT CCAGATAACC TTCACTGTGG AAGACGTCAA CGACAATCCT 300
 GCCACATGCC AAAAGTTCAC CTTAGCATT ATGGTGCCGG AAAGAACAGC CAAGGGGACG 360
 TTGCTTCTTG ACCTAAACAA GTTCTGCTTT GATGATGACA GTGAGGCACC AAACAACAGA 420
 TTCAACTTCA CCATGCCATC TGGAGTGGGG AGCGGCAGCA GATTTTACA GGATCCAGCT 480
 20 GGCTCTGGGA AGATTGTGCT GATTGTGAT CTAGACTACG AAAATCCAAG TAACCTAGCA 540
 GCCGGCAATA AATATACGGT GATAATCCAG GTGCAGGATG TGGCCCCCCC TTAATAATAA 600
 AATAACGTCT ACCTTTATAT CCTAACAAAGC CCAGAAAATG AGTTTCTCTC CATTTTGTAT 660
 AGGCCATCCT ATGTATTGTA TGTGTGAGAA AGAAGGCCCG CCCAGGGTCA CCTATCAGGT 720
 CCTGAGGAAA AAGCTTTACT CTCCATCTGC ATGGTACGTG CCGTTTGTCA TCACTTTGGG 780
 25 CTCCATATTG CTTCTGGGTC TCCTCGTGTA CCTGGTCGTC CTATTGGCCA AAGCCATCCA 840
 CAGACACTGC CCCTGCAAGA CTGGGAAGAA CAAGGAACCT CTGACAAAGA AAGGAGAAAC 900
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 AGAAGCCATA GATCCAGTGA CCGGGGAAAC ATATGAATTC AACTCAAAAA CTGGAGCCAG 1020
 AAAGTGGAAG GATCCACTAA CCCAAATGCC AAAATGGAAG GAGTCCAGCC ACCAGGGAGC 1080
 30 TGCCCCACGC AGAGTCACTG CTGGGGAAGG GATGGGGTCA CTGAGAAGTG CCAACTGGGA 1140
 AGAAGATGAG CTGAGTGGCA AAGCGTGGGC TGAGGATGCT GGTCTGGGTT CCAGAAATGA 1200
 GGTGGGCAAG CTGGGCAACC CAAAGAACAG AAATCCAGCC TTCAATGAACA GGGCTTACCC 1260
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 40 CTGCCCTCGT TTTAACATCA CCGAGATTTC TTCAGTTATA AATATGCCAT ACACCTTTGT 1740
 AAGTCACTC AATCTTCTT CAAAGAAGC AGAACAGTGA AAAAAACAGA TGAGTAAGTT 1800
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 GGTGTCCGGA TCAGATCTCT GCATGTGAGA TTCATCCACG TTGTCTCTGC TAGCAGTAGT 1920
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 45 CTACACTTGG GTGGCAGCTG CTTAGATTTC TTTACTTTTA AAAAAATATA TTAAGATGTA 2040
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 50 GTGCCACTGC ACTCTAGCCT GGGTGACAAA GCAAGACTCC ATCTCAGAAA AAAAAAATAA 2340
 AAGTGAATTA CAACACT 2357

Seq ID NO: C65 DNA Sequence
 Nucleic Acid Accession #: NM_005266.3
 Coding sequence: 122..1198

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1 11 21 31 41 51
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 60 GATGGGCCAT TGGAGCTTCC TGGGAAATTT CCTGGAGGAA GTACACAAGC ACTCGACCGT 180
 GGTAGGCAAG GTCTGGCTCA CTGTCCTCTT CATATTCCGT ATGCTCGTGC TGGGCACAGC 240
 TGCTGAGTCT TCCTGGGGGG ATGAGCAGGC TGATTTCCGG TGTGATACGA TTCAGCCTGG 300
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 GCAGATCATC TTCGTCTCCA CGCCCTCTCT GGTGTACATG GGCCACGCCA TGCACTCTGT 420
 65 GCGCATGCAG GAGAAGCGCA AGCTACGGGA GGCCGAGAGG GCCAAAGAGG TCCGGGGCTC 480
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 TTCAGATTAC TCATGAAACA GGGTAGAGGG AAAGAAGGGA AGCATGGCAA AAGCTGGCCT 1500
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 CTTCTCCTCC CTCTACTCAG CCTTAAAAAG GGCTTCTTGG AACTTTACCA GCAGCCTCAG 1800
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 GCCCACCTT GGTGATGTTG CAACCTTTCC TTCTGCTAGG GTGTACACCT AGCCTGTGCA 1920
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 TCTGTACCCC TGCAGCTCCT TTACAGTTCA ATCCAATGAT AGAAACCATC CCTTCCCTTT 2040
 TCCCTTGGC TGTTACCCA GCCATTCCCT GAAGGCCCTA CCAACAGGAA TATCCAAGAA 2100
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 CCAGGCCCTG TTAATAAAAA AAAAAAATAA 2190

Seq ID NO: C66 DNA Sequence
 Nucleic Acid Accession #: NM_014459.2
 Coding sequence: 738..3407

1 11 21 31 41 51
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 GCTGGGGAAG CTTCAAAATA TATCTGTGAC TCTGTCTTGG TTGCTCTTCA TCCCATCAA 180
 TTTTCATCAG GGAGGCGAGC AGCAAGTAAG AATTTCACTT TCGGATCTGC CTAGAGACAC 240
 ACCTCCCTGC TCCCTCCCCC ACTCGATGTG AAGAGTATTC CGGAGTCTCC GGGCGGGAGT 300
 AGATTTGCAG CACCTTAGCG GGAGCGAGGA AAACCTACTG ATTCTTTAGC TCATTATCAT 360
 CTCTCCGAGA CGAGATTTCC TTCTTATCGC CTGCCTCATC GCTCAAGTTT GAGCCTCCCG 420
 AAGTCCGGGC GGGAGGAGCG AAACCCCTGG CTCACCCCA GCGCGAGGAA GCCACCGCCT 480
 TGCTCCAAGC CCTTGACAGC CTGCTGCACC GCAGCTTCTC ACCCAGTGGC GATGCTGTAG 540
 ATCAACAGGT TCAGGGAAC TTAGCAGAA TAAAGAGAGC CACCGGGTGC CGCAGCTCGG 600
 GTGCAGAGGG AAAAAAGGAC CCATAGACTT GTGGCTCGCG TCGCGCGCGC ACGCTGCGCC 660
 AGGGCCCGAG GCTGGCGCGC ACTCCCTCTC TGGCTCCTCC AGTCCGATTG CTCCTGCCCC 720
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 GGGTCACTGA CCGGACTCT GGCAGAACG GACAGCTGCA GTGTCGGGTC CTAGGCGGAG 1920
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 TGACGCCCCG GGTGGAGCTG GTGGTGAAGG TGACCGACCA CGGCAAGCCT ACCCTGTCCG 2760
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 GTCTGTAGG GAGGCACTCA AGATGAAAAC TACTTCACT AAAAGCCAAC CACTTGAACA 3540
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 GTGCTGGATG CCACAGTTCC CTGCAGCCAA TCAGGCTGAA AATGCAGATT ACCGCACAAA 3660
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 TGCCAAAGCT AAACCTTATT TAAAGCCAA ACGTGCCTG AGCCCTCTCC TCCAAGAGGT 3840
 CCCCTCAGCA TCAAGCAGCC CAACCAAGGC GTGCATCGAG CCTTGCACCT CAACAAAAGG 3900
 CTCCCTGGAT AGCTGTGAAG CAAACACAGG AGCCCTGGCT GAAGCAGACA GTCAGTACTT 3960
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5 TTCCGATCAG ATGGCAAGGG TCTTTCAGAG TGTGCATTCC AGAGCCAGCC GGGATTCCAG 4080
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 TGTGGATGCA GAGGAAGTTG TGAGAGAAAT TGATAAGCTT TTGCAAGACT GCCGGGGAAG 4200
 CGACCCCTGT GCTGTGAGAA AGTGAAAAAA GAAAAAAGAA AAGGCATTGG CATTCTCTTG 4260
 10 TCTCTTCTGT TGATTAAAA ATGATCCCTC CTGGTGATAA CCAATTTTAC AGGGATGAAG 4320
 AAAGACCAAT GCTGCTTTAA GGCTTTTAGT GAACATCTGA AGTGCCACA AGTATGTTCT 4380
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 15 ATAAACACAA GGAACATTCC ATATCATTAG TCGAAAAA AAACAAAAAA AAAACCTTTG 4860
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Seq ID NO: C67 DNA Sequence
 Nucleic Acid Accession #: NM_005601.2
 Coding sequence: 101..598

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1 11 21 31 41 51
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 TCTTCCTCCT CCAGGACCCA GAAGCCCTGA GCTTATCCCC ATGGAGCTCT GCCGGTCCCT 120
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 CTGGTTGAG GCTGTGGGTC CCACCCACTC AGCTCACTCG GGCCTCTGGC CAACAGGGCA 240
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 AAA 783

Seq ID NO: C68 DNA Sequence
 Nucleic Acid Accession #: NM_006433.2
 Coding sequence: 129..566

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 GCCCACCAT GGTACTCTGG GCCCTCTGCT TCCTTGACAG CATGCTCTG GGCACCCAG 180
 GTCTGGTCTT CTCTGCTGCT AGCCCTGAGT ACTACGACCT GGCAGAGCC CACCTGCTG 240
 ATGAGGAGAA ATCTCTGCCC TGCCCTGGCC AGGAGGGCCC CCAGGGTGAC CTGTTGACCA 300
 AAACACAGGA GCTGGGCGGT GACTACAGGA CCTGTCTGAC GATAGTCAA AACTGAAGA 360
 AGATGGTGGG TAAAGCCACC CAGAGAAGTG TTTCCAATGC TGCAGCCCG GTGTGTAGGA 420
 CGGGGAGGTC AAGATGGCGC GACGTCTGCA GAAATTTTAT GAGGAGGTAT CAGTCTAGAG 480
 TTACCCAGGG CCTCTGGGCC GGAGAAACTG CCCAGCAGAT CTGTGAGGAC CTAGGTTGT 540
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 CTCCTGTCTC CAGATCCCGG GAACCTCAGC AACCTCTGCC GGTCTCTCGC TTCTCTGATC 660
 CAGAATCCAC TCTCCAGTCT CCCTCCCCTG ACTCCCTCTG CTGTCTCTCC CTCTCAGAG 720
 AATAAAGTGT CAAGCAAG 738

Seq ID NO: C69 DNA Sequence
 Nucleic Acid Accession #: NM_002985.2
 Coding sequence: 69..344

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 GCGCTCCTGC ATCTGCTCTC CCATATTCTT CGGACACCAC ACCCTGCTGC TTTGCTTACA 180
 TTGCCCGCCC ACTGCCCGCT GCCCACATCA AGGAGTATTT CTACACCACT GGCAGAGTCT 240
 CCAACCCAGC AGTCTCTTTT GTCAACCGAA AGAACCGCCA AGTGTGTGCC AACCAGAGA 300
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 ACCTGAACCT ACACAAATTT GCCTGTTTCT GCTTGCTCTT GTCCTAGCTT GGGAGGCTTC 420
 CCCTCACTAT CCTACCCAC CCGCTCCTTG AAGGGCCAG ATTCTACCAC ACAGCAGCAG 480
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 TGAAACCCCA TCTCTACTAA AAATACAAAA AATTAGCCGG GCGTGGTAGC GGGCGCTGT 660
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 GCAGTGAGCC GAGATCGCGC CACTGCACTC CAGCCTGGGC GACAGAGCGA GACTCCGTCT 780
 CAAAAAAGAA AAAAAAAGAA AAAATACAAA AATTAGCCGG GCGTGGTGGC CCACGCTGT 840
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 GCAGTGAGCT GAGATTGTGC CACTTCACTC CAGCCTGGGT GACAAAGTGA GACTCCGTCA 960
 CAACACAAAC AAAAAAAGC TTCCCAACT AAAGCCTAGA AGAGCTTCTG AGGCGCTGCT 1020
 TTGTCAAAG GAAGTCTCTA GGTCTGAGC TCTGGCTTTG CCTTGGCTTT GCCAGGGCT 1080

TGTGACCAGG AAGGAAGTCA GCATGCCTCT AGAGGCAAGG AGGGGAGGAA CACTGCACTC 1140
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 TACCATTAAA GTTCTCAATG CAACCATAAA AAAAAA 1237

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Seq ID NO: C70 DNA Sequence
 Nucleic Acid Accession #: NM_022154.2
 Coding sequence: 1381..1722

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 15 CTGGTGGCCT TTATCTCTGT CCCCTTTTGT CCTCTTTATC TCAGGCTCTC CAGGAGGCCG 240
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 CTCGGAGCAG CGCCGAGCAC TGACGCTCCC GCCCTTGGGC AAGGACGCCA GTGCGCCCGC 420
 20 GCGCGTCCCT CTGCGCGGCA GCCCGTCGCG GGCCCTCAAG GGGAAAGCCA GGCCAGGATG 480
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 AGCCTGTGCG CGGCGCAGCT CCAGCACTTG CTGAGCAGA TGGGAGCCGC CTCGCGCTG 600
 GCGCTCCCG AGCCTGGCCA GCTGCACTTC AACCACTGTT TAAGTCTGA AGAGATCTTT 720
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 25 CCAGCAGTCT TACAGCAATT GAACCTTCAC CCATGTGAGG ATCGGCCCAA GCACAAAACA 840
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 30 ATTCAGAGG CATTTGGATT TGATCCCAA GTGACAGTT ATGTTGAGAA GGCAGTTGCT 1080
 GTGTTTGGTG GATTTTACCT ACTTTCTTT TTTGAAAGAA TGCTAAAGAT GTTATTAAAG 1140
 ACATATGGTC AGAATGGTCA TACCACTTT GGAAATGATA ACTTTGGTCC TCAAGAAAAA 1200
 ACTCATCAAC CTAAGCATT ACCTGCCATC AATGGTGTGA CATGCTATGC AAATCCTGCT 1260
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 55 TCCTAAGTIN TAAACTTCAC CAGATTCCAC GAAAGCTGG ATAGCTTTTT TTCTGACTTA 2580
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70

Seq ID NO: C71 DNA Sequence
 Nucleic Acid Accession #: NM_004184.2
 Coding sequence: 188..1603

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10	AGACAGGACG	GATATCCAGT	GCCTTATCCC	ATGTGCCATT	GACCAGGATC	CTTACTTTAG	1140
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	CCTGGCTGTG	TCTTGGACGG	GTGGACTTAG	CTAGGGAGAA	AGTCGAGGCA	GCAGCCCTCG	2520
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Seq ID NO: C72 DNA Sequence

Nucleic Acid Accession #: NM_004938.1

Coding sequence: 337..4632

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	GCCTCCGACA	GCGCTCCGGA	GGGACCGGGG	GAGCTCCAG	GCGCCCGGGA	CTGGAGACTG	240
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55	GAATCTTTAA	CTGAAGAGGA	AGCAACTGAA	TTTCTCAAAC	AAATTTCTTAA	TGTTGTTTAC	720
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	GACTTTGGAA	ATGAATTTAA	AAACATATTT	GGGACTCCAG	AGTTTGTGCG	TCCTGAGATA	900
	GTCAACTATG	AACCTTCTGG	TCTTGAGGCA	GATATGTGGA	GTATCGGGGT	AATAACCTAT	960
60	ATCCTCCTAA	GTGGGGCCTC	CCCATTTCTT	GGAGACATTA	AGCAAGAAAC	TTTAGCAAT	1020
	GTATCCGCTG	TCAACTACGA	ATTTGAGGAT	GAATACTTCA	GTAATACCGA	TGCCCTAGCC	1080
	AAAGATTTCA	TAAGAAGACT	TCTGGTCAAG	GATCCAAAGA	AGAGAATGAC	AATTCAAGAT	1140
	AGTTTGCAGC	ATCCCTGGAT	CAAGCCTAAA	GATACACAAC	AGGCACCTAG	TAGAAAAGCA	1200
	TCAGCAGTAA	ACATGGAGAA	ATTCAAGAA	TTTGACGCC	GGAAAAAATG	GAAACAATCC	1260
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	CTTCACTCTG	CTGTAAGACG	GTGTCAAGAT	GAGGTAATCA	AGACTCTCCT	CAGCCAAAGG	2040
	TGTTTCGTGC	ATTATCAAGA	CAGGCACGGC	AATACTCCCC	TCCATGTGGC	ATGTAAGAT	2100
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	GGTCTTACCA	AAGGGATGCT	GGAGGTGTTT	GTGGCCCCGA	CCCACCACCC	GCACTGCTCG	2700
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15	CTGCAGCAGT	TTGTGTACGA	CGTGACAGGAC	CAGCTGAACC	CCCTGGCCAG	CGAGGAGGAC	3360
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	ACAGTTCAGG	ACGTGCTGCT	CCTGGACCCC	CGCTGGCTCT	GCACAAACGT	CCTGGGGGAG	3480
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20	ATGGACATCT	GCGCCCGGGA	CCTGAGCAGC	GGGACCATGG	TGGACGTCCC	AGCCCTGATC	3660
	AAGACAGACA	ACCTGCACCG	CTCCTGGGCT	GATGAGGAGG	ACGAGGTGAT	GGTGTATGGT	3720
	GGCGTGGCGA	TGCTGCCCGT	GGAACACCTC	ACCCCTTCCC	CATGTGGCAT	CTTTCACAA	3780
	GTCCAGGTGA	ACCTGTGCCG	GTGGATCCAC	CAGCAAAGCA	CAGAGGGCGA	CGCGGACATC	3840
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Seq ID NO: C73 DNA Sequence
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Seq ID NO: C74 DNA Sequence
Nucleic Acid Accession #: BC030205.1
Coding sequence: 45..878

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CAACTTACAA GCAGCTAGAG GCAGCCAGAA AAATGGATT TCATGTCTGT GCTGCTGGAT 300
GGATGGCTAA GGGCAGAGTT GGATACCCCA TTGTGAAGCC AGGGCCCAAC TGTGGATTG 360
GAAAAACTGG CATTATTGAT TATGGAATCC GTCTCAATAG GAGTGAAAGA TGGGATGCCT 420
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TTAAATCTCC AGGCTTCCCA AATGAGTACG AAGATAACCA AATCTGTCTG TGGCAGATTA 540
GACTCAAGTA TGGTCAGCGT ATTCACCTGA GTTTTTTGA TTTTGACCTT GAAGATGACC 600
CAGGTGTCTT GGCTGATTAT GTTGAAATAT ATGACAGTTA CGATGATGTC CATGGCTTGT 660
TGGGAAGATA CTGTGGAGAT GAGCTTCCAG ATGACATCAT CAGTACAGGA AATGTCATGA 720
CCTTGAAGTT TCTAAGTGAT GCTTCAGTGA CAGCTGGAGG TTTCCAAATC AAATATGTTG 780
CAATGGATCC TGTATCCAAA TCCAGTCAAG GAAAAAATAC AAGTACTACT TCTACTGGAA 840
ATAAAAACTT TTTAGCTGGA AGATTTAGCC ACTTATAAAA AAAAAAAGG GATGATCAAA 900
ACACACAGTG TTTATGTTGG AATCTTTTGG AACTCCTTGT ATCTCACTGT TATTATTAAC 960
ATTTATTTAT TATTTTCTA AATGTGAAG CAATACATAA TTTAGGGAAA ATTGGAAAAT 1020
ATAGGAACTT TAAACGAGA AAATGAAACC TCTCATAATC CCAGTGCATA GAAATAACAA 1080
GCGTTAACAT TTTTATATTT TTTTCTTTCA GTCATTTTTC TATTGTGGT ATATGTATAT 1140
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TTATACTTTT TAAATCTTGA ACTTTATAAA CATTTTCTGA AATCATTGAT TATTCTACAA 1260
AAACATGATT TTAACAGCT GTAAATATT CTATGATATG AATGTTTAT GCATTATTTA 1320
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Seq ID NO: C75 DNA Sequence
Nucleic Acid Accession #: NM_001982.1
Coding sequence: 199..4227

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TTGCAATTTG CAACCTCCGC TGCCGTCGCC GCAGCAGCCA CCAATTCGCC AGCGGTTCAG 120

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	AGCCTGGCCC	GGGGCTCCGA	GGTGGGCAAC	TCTCAGGCAG	TGTGTCTCTGG	GACTCTGAAT	300
5	GGCCTGAGTG	TGACCGGCCA	TGCTGAGAAC	CAATACCAGA	CACGTACAAA	GCTCTACGAG	360
	AGGTGTGAGG	TGGTGATGGG	GAACCTTGAG	ATTGTGCTCA	CGGGACACAA	TGCCGACCTC	420
	TCCTTCCTGC	AGTGGATTGG	AGAAGTGACA	GGCTATGTCC	TCGTGGCCAT	GAATGAATTC	480
	TCTACTCTAC	CATTGCCCAA	CCTCCGCTG	GTGCGAGGGA	CCCAGGTCTA	CGATGGGAAG	540
	TTTGCCATCT	TCGTATGTTT	GAACTATAAC	ACCAACTCCA	GCCACGCTCT	GCGCCAGCTC	600
10	CGCTTGACTC	AGCTCACCGA	GATTCTGTCA	GGGGGTGTTT	ATATTGAGAA	GAACGATAAG	660
	CTTTGTGACA	TGGACACAAT	TGACTGGAGG	GACATCGTGA	GGGACCGAGA	TGCTGAGATA	720
	GTGGTGAAGG	ACAATGGCAG	AAGCTGTCCC	CCCTGTCATG	AGGTTTGCAA	GGGGCGATGC	780
	TGGGGTCTCT	GATCAGAAGA	CTGCCAGACA	TTGACCAAGA	CCATCTGTGC	TCCTCAGTGT	840
	AATGGTCACT	GCTTTGGGCC	CAACCCCAAC	CAGTGCTGCC	ATGATGAGTG	TGCCGGGGGC	900
	TGCTCAGGCC	CTCAGGACAC	AGACTGCTTT	GCCTGCCGGC	ACTTCAATGA	CAGTGGAGCC	960
15	TGTGTACCTC	GCTGTCCACA	GCCTCTGTG	TACAACAAGC	TAACTTTCCA	GCTGGAACCC	1020
	AATCCCCACA	CCAAGTATCA	GTATGGAGGA	GTTTGTGTAG	CCAGCTGTCC	CCATAACTTT	1080
	GTGGTGGATC	AAACTCTCTG	TGTCAGGGCC	TGTCCTCTCT	ACAAGATGGA	AGTAGATAAA	1140
	AATGGGCTCA	AGATGTGTGA	GCCTTGTGGG	GGACTATGTC	CCAAAGCCTG	TGAGGGAACA	1200
20	GGCTCTGGGA	GCCGCTTCCA	GACTGTGGAC	TCGAGCAACA	TTGATGGATT	TGTGAAGTGC	1260
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	GGTTACCTGA	ACATCCAGTC	CTGGCCGCCC	CACATGCACA	ACTTCAGTGT	TTTTTCCAAT	1440
	TTGACAACCA	TTGAGGCGAC	AAGCCTCTAC	AACCGGGGCT	TCTCATGTGT	GATCATGAAG	1500
25	AACTTGAATG	TCACATCTCT	GGGCTTCCGA	TCCCTGAAGG	AAATTAGTGC	TGGGCGTATC	1560
	TATATAAGTG	CCAATAGGCA	GCTCTGCTAC	CACCACCTCT	TGAACCTGGAC	CAAGGTGCTT	1620
	CGGGGGCTTA	CGGAAGAGCG	ACTAGACATC	AAGCATAATC	GGCCGCGCAG	AGACTGCGTG	1680
	GCAGAGGGCA	AAGTGTGTGA	CCCACTGTGC	TCCTCTGGGG	GATGCTGGGG	CCCAGGCCCT	1740
	GGTCAGTGCT	TGTCTCTGTC	AAATTATAGC	CGAGGAGGTG	TCTGTGTGAC	CCAATGCAAC	1800
30	TTTCTGAATG	GGGAGGCTCG	AGAATTGTGC	CATGAGGCGG	AATGCTTCTC	TGCCACCCCG	1860
	GAATGCCAAC	CCATGGGGGG	CACCTGCCACA	TGCAATGGCT	CGGGCTCTGA	TACTTGTGCT	1920
	CAATGTGCCC	ATTTTGGCGA	TGGGCCCCAC	TGTGTGAGCA	GCTGCCCCCA	TGGAGTCCCTA	1980
	GGTGCCAAGG	CCCCAATCTA	CAAGTACCCA	GATGTTTCTA	ATGAATGTCG	GCCCTGCCAT	2040
	GAGAACTGCA	CCCAGGGGTG	TAAAGGACCA	GAGCTTCAAG	ACTGTTTAGG	ACAAACACTG	2100
35	GTGCTGATCG	GCAAAACCCA	TCTGACAATG	GCTTTGACAG	TGATAGCAGG	ATTGGTAGTG	2160
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	AGGGCTATGA	GGCGATACTT	GGAACGGGGT	GAGAGCATAG	AGCCTCTGGA	CCCCAGTGAG	2280
	AAGGCTAACA	AAGTCTTGGC	CAGAATCTTC	AAAGAGACAG	AGCTAAGGAA	GCTTAAAGTG	2340
	CTTGGCTCGG	TGCTCTTTGG	AACTGTGCAC	AAAGGAGTGT	GGATCCCTGA	GGGTGAATCA	2400
40	ATCAAGATTG	CAGTCTGCAT	TAAAGTCATT	GAGGACAAGA	TGGAGCGGCA	GAGTTTTCAT	2460
	GCTGTGACAG	ATCATATGCT	GGCCATTGGC	AGCCTGGACC	ATGCCACAT	TGTAAGGCTG	2520
	CTGGGACTAT	GCCAGGGGTC	ATCTCTGCAG	CTTGTCACTC	AAATTTTGCC	TCTGGGTTCT	2580
	CTGCTGGATC	ATGTGAGACA	ACACCGGGGG	GCACTGGGGC	CACAGCTGCT	GCTCAACTGG	2640
	GGAGTACAAA	TTGCCAAGGG	AATGTACTAC	CTTGAGGAAC	ATGGTATGGT	GCATAGAAAC	2700
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	GTGGCTGACC	TGCTGCCCTC	TGATGATAAG	CAGCTGCTAT	ACAGTGAGGC	CAAGACTCCA	2820
	ATTAAGTGGA	TGGCCCTTGA	GAGTATCCAC	TTTGGGAAAT	ACACACACCA	GAGTGATGTC	2880
	TGGAGCTATG	TGTGTGACAT	TTGGGAGTTG	ATGACCTTCG	GGGCAGAGCC	CTATGCAAGG	2940
	CTACGATTGG	CTGAAGTACC	AGACCTGCTA	GAGAAGGGGG	AGCGGTTGGC	ACAGCCCCAG	3000
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	CGCCCAACCT	TTAAAGAACT	AGCCAAATGAG	TTCAACAGGA	TGGCCCGAGA	CCCCACCGG	3120
	TATCTGGTCA	TAAAGAGAGA	GAGTGGGCCT	GGAATAGCCC	CTGGGCCAGA	GCCCCATGGT	3180
	CTGACAAACA	AGAAGCTAGA	GGAAGTAGAG	CTGGAGCCAG	AACCTAGACCT	AGACCTAGAC	3240
	TTGGAGGACG	AGGAGGACAA	CCTGGCAACC	ACCACACTGG	GCTCCGCCCT	CAGCCTACCA	3300
55	GTGGGAACAC	TTAATCGGCC	ACGTGGGAGC	CAGAGCCTTT	TAAGTCCATC	ATCTGGATAC	3360
	ATGCCCATGA	ACCAGGGTAA	TCTTGGGGGG	TCTTGCCAGG	AGTCTGCAGT	TTCTGGGAGC	3420
	AGTGAACGGT	GGCCCCGTCC	AGTCTCTCTA	CACCCAATGC	CACGGGGATG	CCTGGCATCA	3480
	GAGTCATCAG	AGGGGCATGT	AACAGGCTCT	GAGGCTGAGC	TCCAGGAGAA	AGTGTCAATG	3540
	TGTAGAAGCG	GGAGCAGGAG	CCGGAGCCCA	CGGCCACGCG	GAGATAGCGC	CTACCATTC	3600
60	CAGCGCCACA	GTCGTCTGAC	TCTTGTATCC	CCACTCTCCC	CACCCGGGTT	AGAGGAAGAG	3660
	GATGTCAACG	GTTATGTCTAT	GCCAGATACA	CACCTCAAAG	GTACTCCCTC	CTCCCGGAA	3720
	GGCACCCCTT	CTTCAGTGGG	TCTCAGTTCT	GTCCTGGGTA	CTGAAGAAGA	AGATGAAGAT	3780
	GAGGAGTATG	AATACATGAA	CCGGAGGAGA	AGGCACAGTC	CACCTCATCC	CCCTAGGCCA	3840
	AGTTCCCTTG	AGGAGCTGGG	TTATGAGTAC	ATGGATGTGG	GGTCAGACCT	CAGTGCCTCT	3900
65	CTGGGCAGCA	CACAGAGTTG	CCCACTCCAC	CCTGTACCCA	TCATGCCCCAC	TGCAGGCACA	3960
	ACTCCAGATG	AAGACTATGA	ATATATGAAT	CGGCAACGAG	ATGGAGGTGG	TCCTGGGGGT	4020
	GATTATGCAG	CCATGGGGGC	CTGCCAGCA	TCTGAGCAAG	GGTATGAAGA	GATGAGAGCT	4080
	TTTCAGGGGC	CTGACATCA	GGCCCCCAT	GTCCATTATG	CCCGCCTAAA	AACTCTACGT	4140
	AGCTTAGAGG	CTCAGACTC	TGCCCTTGAT	AACCTGATT	ACTGGCATAG	CAGGCTTTTC	4200
70	CCCAAGGCTA	ATGCCAGAG	AACGTAATC	CTGCTCCCTG	TGGCACTCAG	GGAGCATTTA	4260
	ATGGCAGTCA	GTGCCCTTAG	AGGGTACCGT	CTTCTCCCTA	TTCCCTCTCT	CTCCAGGTC	4320
	CCAGCCCTTT	TTCCCCAGTC	CCAGACAATT	CCATTCAATC	TTTGGAGGCT	TTTAAACATT	4380
	TTGACACAAA	ATCTTATGAG	TATGTAGCCA	GCTGTGCACT	TTCTTCTCTT	TCCCAACCCC	4440
	AGGAAAGGTT	TTCTTATTTT	TGTGTGCTTT	CCCAGTCCCA	TTCTTCAGCT	TCTTCACAGG	4500
75	CACCTCTGGA	GATATGAAGG	ATTACTCTCC	ATATCCCTTC	CTCTCAGGCT	CTTGACTACT	4560
	TGGAAGTACG	CTCTTATGTG	TGCCCTTGTG	TCCCATCAGA	CTGTCAAGAA	GAGGAAAGGG	4620
	AGGAAACCTG	GCAGAGGAAA	GTGTAATTTT	GGTTTATGAC	TCTTAACCCC	CTAGAAAGAC	4680
	AGAAGCTTAA	AATCTGTGAA	GAAAGAGGTT	AGGAGTAGAT	ATTGATTACT	ATCATAATTC	4740
	AGCACTTAAC	TATGAGCCAG	GCATCATACT	AAACTTCACC	TACATTATCT	CACCTAGTCC	4800
80	TTTATCATCC	TTAAACAAT	TCTGTGACAT	ACATATTATC	TCATTTTACA	CAAAGGGAAG	4860
	TCGGGCATGG	TGGCTCATGC	CTGTAATCTC	AGCACTTTGG	GAGGCTGAGG	CAGAGGAGTT	4920
	ACCTGAGGCA	AGGAGTTTGA	GACCAGCTTA	GCCAACATAG	TAAGACCCCC	ATCTC	4975

Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCAGAGGT TGGCCCGGAT GCAGGAGGAT 180
TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGCCGAGGA GGATCTGCCC 240
AGTGAAGAGG ATTCAACCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAATCAGA AGAAGAGGGC 360
TCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCAG 420
AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480
CCGCCCTGGC CCGGGGTGTC CCCAGCCTGC GCGGGCCGCT TCCAGTCCCC GGTGGATATC 540
15      CGCCCCAGC TCGCCGCTT CTGCCCGGCC CTGCCGCCCT TGGAACTCCT GGGCTTCCAG 600
CTCCCGCCGC TCCAGAACT GCGCTGCGC AACAATGGCC ACAGTGTGCA ACTGACCCCTG 660
CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT 720
CTGCACTGGG GGGCTGCAAG TCGTCCGGGC TCGGAGCACA CTGTGGAAG CCACCGTTTC 780
20      CCTGCCGAGA TCCACGTGGT TCACCTCAGC ACCGCCTTGT CCAGAGTTGA CGAGGCCCTT 840
GGGCGCCCCG GAGGCCTGGC CGTGTGGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC 900
AGTGCCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960
CAGTCCAGG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA 1020
TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAA 1080
25      CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCCTCT CTGACACCCT GTGGGGACCT 1140
GGTGACTCTC GGTCTACAGT GAACCTCCGA GCGACGCAGC CTTTGAATGG GCGAGTGATT 1200
GAGGCCTCTT TCCCTGCTGG AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGTTT TTGGCCTCCT TTTTGCTGTC 1320
ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380
30      GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA 1440
TGTGAGAAAG CAGCCAGAGG CATCTGAGGG GGAGCCGGTA ACTGTCTCTG CTGCTCATT 1500
ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTATA AT 1552

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Seq ID NO: C77 DNA Sequence

Nucleic Acid Accession #: NM_004207.1
Coding sequence: 63..1460

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GGGGCTGGGC CGTGTCTTTC GGCTGTTTGG TCATCACTGG CTTCCTCTAC GCCTTCCCCA 180
AGGCGGTGAG TGTCTTCTTC AAGGAGCTCA TACAGGAGTT TGGGATCGGC TACAGCGACA 240
CAGCCTGGAT CTCTCCATGC CTGCTGGCCA TGCTCTACGG GACAGGTCGG CTCTGCAGTG 300
TGTGCGTGAA CCGCTTGGC TGCCCGCCCG TCATGCTTGT GGGGGGTCTC TTTGCGTGC 360
45      TGGGCATGGT GGCCTGCGTCC TTTTGCCGGA GCATCATCCA GGTCTACCTC ACCACTGGGG 420
TCATCAGCGG GTTGGGTTTG GCACTCAACT TCCAGCCCTC GCTCATCATG CTGAACCGCT 480
ACTTCAGCAA GCGGCGCCCC ATGGCCAACG GGCTGGCGGC AGCAGGTAGC CCGTCTCTCC 540
TGTGTGCCCT GAGCCCGCTG GGGCAGCTGC TGCAGGACCG CTACGGCTGG CGGGGCGGCT 600
50      TCCTCATCCT GGGCGGCCTG CTGCTCAACT GCTGCGTGTG TGCCGCACTC ATGAGGCCCC 660
TGTGTGTACG GGGCGGCGGC GGCTCGGGGC CGCCGCGACC CTCCGCGGCG CTGCTAGACC 720
TGAGGCTCTT CCGGAGCCGC GGCTTTGTGC TTTACGCCGT GGCCGCTCG GTCTAGGTGC 780
TGGGGCTCTT CGTCCCGCCC GTGTTCTGTT TGAGCTACGC CAAGGACCTG GGCGTGCCCG 840
ACACCAAGGC CGCTTTCCTG CTCACCATCC TGGGCTTCAT TGACATCTTC GCGGCGCCGG 900
CGCGGGGCTT CGTGGCGGGG CTGCGGAAGG TGCGGCCCTA CTCCGTCTAC CTCTTCAGCT 960
55      TCTCATGTTT CTTCAACGGC CTCGCGGACC TGGCGGGCTC TACGGCGGGC GACTACGGCG 1020
GCCTCGTGGT CTTCTGATC TTCTTTGGCA TCTCTACGG CATGGTGGGG GCCCTGCAGT 1080
TCGAGGTGCT CATGGCCATC GTGGGCACCC ACAAGTTCTC CAGTGCCATT GGCCTGGTGC 1140
TGCTGATGGA GGCCTGTGGC GTGCTCGTGC GGGCCCTTTC GGGAGGCCAA CTCTGGATG 1200
CGACCCAGCT CTACATGATC GTGTTTCATC TGGCGGGGGC CGAGGTGCTC ACCTCCTCCC 1260
60      TGATTTTGGT GCTGGGCAAC TTCTTCTGCA TTAGGAAGAA GCCCAAGAG CCACAGCCTG 1320
AGGTGGCGGC CGCGGAGGAG GAGAAGCTCC ACAAGCCTCC TGCAGACTCG GGGGTGGACT 1380
TGCGGGAGGT GGAGCATTTT CTGAAGGCTG AGCCTGAGAA AAACGGGGAG GTGGTTTACA 1440
CCCCGGAAC AAGTGTCTGA GTGGCTGGGC GGGGCGGCA GGCACAGGGA GGAGGTACAG 1500
AAGCCGGCAA CGCTTGTCTT TTATTTTACA AACTGGACTG GCTCAGGCA GGCCACGGCT 1560
65      GGGCTCAGC TGCCGGCCCA GCGATCTGTC GCCGATCAG TGTTTGAGG GGAAGGTGG 1620
CGGGGTGGGA ACCGTGTCTT TCCAGAGTGG ATCTGCGGTG AAGCCAAAGC GCAAGGTTAC 1680
AAGGCATCCT CACCAAGGGC CCCGCTCTCT GCTCCAGGT GGCCTGCGGC CACTGCTATG 1740
CTCAAGGACC TGGAAACCCA TGCTTCGAGA CAACGTGACT TTAATGGGAG GGTGGGTGGG 1800
CGCAGACAG GCTGGCAGGG CAGGTGCTGC GTGGGGCCCT CTCCAGCCCG TCCTACCCCTG 1860
70      GGCTCACATG GGGCCTGTGC CCACCCCTCT TGAGTGTCTT GGGGACAGCT CTTTCCACCC 1920
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TT 1982

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Seq ID NO: C78 DNA Sequence

Nucleic Acid Accession #: NM_000358.1
Coding sequence: 48..2099

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TGCGGCTGCT GGCTCTCGCC CTGGCTCTGG CCCTGGGCCC CGCCGCGACC CTGGCGGGTC 120
CCGCCAAGTC GCCCTACCAG CTGGTGTCTG AGCACAGCAG GCTCCGGGGC CGCCAGCACG 180
GCCCCAAGCT GTGTGCTGTG CAGAAGGTTA TTGGCACTAA TAGGAAGTAC TTCACCAACT 240

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5	GCAAGCAGTG	GTACCAAAAGG	AAAATCTGTG	GCAAATCAAC	AGTCATCAGC	TACGAGTGTCT	300
	GTCTCTGGATA	TGAAAAAGGTC	CCTGGGGGAGA	AGGGCTGTCC	AGCAGCCCTA	CCACTCTCAA	360
	ACCTTTACGA	GACCCCTGGGA	GTGCTTGGAT	CCACCACCAC	TCAGCTGTAC	ACGGACCGCA	420
	CGGAGAAGCT	GAGGCCTGAG	ATGGAGGGGC	CCGGCAGCTT	CACCATCTTC	GCCCTTAGCA	480
	ACCAGGGCTG	GGCTCTCTTG	CCAGCTGAAG	TGCTGGACTC	CCTGGTCAAG	AATGTCAACA	540
	TTGAGCTGCT	CAATGCCCTC	CGTACCATA	TGGTGGGCG	GCGAGTCTG	ACTGATGAGC	600
	TGAAACACGG	CATGACCCCT	ACCTCTATGT	ACCAGAATTC	CAACATCCAG	ATCCACCACT	660
	ATCCTAATGG	GATTGTAAC	GTGAACCTGT	CCCGGCTCCT	GAAAGCCGAC	CACCATGCAA	720
10	CCAACGGGGT	GGTGCACCTC	ATCGATAAGG	TCATCTCCAC	CATCACCAC	AACATCCAGC	780
	AGATCATTGA	GATCGAGGAC	ACCTTTGAGA	CCCTTCGGGC	TGCTGTGGCT	GCATCAGGGC	840
	TCAACACGAT	GCTTGAAGGT	AACGGCCAGT	ACACGCTTTT	GGCCCCGACC	AATGAGGCCT	900
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	ACCTGCTGAA	CAACCACATC	TTGAAGTCAG	CTATGTGTGC	TGAAGCCATC	GTTGCGGGGC	1020
	TGCTGTAGA	GACCCCTGGAG	GGCAGGACAC	TGGAGGTGGG	CTGCAGCGGG	GACATGCTCA	1080
15	CTATCAACGG	GAAGGCGATC	ATCTCCAATA	AAGACATCCT	AGCCACCAAC	GGGGTGATCC	1140
	ACTACATTGA	TGAGCTACTC	ATCCCAGACT	CAGCCAAGAC	ACTATTGTA	TTGGCTGAC	1200
	AGTCTGATGT	GTCCACAGCC	ATTGACCTTT	TCAGACAAGC	CGGCCTCGGC	AATCATCTCT	1260
	CTGGAAGTGA	GCGGTTGACC	CTCCTGGCTC	CCCTGAATTC	TGTATTCAAA	GATGGAAACC	1320
20	CTCCAATTGA	TGCCCCATACA	AGGAATTTTG	TTCGGAACCA	CATAATTAAA	GACCAGCTGG	1380
	CCTCTAAGTA	TCTGTACACT	GGACAGACCC	TGGAACCTCT	GGGCGGCAAA	AAACTGAGAG	1440
	TTTTTTGTTA	TCGTAATAGC	CTCTGCATTG	AGAACAGCTG	CATCGCGGCC	CACGACAAGA	1500
	GGGGGAGGTA	CGGGACCCTG	TTACAGATGG	ACCGGGTGCT	GACCCCCCA	ATGGGGACTG	1560
	TCATGGATGT	CCTGAAGGGA	GACAATCGCT	TTAGCATGCT	GGTAGCTGCC	ATCCAGTCTG	1620
25	CAGGACTGAC	GGAGACCCCT	AACCGGGAAG	GAGTCTACAC	AGTCTTTGCT	CCCAACAAAT	1680
	AAGCCTTCCG	AGCCCTGCCA	CCAAGAGAAC	GGAGCAGACT	CTTGGGAGAT	GCCAAGGAAC	1740
	TTGCCAACAT	CCTGAAATAC	CACATTGGTG	ATGAAATCCT	GTTAGCGGA	GGCATCGGGG	1800
	CCCTGGTGCG	GCTAAAGTCT	CTCCAAGGTG	ACAAGCTGGA	AGTCAGCTTG	AAAAACAATG	1860
	TGGTGAGTGT	TCTGAAGGAG	CCTGTTGCCG	AGCCTGACAT	CATGGCCACA	AATGGCGTGG	1920
30	TCATGTGCT	CACCAATGTT	CTGCAGCCTC	CAGCCAACAG	ACCTCAGGAA	AGAGGGGATG	1980
	AACCTGCAGA	CTCTGCGCTT	GAGATCTTCA	ACAAGCATC	AGCGTTTTTC	AGGGCTTCCC	2040
	AGAGGTCTGT	GCGACTAGCC	CCTGTCTATC	AAAAGTTATT	AGAGAGGATG	AAGCATTAGC	2100
	TTGAAGCACT	ACAGGAGGAA	TGCACCACGG	CAGCTCTCCG	CCAATTCTTC	TCAGATTTC	2160
	ACAGAGACTG	TTTGAATGTT	TTCAAAACCA	AGTATCACAC	TTTAATGTAC	ATGGGCGGCA	2220
35	CCATAATGAG	ATGTGAGCCT	TGTGCATGTG	GGGGAGGAGG	GAGAGAGATG	TACTTTTTTA	2280
	ATCATGTTCC	CCCTAAACAT	GGCTGTTAAC	CCACTGCATG	CAGAAACTTG	GATGTCACTG	2340
	CCTGACATT	ACTTCCAGAG	AGGACCTATC	CCAAATGTGG	AATTGACTGC	CTATGCCAAG	2400
	TCCTGGGAAA	AGGAGCTTCA	GTATTGTGGG	GCTCATAAAA	CATGAATCAA	GCAATCCAGC	2460
40	CTCATGGGAA	GTCTGGCAC	AGTTTTGTGA	AAGCCCTTGC	ACAGCTGGAG	AAATGGCATC	2520
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	AGGCTTTTAT	GGGGCCCTGT	CCAGGTAGAA	AAGAAATGGT	ATGTAGAGCT	TAGATTTCCT	2640
	TATTGTGACA	GAGCCATGGT	GTGTTGTGTA	TAATAAAACC	AAAGAAACAT	A	2691

Seq ID NO: C79 DNA Sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109..2940

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	AGCATTGCAG	GTCTATTTTG	CAACCTGAAG	TTTGTGACTC	TCCTGGTTGC	CTTAAGTTCA	180
	GAACTCCCAT	TCCTGGGAGC	TGGAGTACAG	CTTCAAGACA	ATGGGTATAA	TGGATTGCTC	240
55	ATTGCAATTA	ATCCTCAGGT	ACCTGAGAA	CAGAACCTCA	TCTCAACAT	TAAAGAAATG	300
	ATAACTGAAG	CTTCATTTTA	CCTATTTAAT	GCTACCAAGA	GAAGAGTATT	TTTCAGAAAT	360
	ATAAAGATT	TAATACCTGC	CACATGGAAA	GCTAATAATA	ACAGCAAAAT	AAAACAAGAA	420
	TCATATGAAA	AGGCAAAATG	CATAGTGACT	GACTGGTATG	GGGCACATGG	AGATGATCCA	480
	TACACCTTAC	AATACAGAGG	GTGTGGAAAA	GAGGGAAAAAT	ACATTCATTT	CACACCTAAT	540
60	TTCTTACTGA	ATGATAACTT	AACAGCTGGC	TACGGATCAC	GAGGCCGAGT	GTTTGTCCAT	600
	GAATGGGCCC	ACCTCCGTTG	GGGTGTGTTT	GATGAGTATA	ACAATGACAA	ACCTTTCTAC	660
	ATAAATGGGC	AAAATCAAAT	TAAAGTGACA	AGGTGTTTCT	CTGACATCAC	AGGCATTTTT	720
	GTGTGTGAAA	AAGGTCCTTG	CCCCAAGAA	AACGTGATTA	TTAGTAAGCT	TTTTAAAGAA	780
	GGATGCACCT	TTATCTACAA	TAGCACCCAA	AATGCAACTG	CATCAATAAT	GTTTCATGCA	840
65	AGTTTATCTT	CTGTGGTTGA	ATTTTGTAAT	GCAAGTACCC	ACAACCAAGA	AGCACCAAAC	900
	CTACAGAACC	AGATGTGCAG	CCTCAGAAGT	GCATGGGATG	TAATCACAGA	CTCTGCTGAC	960
	TTTCACCACA	GCTTTCCCAT	GAATGGGACT	GAGCTTCCAC	CTCCTCCAC	ATTCTCGCTT	1020
	GTACAGGCTG	GTGACAAAGT	GGTCTGTTTA	GTGCTGGATG	TGTCACGAA	GATGGCAGAG	1080
	GCTGACAGAC	TCCTTCAACT	ACAACAAGCC	GCAGAATTTT	ATTTGATGCA	GATTGTTGAA	1140
70	ATTCATACCT	TCGTGGGCAT	TGCCAGTTTC	GACAGCAAAG	GAGAGATCAG	AGCCCCAGTA	1200
	CACCAAAATTA	ACAGCAATGA	TGATCGAAAG	TTGCTGGTTT	CATATCTGCC	CACCACTGTA	1260
	TCAGCTAAAA	CAGACATCAG	CATTTGTTCA	GGGCTTAAGA	AAGGATTGTA	GGTGGTTGAA	1320
	AAACTGAATG	GAAGAAGCTTA	TGGCTCTGTG	ATGATATTAG	TGACCAGCGG	AGATGATAAG	1380
	CTTCTTGGCA	ATTGCTTTACC	CACCTGTGCTC	AGCAGTGGTT	CAACAATTCA	CTCCATTGCC	1440
75	CTGGGTTTAT	CTGCAGCCCC	AAATCTGGAG	GAATTATCAC	GTCTTACAGG	AGGTTTAAAG	1500
	TTCTTTGTTT	CAGATATATC	AAACTCCAAT	AGCATGATTG	ATGCTTTTCA	TAGAAATTTCC	1560
	TCTGGAACCTG	GAGACATTTT	CCAGCAACAT	ATTCAGCTTG	AAAGTACAGG	TGAAATATGC	1620
	AAACCTCACC	ATCAATTGAA	AAACACAGTG	ACTGTGGATA	ATACTGTGGG	CAACGACACT	1680
80	ATTGTTCTAG	TTACGTGGCA	GGCCAGTGGT	CCTCCTGAGA	TTATATTATT	TGATCCTGAT	1740
	GGACGAAAAT	ACTACACAAA	TAATTTTATC	ACCAATCTAA	CTTTTGGGAC	AGCTAGTCTT	1800
	TGGATTCCAG	GAACAGCTAA	GCCTGGGCAC	TGGACTTACA	CCCTGAACAA	TACCCATCAT	1860
	TCTCTGCAAG	CCCTGAAAGT	GACAGTGACC	TCTCGGCCT	CCAACCTCAG	TGTGCCCCCA	1920
	GCCACTGTGG	AGCCCTTTGT	GGAAAGAGAC	AGCCTCCATT	TTCTCATCC	TGTGATGATT	1980
	TATGCCAATG	TGAAACAGTG	ATTTTATCCC	ATTCTTAATG	CCAATCTCAC	TGCCACAGTT	2040
	GAGCCAGAGA	CTGGAGATCC	TGTTACGCTG	AGACTCCTTG	ATGATGGAGC	AGGTGCTGAT	2100

GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTCTCT CCTTTGCTGC AAATGGTAGA 2160
 TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCACGC CCACTCTATT 2220
 CCAGGGAGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280
 GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGCTT TAGCCGAGTC 2340
 AGCTCAGGAG GCTCCTTTTC AGTGTCTGGA GTTCCAGCTG GCCCCACCC TGATGTGTTT 2400
 CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAAT GACCCATCT 2460
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 AGTAAAAGTC TACAGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA 2580
 AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTCC 2640
 ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTTATGTT 2700
 GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCCAGGCG 2760
 CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
 GGAGTTTAA CAGCAATGGG TTTGATAGGA ATCATTGCCC TTATTATAGT TGTGACACAT 2880
 CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA 2940
 ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCCTCG ACTACAAAAA 3000
 CATACTAAAC AAGTCAAAAT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTACA 3060
 ATACAGATAA GATTTTAAAC TGGTAGATCA ACAATCTTTT TTGGGGGTAG ATTAGAAAAA 3120
 CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAAGTAAT GTCTTTAAAG 3180
 GCAAAGGGAA GGGTAAAGTC GGACCAAGTGT CAAGGAAAGT TTGTTTATT GAGGTGGA 3240
 AATAGCCCAA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACGTCTCT TGTGAAGCAA 3300
 TCATTAGTAT ACTTTGATTA ATTTTCTTT TCTCCTTATC TGTGCAGTAC AGGTGTGCTT 3360
 TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAG CTCTTTACCT 3420
 CTTGCTATTT TGTATATAT ATTTAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
 TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540
 TTTATGACAA AGGTCTATTG AATTTATTG TMTGTAAGTT TCTACTCCCA TCAAAGCAGC 3600
 TTTCTAAGTT TATTGCCTTG GGTATTATG GAATGATAGT TATAGCCCN TATAATGCCT 3660
 TACCTAGGAA A 3671

Seq ID NO: C80 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1413

1 11 21 31 41 51
 ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCCTGAAC 60
 AGCTCTACAA GCCTGGAAAA AAATAATGTG CTATTGGTGG AAAGATACTT AGAAAAATTT 120
 TATGGCCTTG AGATAAACAA ACTTCCAGTG ACAAATAATGA AATATAGTGG AAACCTTAATG 180
 AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240
 ACATCTAACC TGGAGATGAT GCACGCACCT CGATGTGGAG TCCCGATGT CCATCATTTT 300
 AGGGAAATGC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT 360
 TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCCGGAAGC TTTCGAAGTA 420
 TGGAGTAATG TTACCCCTTT GAAATTCAGC AAGATTAAAC CAGGCATGGC TGACATTTTG 480
 GTGGTTTTTG CCCGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540
 CTAGCCCATG CTTTGGGACC TGGATCTGGC ATTGGAGGGG ATGCACATTT CGATGAGGAC 600
 GAATCTTGGA CTACACATTC AGGAGGCACA AACTTGTTC TCATGCTGT TCACGAGATT 660
 GGCCATTCTCT TAGGTCTTGG CCATTCTAGT GATCCAAAGG CCGTAATGTT CCCACCTAC 720
 AAATATGTTG ACATCAACAC ATTTGCGCTC TCTGCTGATG ACATACGTGG CATTCAGTCC 780
 CTGTATGGAG ACCCAAAAGA GAACCAACGC TTGCCAAATC CTGACAATTC AGAACCAGCT 840
 CTCTGTGACC CCAATTTGAG TTTTGTGCTG GTCACACCG TGGGAAATAA GATCTTTTTC 900
 TTCAAAGACA GGTTCCTCTG GCTGAAGGTT TCTGAGAGAC CAAAGACCAG TGTTAATTTA 960
 ATTTCTTCTCT TATGGCCAACT CTGCACTCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020
 AGAAATCAAG TTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080
 GAGCCAAATT ATCCCAAGAG CATACATTCT TTTGGTTTTT CTAACCTTGT GAAAAAATT 1140
 GATGCAGCTG TTTTAAACCC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAACCAGTAT 1200
 TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCCCTGTT ATCCCAACT GATTACCAAG 1260
 AACTTCCAAG GAATCGGGCC TAAATTTGAT GCAGTCTCT ACTCTAAAA CAAATACTAC 1320
 TATTTCTTCC AAGGATCTAA CCAATTTGAA TATGACTTCC TACTCCAACG TATACCCAAA 1380
 ACATGAAAAA GCAATAGCTG GTTTGGTGTG TGA 1413

Seq ID NO: C81 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1413

1 11 21 31 41 51
 ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCCTGAAC 60
 AGCTCTACAA GCCTGGAAAA AAATAATGTG CTATTGGTGG AAAGATACTT AGAAAAATTT 120
 TATGGCCTTG AGATAAACAA ACTTCCAGTG ACAAATAATGA AATATAGTGG AAACCTTAATG 180
 AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240
 ACATCTAACC TGGAGATGAT GCACGCACCT CGATGTGGAG TCCCGATGT CCATCATTTT 300
 AGGGAAATGC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT 360
 TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCCGGAAGC TTTCGAAGTA 420
 TGGAGTAATG TTACCCCTTT GAAATTCAGC AAGATTAAAC CAGGCATGGC TGACATTTTG 480
 GTGGTTTTTG CCCGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540
 CTAGCCCATG CTTTGGGACC TGGATCTGGC ATTGGAGGGG ATGCACATTT CGATGAGGAC 600
 GAATCTTGGA CTACACATTC AGGAGGCACA AACTTGTTC TCATGCTGT TCACGCCATT 660
 GGCCATTCTCT TAGGTCTTGG CCATTCTAGT GATCCAAAGG CCGTAATGTT CCCACCTAC 720
 AAATATGTTG ACATCAACAC ATTTGCGCTC TCTGCTGATG ACATACGTGG CATTCAGTCC 780
 CTGTATGGAG ACCCAAAAGA GAACCAACGC TTGCCAAATC CTGACAATTC AGAACCAGCT 840
 CTCTGTGACC CCAATTTGAG TTTTGTGCTG GTCACACCG TGGGAAATAA GATCTTTTTC 900
 TTCAAAGACA GGTTCCTCTG GCTGAAGGTT TCTGAGAGAC CAAAGACCAG TGTTAATTTA 960
 ATTTCTTCTCT TATGGCCAACT CTGCACTCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020
 AGAAATCAAG TTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080
 GAGCCAAATT ATCCCAAGAG CATACATTCT TTTGGTTTTT CTAACCTTGT GAAAAAATT 1140

GATGCAGCTG TTTTAAACCC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAACCAGTAT 1200
 TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCCTGGTT ATCCCAAACT GATTACCAAG 1260
 AACTTCCAAAG GAATCGGGCC TAAATTTGAT GCAGTCTTCT ACTCTAAAAA CAAATACIAC 1320
 TATTTCTTCC AAGGATCTAA CCAATTTGAA TATGACTTCC TACTCCAACG TATCACCAAA 1380
 AACTGAAAA GCAATAGCTG GTTTGGTTGT TGA 1413

Seq ID NO: C82 DNA Sequence
 Nucleic Acid Accession #: NM_006952.1
 Coding sequence: 11..793

1 11 21 31 41 51
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 TGGAAATGTG ATTATTTGTT GTTGCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120
 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
 GGCTGCCTGG ATCGGCATAT TGTGGGGCAT CTGCCCTCTC TGCCCTGTCTG TTCTAGGCAT 240
 TGTAGGCATC ATGAAGTCCA GCAGGAAAA TCTTCTGGCG TATTTCAATC TGATGTTTAT 300
 AGTATATGCC TTGGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
 ACCCAACCTC TTCTGAAGC AGATGCTAGA GAGGTACCAA AACCAACGCC CTCCAAACAA 420
 TGATGACCA TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
 CAATTGCTGT GGGCTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540
 TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
 AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTATC ACAATCAGGG 660
 CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG 720
 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTGGGT ACCATGTCTT ACTGGAGCAG 780
 AATTGAATAT TAAGAA 796

Seq ID NO: C83 DNA Sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

1 11 21 31 41 51
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTCGC GGCAGCTGCT TCACCCCTCT 60
 CTCTGCAGCC ATGGGGCTCC CTGCTGGACC TCTCGCGTCT CTCCCTCCTTC TCCAGGTTTG 120
 CTGGCTGCA TGC CGCGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
 CTTGGAGGCG GAGGCGCGCG AGCAGGAGCC CCGCCAGGCG CTGGGGAAG TATTCATGGG 240
 CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
 TGGCGAGACA GTCCAGGAAA GAAGGTCAC TGAAGGAAAG AATCCATTGA AGATCTTCCC 360
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
 TGAAAAATGC AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAACTCTA ATAAAGATAG 480
 AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540
 CTTCTGCTGA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
 GATTGCCAAG TATGACTCTT TTGGCCACGC TGTGTGACAG AATGGTGGCT CAGTGGAGGA 660
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAGGT 780
 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
 CCATAGCCAA GAACCAAGAG ACCCACACGA CCTCATGTTT ACCATTACCC GGAGCACAGG 900
 CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAGAA GTCCCTGAGT ACACACTGAC 960
 CATCCAGGCC ACAGACATGG ATGGGGACGG CTCACCACC ACCGGCAGTGG CAGTAGTGGA 1020
 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
 GCCTGAGAA TATGAGTGGC ATGAGGTGCA GAGGCTGACG GTCAGTGATC TGGACGCCCC 1140
 CAACTACCA CGGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
 TACCATCACC ACCCACCTTG AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGGA 1260
 TTTTGAGGCC AAAAACCCAGC ACACCTGTA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
 ACCTGTGTTT GTCCCGCGT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
 GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAGA TCAGCTACCG 1500
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 GTTCTTGGCC ATGGACAATG GAAGCCTTCC CACCACGGC ACGGGAACCC TTCTGCTAAC 1680
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 CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
 CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
 GGAAGGTGAC ACAGTGTGCT TGTCCCTGAA GAAGTTCTTG AAGCAGGATA CATATGACGT 1920
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAGGGAG GTTTCATCCT 2040
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCCCTCTG CTGGTGTGCT TTTTGTGGT 2100
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 GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGACG TGGACCAAC 2280
 CATCATCCCG ACACCCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCACA GCCCCGCCCT ACGACACCTT 2400
 CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCTGAGCT CCCTCACTC 2460
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 GGGACCAAAC CTGAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG 2640
 GACTTCGAGG TTTGTGAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
 ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAAGCC 2820
 TTTACTCTGC CTAAACCTGT TCAACCTGTG GTCCCTGGCC TTGGCCTGCT GTGACTGACC 2880
 TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
 TTTTTTTAA TCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
 GCTGGGCCCA GTGCCCTTCC TGCATTTCTG GTTTCAGAC CCAATGCCT CCCATTCGGA 3060

TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTTT TATTTTCCCT 3120
 GTTGC GTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
 TAAAGAAACT TTTCCAGAA AAAAA 3205

5

Seq ID NO: C84 DNA Sequence
 Nucleic Acid Accession #: NM_005629.1
 Coding sequence: 639..2546

10

1 11 21 31 41 51
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 CCGCCGCGCAC CACCGCCACC GGAGTCGCGG GCCAGCCGGG CAGCCTCCGC GGGCCCGCGC 180
 CGGGGCGGGG GGGCGGGGCC ACAGGCCCCC GCTCCGGCCG TCGTTTGCAG ACCGCGGGCG 240
 15 CCGATGTGCG CCGCGCCCCG TTAGGATGAG TCTCGGGTCG GCGGAGGAGC CGCGCGAGCC 300
 GCCGCGCGCC GAGCCGCGGG CAGGAGCCTC GGGAGCCGCC GCCGCGCGCG CGCGCGCGCG 360
 GCCGGGCCCC GAGCGCGCCC GCGCGCCCCC GGGCCCCCGA CACACATGAG ATTCTTCAGG 420
 CTCACTTTCA AGTGCTTCGT GGACTGCTTC TGACTGCGCC GCCCGCGCCC CGCACCCCGC 480
 CGTCCGCGCG CCGCCCCGTC CCGCGCCCCG GCCCGCCCCG GCGCCCGCGC CGCGCGCGCG 540
 20 CTTGCGGGCC CTCCCCGGTG CCGCCCGGTG CCCCCGCTG ACCGCGCGCC CCCGTGAGGC 600
 GCCGCGACCC CGGCCGCGCC GTGCGGCCCC CCGGGGCCAT GCGGAAGAAG AGCGCCGAGA 660
 ACGGCATCTA TAGCGTGTCC GCGGACGAGA AGAAGGGCCC CCTCATCGCG CCGGGCGCGC 720
 ACGGGGCCCC GCGCAAGGGC GACGCGCCCC TGGCCTGGG GACACCCGGC GCGCGCCTGG 780
 CCGTGCCGCC GCGCGAGACC TGGACGCGCC AGATGGAATT CATCATGTCT TCGTGGGCT 840
 25 TCGCCGTGGG CTTGGGCAAC GTGTGGCGCT TCCCTTACCT GTGCTACAAG AACGCGGAG 900
 GTGTGTTCTT TATTCCTTAC GTCTGATCG CCTGTGTTGG AGGAATCCCC ATTTTCTTCT 960
 TAGAGATCTC GCTGGGCCAG TTCTATGAAG CCGGCAGCAT CAATGTCTGG AACATCTGTC 1020
 CCTGTTCCTA AGCCCTGGGC TACGCTTCCA TGGTGATCGT CTCTACTGTC AACACCTACT 1080
 ACATCATGGT GCTGGCCTGG GGCTTCTATT ACCTGGTCAA GTCCTTTACC ACCACGCTGC 1140
 30 CCTGGGCCAC ATGTGGCCAC ACCTGGAACA CTCGCCACTG CGTGGAGATC TTCCGCCATG 1200
 AAGACTGTGC CAATGCCAGC CTGGCCAACC TCACCTGTGA CCAGCTTGCT GACCGCCGGT 1260
 CCCTGTCTAT CGAGTTCTGG GAGAACAAG TCTTGAGGCT GTCTGGGGGA CTGGAGGTGC 1320
 CAGGGGCCCT CAACTGGGAG GTGACCCCTT GTCTGCTGGC CTGCTGGGTG CTGGTCTACT 1380
 35 TCTGTGTTCT GAAGGGGGTC AAATCCACGG GAAAGATCGT GTACTTCACT GCTACATTCC 1440
 CCTACGTGGT CCTGGTCTGC CTGCTGTTGC GTGGAGTGCT GCTGCTGGC GCCCTGGATG 1500
 GCATCATTTA CTATCTCAAG CCTGACTGGT CAAAGCTGGG GTCCCTCAG GTGTGGATAG 1560
 ATGCGGGGAC CCAGATTTTC TTTTCTTACG CCATTGGCCT GGGGGCCCTC ACAGCCCTGG 1620
 CGAGCTACAA CCGCTTCAAC AACAATGCT ACAAGGACGC CATCATCTCT GCTCTCATCA 1680
 40 ACAGTGGGAC GCGGTACCTT GCTGGCTTCG TGGTCTTCTC CATCCTGGGC TTCTATGGCTG 1740
 CAGAGCAGGG CGTGACATC TCCAAGGTGG CAGAGTCAGG GCCGGGCTCG GCCTTCATCG 1800
 CCTACCCGCG GCGTGTACGC CTGATGCCAG TGGCCCACT CTGGGCTGCC CTGTTCTTCT 1860
 TCATGCTGTT CTGCTTGGT CTGACAGCC AGTTTGTAGG TGTGGAGGGC TTCATCACCG 1920
 GCCTCTCGCA CCGCTCTCCG GCCTCTTACT ACTTCCGTTT CCAAGGGGAG ATCTCTGTGG 1980
 45 CCCTCTGTTG TGGCTCTGTC TTTGTCTATG ATCTCTCCAT GGTGACTGAT GCGGGGATGT 2040
 ACGTCTTCCA GCTGTTTGAC TACTACTCGG CCAGCGGCAC CACCTTGCTC TGGCAGGCCT 2100
 TTTGGGAGTG CGTGGTGGTG GCCTGGGTGT ACGGAGCTGA CCGCTTCATG GACGACATTG 2160
 CCTGTATGAT CCGGTACCGA CCTTGCCCTC GGATGAAATG GTGCTGGTCC TTCTTACACC 2220
 CGCTGGTCTG CATGGGCATC TTCTATCTCA ACGTTGTGTA CTACGAGCCG CTGGTCTACA 2280
 50 ACAACACCTA CGTGTACCCG TGGTGGGGTG AGGCCATGGG CTGGGCTTTC GCCCTGTCTC 2340
 CCATGCTGTG CGTGCCCTGG CACCTCTCTG GCTGCCTCCT CAGGGCCCAAG GGCACCATGG 2400
 CTGAGCGCTG CGAGCACTG ACCCAGCCCA TCTGGGGCCT CCACCACTTG GAGTACCGAG 2460
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 55 GCCATAGCAG CCCCTGCTTC AGCCCCACCG CACCCCTCCA GGGGGCCTGC CTTTCCCTGA 2640
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 TCCCCCTCCA GCCCTAGCCG AGCTGCTCCT AGGCCCGGCC TAGTGCCCCA CCCCCACCA 2820
 CAGTGCTGCA CTCCTCTGTC CCCTGCCACG CCCACCCCTT GCCCACTCTT CCAGGCTCTG 2880
 60 CTCTGCAGCA CACCCGTGGG TGACCCCTCA CCCCAGAAGC AGCAGTGGCA GCTTGGGAAA 2940
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 GAGGGGAGC AGAACCAAG CAAATATTTT AGCTGGGCTA TACCCCTCTC CCCATCCCTG 3060
 TTATAGAAGC TTAGAGAGCC AGCCAGCAAT GGAACCTTCT GGTTCCTGCG CCAATCGCCA 3120
 CCAGTATCAA TTGGTGTGAG TTGGGTGCGA GTGCACGCGT GCGTGAGTAC GGAGAGTATA 3180
 65 TATAGATCTC TATCTCTTAG CAAAGGTGAA TGCCAGATGT AAATGGCGCC TCTGGGCAAA 3240
 GGAGGCTTGT ATTTTGCACA TTTTATAAAA ACTTGAGAGA ATGAGATTTC TGCTTGATA 3300
 TTTCTAAAAA GAGGAAGGAG CCCAAACCAT CCTCTCCTTA CCACTCCCAT CCCTGTGAGC 3360
 CCTACCTTAC CCCTCTGCCC CTAGCCAAAG AGTGTGAATT TATAGATCTA ACTTTCATAG 3420
 70 GCAAAACAAA AGCTTCGAGC TGTGCGTGT GTGAGTCTGT TGTGTGGATG TCGTGTGTG 3480
 GTCCCCAGCC CAGACTGGA TTGGAAGAGT GCATGGTGGG GGCTCGGGG CTGTCCCCAC 3540
 CTTGTCCCTT TGCCACAAGT CTGTGGGGCA AGAGGCTGCA ATATTCGCTC CTGGGTGTCT 3600
 GGGCTGTCAA CCTGGCTTGC TCAGGCTTCC CACCCGTGTC GGGGCACACC CCGAGGAAGG 3660
 GACCTGGAGC ACGGCTCCCA CGTCCAGGCT TAAGGTGGAT GCACCTTCCC CACCTCCAGT 3720
 CTTCTGTGTA CCGCTTTTAA CCCACGTTTG TCTGTACGCT CCAGTCCCGA GACGGCTGAG 3780
 75 TGACCCCAAG AAAGGCTTCC CCGACACCCA GACAGAGGCT GCAGGGCTGG GGCTGGGTGA 3840
 GGGTGGCGGG CTTGCGGGGA CATCTACTGT TGCTAAAAAG CCAGTGCAGA CATAGCAATA 3900
 AAAACATGTC ACTTTCC 3917

80

Seq ID NO: C85 DNA Sequence
 Nucleic Acid Accession #: NM_006516.1
 Coding sequence: 180..1658

1 11 21 31 41 51
 | | | | | |
 TAGTCGCGGG TCCCCGAGTG AGCACGCCAG GGAGCAGGAG ACCAAACGAC GGGGGTCCGA 60

GTCAGAGTCG CAGTGGGAGT CCCCAGGACG GAGCAGGAG CTGAGCGGGA GAGCGCCGCT 120
 CGCACGCCCG TCGCCACCGG CGTACCCGGC GCAGCCAGAG CCACCAGCGC AGCGCTGCCA 180
 TGGAGCCCGC CAGCAAGAAG CTGACGGGTC GCCTCATGCT GGCTGTGGGA GGAGCAGTGC 240
 5 TTGGCTCCCT GCAGTTTGGC TACAACTG GAGTCATCAA TGCCCCCAG AAGGTGATCG 300
 AGGAGTTCTA CAACCAGACA TGGGTCCACC GCTATGGGGA GAGCATCTG CCCACCACGC 360
 TCACCACGCT CTGTTCCCTC TCAGTGGCCA TCTTTCTGT TGGGGGCATG ATTGCTCTCT 420
 TCTCTGTGGG CCTTTCTGTT AACCGCTTTG GCCGGCGGAA TCAATGCTG ATGATGAACC 480
 TGCTGGCCTT CGTGTCCGCC GTGCTCATGG GCTTCTCGAA ACTGGGCAAG TCCTTTGAGA 540
 10 TGCTGATCCT GGGCCGCTTC ATCATCGGTG TGTACTGCGG CCTGACCACA GGCTTCGTGC 600
 CCATGTATGT GGGTGAAGTG TCACCACAG CTTTTCGTGG GGCCCTGGGC ACCCTGCACC 660
 AGCTGGGCAT CGTCTCGGC ATCCTCATCG CCCAGGTGTT CGGCCCTGGAC TCCATCATGG 720
 GCAACAAGGA CCTGTGGCCC CTGCTGCTGA GCATCATCTT CATCCCGGCC CTGCTGCAGT 780
 GCATCGTGCT GCCCTTCTGC CCCGAGAGTC CCCGCTTCTT GCTCATCAAC CGCAACGAGG 840
 15 AGAACCGGGC CAAGAGTGTG TAAAGAAGC TGCGCGGGAC AGCTGACGTG ACCCATGACC 900
 TGCAGGAGAT GAAGAGAAG AGTCCGCGAG TGATGCGGGA GAAGAAGTTC ACCATCTGG 960
 AGCTGTTCCG CTCCCCCGCC TACCGCCAGC CCATCTCAT CGCTGTGGTG CTGCAGCTGT 1020
 CCCAGCAGCT GTCTGGCATC AACCGTGTCT TCTATTACTC CACGAGCATC TTCGAGAAGG 1080
 CGGGGGTGCA GCAGCTGTG TATGCCACCA TTGGCTCCGG TATCGTCAAC ACGGCTTTCA 1140
 20 CTGTCGTGTC GCTGTTTGTG GTGAGCGAG CAGGCGGGCG GACCTGACAC CTCATAGGCC 1200
 TCGCTGGCAT GGGCGGTTGT GCCATACTCA TGACCATCGC GCTAGCACTG CTGGAGCAGC 1260
 TACCCTGGAT GTCCATCTG AGCATCGTGG CCATCTTTGG CTTTGTGGCC TTCTTTGAAG 1320
 TGGGTCTCTG GCCCATCCCA TGGTTTCATG TGGCTGAAC CTTCAGCCAG GGTCCACGTC 1380
 CAGCTGCCAT TGCCGTGCA GGCTTCTCCA ACTGGACCTT AAATTTCTAT GTGGCATGT 1440
 25 GCTTCCAGTA TGTGGAGCAA CTGTGTGGTC CCTACGCTCT CATCATCTTC ACTGTGCTCC 1500
 TGGTTCTGTT CTTCATCTTC ACCTACTTCA AAGTTCTCTG GACTAAAGGC CGGACCTTCG 1560
 ATGAGATCCG TTCCGCTTTC CGGCAGGGGG GAGCCAGCCA AAGTGATAAG ACACCCGAGG 1620
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 GCCTGCTCCC AGCAGCCCTA AGGATCTCTC AGGAGCACAG GCAGCTGGAT GAGACTTCCA 1740
 30 AACCTGACAG ATGTGAGCG AGCCCGGCCCT GGGGCTCCTT TCTCCAGCCA GCAATGATGT 1800
 CCAGAGAAT ATTCAGGACT TAACGGCTCC AGGATTTTAA CAAAGCAAG ACTGTTGCTC 1860
 AAATCTATTG AGACAGCAA CAGGTTTAT AATTTTCTTA TTAAGTATT TGTATTATTT 1920
 ATATCAGCCT GAGTCTCTCG TGCCACATC CCAGGCTTCA CCCTGAATGG TTCCATGCCT 1980
 GAGGGTGGAG ACTAAGCCCT GTGAGACAC TTGCTTCTT CACCCAGCTA ATCTGTAGGG 2040
 35 CTGGACCTAT GTCTTAAGGA CACACTAATC GAACATGAA CTACAAAGCT TCTATCCCA 2100
 GAGGTGGCTA TGGCCACCGG TTCTGTGGC CTGGATCTCC CCACTCTAGG GGTGAGGCTC 2160
 CATTAGGATT TGCCCTTCC CATCTCTCC TACCACCA CTCAAATTAA TCTTCTTTA 2220
 CCTGAGACCA GTTGGAGCA CTGGAGTGCA GGGAGGAGAG GGGAGGGGCC AGTCTGGGCT 2280
 GCCGGGTTCT AGTCTCTTT GCACTGAGGG CCACACTATT ACCATGAGAA GAGGGCCTGT 2340
 40 GGGAGCCTGC AAACCTAGC CTCAAGAAGA CATGGAGACT CTGCCCCTGT TGTGTATAGA 2400
 TGCAAGATAT TTATATATAT TTTTGGTTGT CAATATTAAT TACAGACACT AAGTTATAGT 2460
 ATATCTGGAC AAGCCAACCT GTAAATACAC CACCTCACTC CTGTTACTTA CCTAAACAGA 2520
 TATAAATGGC TGGTTTTTAG AAACATGGTT TTGAAATGCT TGTGGATTGA GGGTAGGAGG 2580
 TTTGGATGGG AGTGAGACAG AAGTAAGTGG GGTGCAACC ACTGCAACCG CTAGACTTTC 2640
 45 GACTCAGGAT GCTAGCCTT ACACGTACCT CTATCATGT TCTCTTGCT CAAAATCTG 2700
 TTTGATCCCT GTTACCAGCA GAATATATAC ATTCTTTATC TTGACATTCA AGGCATTTCT 2760
 ATCACAATAT TGTAGTTGG TGTTCAAAAA AACACTAGTT TGTGCCAGC CGTGATGCTC 2820
 AGGCTTGAAA TCGCATTAAT TTGAATGTGA AGGGAA 2886

Seq ID NO: C86 DNA Sequence
 Nucleic Acid Accession #: XM_035292.2
 Coding sequence: 53..1576

1 11 21 31 41 51
 55 GCTCGCTGGG CGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
 TCGCGGCCCG AAGCGCGCGC CGCTAGCGGC GCCGCGGCC GAGGAGAAGG AAGAGGCGCG 120
 GGAGAAGATG CTGGCCGCGA AGAGCGCGGA CGGCTCGGCG CCGCAGGCG AGGGCGAGGG 180
 CGTGACCCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT 240
 60 TATCGGCTCG GGCATCTTCG TGACGCCAC GGGCGTGCTC AAGGAGGCG GCTCGCCGGG 300
 GCTGGCGCTG TGGTGTGGG CCGCGTGGG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360
 CGCGGAGCTC GGCACACCA TCTCCAAATC GGGCGGCGAC TACGCTTACA TGCTGGAGGT 420
 CTACGGCTCG CTGCCCGCTT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGGCCTTC 480
 ATCGAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAAGCCG TCTTCCCCAC 540
 65 CTGCCCCTG CCGGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCTGCT TGCTGCTCAC 600
 GGCCGTGAAC TGCTACAGCG TGAAGGCGG CACCCGGGTC CAGGATGCCT TTGCCCGCGC 660
 CAAGCTCTCT GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGACCA AAACCTGGATG TGGGGAACAT 780
 TGTGTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGGAAATTACT TGAATTTCTG 840
 70 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTG GCCATCATCA TCTCCCTGCC 900
 CATCGTGACG CTGGTGTACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCACCCGA 960
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACATACAC TGGGCGTCA 1020
 GTCTTGATAT ATCCCGTCT TCGTGGGCTT GTCTGTCTTC GGCTCCGTC ATGGGTCCCT 1080
 GTTCAATCTC TCAAGGCTCT TCTCTGTGG GTCCCGGAA GGCCACCTGC CCTCCATCT 1140
 75 CTCCATGATC CACCCACAGC TCCTCACCCC CGTGCCGCTC CTGCTGTTC CTGTGTGAT 1200
 GACGCTGCTC TACGCTTCT CCAAGGACAT CTCTCCGTC ATCAACTTCT TCAGCTTCT 1260
 CAACCTGCTC TAGCTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
 TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCCTGCCT GTGTTCTTCA TCCTGGCCTG 1380
 CCTCTTCTG ATGCCGCTC CTCTCTGGAA GACACCGTG GAGTGTGGCA TCGGCTTAC 1440
 80 CATCATCTC AGCGGCTGC CCGTCTACTT CTTGCGGGTC TGGTGGAAA ACAAGCCCAA 1500
 GTGGCTCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAAGTGGT 1560
 CCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC 1609

Seq ID NO: C87 DNA Sequence
 Nucleic Acid Accession #: NM_005268.1

Coding sequence: 168..989

	1	11	21	31	41	51	
5	TAAAAAGCAA	AAGAATTTCG	GGCCGCGTCG	ACACGGGCTT	CCCCGAAAAC	CTTCCCGCT	60
	TCTGGATATG	AAATTCAAGC	TGCTTGCTGA	GTCTTATTGC	CGGCTGCTGG	GAGCCAGGAG	120
	AGCCCTGAGG	AGTAGTCACT	CAGTAGCAGC	TGACGCGTGG	GTCCACCATG	AACTGGAGTA	180
	TCTTTGAGGG	ACTCTGAGT	GGGGTCAACA	AGTACTCCAC	AGCCTTTGGG	CGCATCTGGC	240
10	TGTCTCTGGT	CTTCACTCTC	CGCGTGCTGG	TGTACTTGGT	GACGGCCGAG	CGTGTGTGGA	300
	GTGATGACCA	CAAGGACTTC	GACTGCAATA	CTCGCCAGCC	CGGCTGCTCC	AACGTCTGCT	360
	TTGATGAGTT	CTTCCCTGTG	TCCCATGTGC	GCCTCTGGGC	CCTGCAGCTT	ATCCTGGTGA	420
	CATGCCCTTC	ACTGCTCGTG	GTCAATGCAG	TGGCCTACCG	GGAGGTTTCA	GAGAAGAGGC	480
	ACCGAGAAGC	CCATGGGGAG	AACAGTGGGC	GCCTCTACCT	GAACCCCGGC	AAGAAGCGGG	540
	GTGGGCTCTG	GTGGACATAT	GTCTGCAGCC	TAGTGTTCAC	GGCGAGCGTG	GACATCGCCT	600
15	TTCTCTATGT	GTCCACTCA	TTCTACCCCA	AATATATCCT	CCCTCCTGTG	GTCAAGTGCC	660
	ACGCAGATCC	ATGTCCCAAT	ATAGTGGACT	GCTTCACTCT	CAAGCCCTCA	GAGAAGAAC	720
	TTTTCACTCT	CTTCACTGGT	GCCACAGCTG	CCATCTGCAT	CCTGCTCAAC	CTCGTGGAGC	780
	TCATCTACCT	GGTGAGCAAG	AGATGCCACG	AGTGCCTGGC	AGCAAGGAAA	GCTCAAGCCA	840
20	TGTGCACAGG	TCATCACCCC	CACGCTACCA	CCTCTTCCTG	CAAACAAGAC	GACCTCCTTT	900
	CGGGTGACCT	CATCTTTCTG	GGCTCAGACA	GTCACTCTCC	TCTCTTACCA	GACCGCCCCC	960
	GAGACCATGT	GAAGAAAACC	ATCTTGTGAG	GGGCTGCTTG	GACTGTGCTG	GCAGGTGGGG	1020
	CCTGGATGGG	GAGGCTCTAG	CATCTCTCAT	AGGTGCAACC	TGAGAGTGGG	GGAGCTAAGC	1080
	CATGAGGTAG	GGCAGGTAG	GAGAGAGGAT	TCAGACGCTC	TGGGAGCCAG	TTCTTAGTCC	1140
25	TCAACTCCAG	CCACCTGCCC	CAGCTCGACG	GCACTGGGCC	AGTTCCCCCT	CTGCTCTGCA	1200
	GCTCGGTTTC	CTTTCTAGA	ATGGAAATAG	TGAGGGCCAA	TGC		1243

Seq ID NO: C88 DNA Sequence
Nucleic Acid Accession #: NM_005130
Coding sequence: 98..802

	1	11	21	31	41	51	
30	CTCTACCTGA	CACAGCTGCA	GCCTGCAATT	CACTCCCACT	GCCTGGGATT	GCACTGGATC	60
	CGTGTGCTCA	GAACAAGGTG	AACGCCACGC	TGCAGCCATG	AAGATCTGTA	GCCTCACCTT	120
35	GCTCTCCTTC	CTCTACTGCG	CTGCTCAGGT	GCTCCTGGTG	GAGGGGAAAA	AAAAAGTGAA	180
	GAATGGACTT	CACAGCAAAG	TGGTCTCAGA	ACAAAAGGAC	ACTCTGGGCA	ACACCCAGAT	240
	TAAGCAGAAA	AGCAGGCCCG	GGAAACAAAG	CAAGTTTGTG	ACCAAAGACC	AAGCCAACTG	300
	CAGATGGGCT	GCTACTGAGC	AGGAGGAGGG	CATCTCTCTC	AAGGTTGAGT	GCACTCAATT	360
40	GGACCATGAA	TTTTCCTGTG	TCTTGTCTGG	CAATCCAACC	TCATGCCTAA	AGCTCAAGGA	420
	TGAGAGAGTC	TATTGGA AAC	AAGTTGCCCG	GAATCTGCGC	TCACAGAAAG	ACATCTGTAG	480
	ATATTCCAAG	ACAGCTGTGA	AAACCAGAGT	GTGCAGAAAG	GATTTTCCAG	AATCCAGTCT	540
	TAAGCTAGTC	AGCTCCACTC	TATTTGGGAA	CACAAAGCCC	AGGAAGGAGA	AAACAGAGAT	600
	GTCCCCCAGG	GAGCAGATCA	AGGGCAAAGA	GACCACCCCC	TCTAGCCTAG	CAGTGACCCA	660
45	GACCATGGCC	ACCAGAGCTC	CCGAGTGTGT	GGAGGACCCA	GATATGGCAA	ACCAGAGGAA	720
	GACTGCCCTG	GAGTTCGTGT	GAGAGACTTG	GAGCTCTCTC	TGCACATTCT	TCTCAGCAT	780
	AGTGACAGAC	ACGTCTAGTC	AATGAGGTCA	AAAGAGAACG	GGTTCCTTTA	AGAGATGTCA	840
	TGTCTAAGT	CCCTCTGTAT	ACTTTAAAGC	TCTCTACAGT	CCCCCAAAA	TATGAACCTT	900
	TGTGCTTAGT	GAGTGCAACG	AAATATTATA	ACAAGTTTGT	TATTTTGTGC	TTTGTGTTT	960
50	TGGAATTTCG	CTTATTTTTC	TTGGATGCGA	TGTTTCAGAGG	CTGTTTCTCG	CAGCATGTAT	1020
	TTCCATGGCC	CACAGAGCTA	TGTGTTTGTG	CAGCGAAGAG	TCTTTGAGCT	GAATGAGCCA	1080
	GAGTGATAAT	TTCACTGCAA	CGAAGTTTCT	GCTGAATTAA	TGTTAATAAA	ACTCTGGGTG	1140
	TTTTTCAAAA	AAAAAATAAA	AAA				1163

Seq ID NO: C89 DNA Sequence
Nucleic Acid Accession #: BC022542
Coding sequence: 274..927

	1	11	21	31	41	51	
60	ACTTGGTCCC	AGCCGATAAA	TCTGGGGCAG	CGCGCGGTAG	GAGCTGCGGG	CGGCCAGGCC	60
	CCTTCCTGCG	TCCGCACCTG	GCCCCGCGCG	CCCCTCTCGG	CGCTCCGGCT	TCCGGCGTCC	120
	TGGGCGGCTG	GGTGGCGGCG	GTTGCGGGCG	CCGCTCTGGT	GCTCCTCGGG	GCGGCGACGG	180
	GGCTCACGCG	CGGGCCCGCC	ACGGCCTTCA	CCGCCGCGCG	CTCTGACGCC	GGCATAAGGG	240
65	CCATGTGTTT	TGAATATTAT	TTGAGGCAAG	AAGTTTGTAA	AGATGGTTTC	CACAGAGACC	300
	TTTTAATCAA	AGTGAAGTTT	GGGGAAGCA	TTGAGGACTT	GCACACGTGC	CGTCTCTTAA	360
	TTAAACAGGA	CATTCCTGCA	GGACTTTATG	TGGATCCGTA	TGAGTTGGCT	TCATTACGAG	420
	AGAGAAACAT	AACAGAGGCA	GTGATGGTTT	CAGAAAATTT	TGATATAGAG	GCCCCTAATC	480
	ATTTGTCCAA	GGAGCTGTA	GTTCTCATTT	ATGCCAGACG	AGATTACAG	TGCATTGACT	540
70	GTTTTCAGC	CTTTTTCGCT	GTGCACTGCC	GCTATCATCG	CCCGCACAGT	GAAGATGGAG	600
	AAGCCTCGAT	TGTGGTCAAT	AACCCAGATT	TGTTGATGTT	TTGTGACCAA	GAGTTCCTCG	660
	TTTGAAGATG	CTGGGCTCAC	TCAGAAAGTG	CAGCCCCCTG	TGCTTTGGAT	AATGAGGATA	720
	TATGCCAATG	GAACAAGATG	AAGTATAAAT	CAGTATATAA	GAATGTGATT	CTACAAGTTC	780
	CAGTGGGACT	CAGTGTACAT	ACCTCTCTAG	TATGTTCTGT	GACTCTGCTC	ATTACAATCC	840
75	TGTGCTCTAC	ATTGATCCTT	GTAGCAGTTT	TCAAATATGG	CCATTTTTC	CTATAAGTTT	900
	TATGTAGTTA	AATGCTTCTT	AGAAACCTAA	ATAAGATCTA	TTAATTTCTG	ACGAGAGGTT	960
	TTCTCTAGTA	ATTAATTTCT	TTTATCTTTT	GTCTTCATTT	GTGGCCAAAA	TTATGTTTAC	1020
	TAGAGGAAAT	TTGGGATCAT	TCTCAGCTAA	TTCCAAAATG	TAGTGCTCTA	TTGCATGGAT	1080
	CCTTGGTAAT	CCTCAAGCAT	CAGATGCCAT	AAGGGGAAC	TTAATTTCTG	TAAATTAATG	1140
80	TTTATTTTGT	GAGAAGTGAC	TTTATCTTCA	TTTGGGGTAG	AAAAATTATT	TCTTTATGTA	1200
	GTAGAGACAA	ATTATTCTCA	TTTTGCAAGT	ACTTTCAATT	TAGACTACAA	ATTGAGAAAA	1260
	CCGTTATAAA	TAAGAAATAA	ATAGGCCAGG	CACAGTGGCT	CACACCTGTA	ATCCAGCAGC	1320
	TTTGGGAGGC	CGAGGTGGGC	GGATCACCAG	AGGTCAAGAG	TTTGAGACCA	GCTTGGTGAA	1380
	ACCTGTCTCT	TACTAAAAAT	ACAAAAGTTA	GCTGGGGCTG	GTGGTGGGCA	TCTGTAGTCC	1440
	CAGCTAATTG	GAAGGGTGAG	GCGGGAGGAT	CGCTGAACC	TGGGAGGCGG	AGGTTCCAGA	1500

GAGCCAAGAT CGCACCCTG CACTACAGCC TGGGCGACAG AACGAGACCC TGTCTCCAAA 1560
 GGA AAAACAA AAAAGAAGAA TAAAAAATT TGGATGAAAA TCATGTTTAT TTAATAAGTA 1620
 ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTTCATGA AAATCATTAA AGTAGGACAG 1680
 CTAAGAAAT AATATTAAAT TAAAAATTAT TGATAATCTT AAATATTATGA TTATTCCCTTA 1740
 ACGCACTCCA TTCTCCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800
 GGA CTGATG AACTGAGTA CTAAGATTG GTACAGAGTA TGTGAGGAAG ACAACTCAGA 1860
 TTGCCATTTT AAATAAAGTT GTACATGAAC AAAAAAAAAA AAAAAA 1906

Seq ID NO: C90 DNA Sequence
 Nucleic Acid Accession #: NM_004994
 Coding sequence: 20..2143

1 11 21 31 41 51
 15 AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCCTG GTCCTGCTGC TCCTGGTGCT 60
 GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTGTGCTCT TCCTGGAGA 120
 CCTGAGAAC AATCTCACC ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA 180
 CACTCGGGTG GCAGAGATGC GTGGAGATC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT 240
 20 CCAGAAGCAA CTGTCCCTGC CCGAGACCAG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT 300
 GCGAACCCCA CGGTGCGGGG TCACAGACCT GGGCAGATTC CAAACCTTTG AGGCGGACCT 360
 CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGCCGCG 420
 GGCCTGTGAT GACGACGCTT TTGCCCGCGC CTTCGCACTG TGGAGCGCGG TGACGCGCGT 480
 CACCTTCACT CGCGTGTACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTGCGCGA 540
 25 GCACGAGAGC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTCTCTCC 600
 TGGCCCCGGC ATTTCAGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA 660
 GGGCGTCTGT GTTCCAACTC GGTTCGAAA CGCAGATGGC GCGGCTGACC ACTTCCCTTT 720
 CATCTTCGAG GGCCTCTCCT ACTCTGCTTG CACCACCGAC GGTCTGCTCG ACGGCTTGCC 780
 CTGGTGCAGT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCCAGCGA 840
 30 GAGACTCTAC ACCCGGGACG GCAATGCTGA TGGGAAACCC TGCCAGTTTC CATTCATCTT 900
 CCAAGGCCAA TCTTACTCCG CCTGCACCAC GGACGGTCTG TCCGACGGCT ACCGCTGGTG 960
 CGCCACCACC GCCAACATACG ACCGGGACAA GCTCTTCGGC TTCTGCCGA CCGAGCTGA 1020
 CTCGACGGTG ATGGGGGGCA ACTCGGCGGG GGAGCTGTGC GTCTTCCCTT TCACTTCTCT 1080
 GGGTAAGGAG TACTCGACCT GTACGACGCA GGGCCGCGGA GATGGGCGCC TCTGGTGCGC 1140
 35 TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG 1200
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 40 TGTCACCCCT TCAGAGCGCC CCACAGCTGG CCCCACAGGT CCCCCCTCAG CTGGCCCCAC 1500
 AGGTCCCCCT ACTGCTGGCC CTTCTACGGC CACTACTGTG CCTTTGAGTC CGGTGGACGA 1560
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 CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGGG AGCCGGCGCG AGGGCCCTTT 1680
 45 CCTTATCGCC GACAGTGGC CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC 1740
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 GGTGCTGGGG CCGAGGGGCT TGGACAAGCT GGGCCTGGGA GCCGACGTGG CCGAGGTGAC 1860
 CGGGGCCCTC CCGAGTGGCA GGGGGAAGAT GCTGCTGTTC AGCGGGCGGC GCCTCTGGAG 1920
 GTTCGACGTG AAGCGGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT 1980
 CCCCAGGGTG CCTTTGGACA CGCAGCAGCT CTTCCAGTAC CGAGAGAAAG CCTATTCTCT 2040
 50 CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGGAGTGAG TTGAACACAG TGGACCAAGT 2100
 GGGCTACGTG ACCTATGACA TCCTGCACTG CCCTGAGGAC TAGGGCTCCC GTCTGCTTTT 2160
 GCAGTGCCAT GTAATATCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA 2220
 CAAACTGGTA TTCGTGTTCT GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC 2280
 TCACCTTTGT TTTTGTGGG AGTGTTCCTA ATAAACTTGG ATTCTCTAAC CTTT 2334

Seq ID NO: C91 Sequence
 Nucleic Acid Accession #: NM_000213
 Coding sequence: 188..5656

1 11 21 31 41 51
 60 GCGCTGCCCG CCTCGTCCCC ACCCCCCAAC CCCCCGCGCC GCGCCTCGGA CAGTCCCTGC 60
 TCGCCCGCGC GCTGCAGCCC CATCTCCTAG CGGCAGCCCA GCGCGGAGG GAGCGAGTCC 120
 GCCCCGAGGT AGGTCCAGGA CGGGCGCACA GCAGCAGCCG AGGCTGGCCG GGAGAGGGAG 180
 65 GAAGAGGATG GCAGGGCCAC GCCCCAGCCC ATGGGCCAGG CTGCTCCTGG CAGCCTTGAT 240
 CAGCGTCAGC CTCTCTGGGA CCTTGGCAAA CCGCTGCAAG AAGGCCCCAG TGAAGAGCTG 300
 CACGGAGTGT GTCCGTGTGG ATAAGGACTG CGCCTACTGC ACAGACGAGA TGTTCAGGGA 360
 CCGGCGCTGC AACACCCAGG CGGAGCTGCT GGC CGCGGGC TGCCAGCGGG AGAGCATCGT 420
 GGT CATGGAG AGCAGCTTCC AAATCACAGA GGAGACCCAG ATTGACACCA CCCTGCGGCG 480
 70 CAGCCAGATG TCCCCCAAG GCCTGCGGGT CCGTCTGCGG CCCGGTGAGG AGCGGCATTT 540
 TGAGCTGGAG GTGTTTGAGC CACTGGAGAG CCCCCTGGAC CTGTACATCC TCATGGACTT 600
 CTCCAACTCC ATGTCCGATG ATCTGGACAA CCTCAAGAAG ATGGGGCAGA ACCTGGCTCG 660
 GGTCTGAGC CAGCTCACCA GCGACTACAC TATTGGATTT GGCAGTTTGT TGGACAAAGT 720
 CAGCGTCCCC CAGACGGACA TGAGGCCTGA GAAGCTGAAG GAGCCCTGGC CCAACAGTGA 780
 75 CCCCCCTTC TCCTTCAAGA AGGTCTACAG CCGTACAGAA GATGTGGATG AGTTCCGGAA 840
 TAAACTCGAG GGAGAGCGGA TCTCAGGCAA CCTGGATGCT CTGAGGGGCG GCTTCGATGC 900
 CATCTCGCAG ACAGCTGTGT GCACAGGGA CATTGGCTGG GCGCCGACA GCACCCACCT 960
 GCTGCTCTTC TCCACCGAGT CAGCCTTCCA CTATGAGGCT GATGGCGCCA ACGTGTGGC 1020
 80 TGGCATCATG AGCCGCAACG ATGAACGGTG CCACCTGGAC ACCAGGGGCA CCTACACCCA 1080
 GTACAGGACA CAGGACTACC CGTCGGTGCC CACCTGGGTG GCGCTGCTCG CCAAGCAAA 1140
 CATCATCCCC ATCTTTGCTG TCACCAACTA CTCCTATAGC TACTACGAGA AGCTTACACT 1200
 CTATTTCCTT GTCTCTCTAC TGGGGGTGCT GCAGGAGGAC TCGTCCAACA TCGTGGAGCT 1260
 GCTGGAGGAG GCCTTCAATC GGATCCGCTC CAACCTGGAC ATCCGGGCCC TAGACAGCCC 1320
 CCGAGGCCCT CGGACAGAGG TCACCTCCAA GATGTTCCAG AAGACGAGGA CTGGGTCTCT 1380
 TCACATCCGG CCGGGGGAAG TGGGTATATA CCAGGTGCAG CTGCGGGCCC TTGAGCAGCT 1440

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GGATGGGACG CACGTGTGCC AGCTGCCGGA GGACCAAGA GGAACATCC ATCTGAAACC 1500
TTCCTTCTCC GAGGCGCTCA AGATGGACGC GGGCATCATC TGTGATGTGT GCACCTGCGA 1560
GCTGCAAAAA GAGGTGGCGT CAGCTCGCTG CAGCTTCAAC GGAGACTTCG TGTGCGGACA 1620
5 GTGTGTGTGC AGCGAGGGGT GAGTGGGCA GACCTGCAAC TGCTCCACCG GCTCTCTGAG 1680
TGACATTGAG CCTGCGCTGC GGGAGGGCGA GGACAAGCCG TGCTCCGGCC GTGGGGAGTG 1740
CCAGTGGCGG CACTGTGTGT GCTACGGCGA AGGCCGCTAC GAGGGTCAGT TCTGCGAGTA 1800
TGACAACTTC CAGTGTCCCC GCACCTCCGG GTTCTGTGTC AATGACCGAG GACGCTGCTC 1860
CATGGGCGCAG TGTGTGTGTG AGCCTGGTTG GACAGGCCCA AGCTGTGACT GTCCCTCAG 1920
CAATGCCACC TGCATCGACA GCAATGGGGG CATCTGTAAT GGACGTGGCC ACTGTGAGTG 1980
10 TGGCCGCTGC CACTGCCACC AGCAGTCGCT CTACACGGAC ACCATCTGCG AGATCAACTA 2040
CTCGGCGATC CACCCGGGCC TCTGCGAGGA CCTACGCTCC TCGGTGAGT GCCAGGCGTG 2100
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Seq ID NO: C92 DNA Sequence
Nucleic Acid Accession #: NM_023915
Coding sequence: 250..1326

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Seq ID NO: C93 DNA Sequence
 Nucleic Acid Accession #: NM_020789.1
 Coding sequence: 208..3699

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Seq ID NO: C94 DNA Sequence
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 Coding sequence: 186..1190

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Seq ID NO: C96 DNA Sequence
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Nucleic Acid Accession #: NM_005688.1
Coding sequence: 126..4439

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10	GTGTGAGGGA	GAGAACACAGC	ACTTCTGGGA	CGCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
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	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
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	TTAAGAAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGCTCCAA	CGATGGGCAG	AGAAATGTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
25	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCTTCTCTGG	ATCAGCTGTT	TTTATCCTCT	TTTATCCAGC	AATGATGTTT	GCATCACGGC	1140
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	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
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30	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTT	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTTCATAT	GACCTTGGGC	TTCGATCTGA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
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Seq ID NO: C106 DNA Sequence
Nucleic Acid Accession #: NM_005562
Coding sequence: 90..3671

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	ATGGGAAGTC	CAGGCAGTGT	ATCTTTGATC	GGGAACCTCA	CAGACAAACT	GCTAATGGAT	240
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Seq ID NO: C110 DNA Sequence
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 Coding sequence: 939..2372

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Coding sequence: 1..1746

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Seq ID NO: C112 DNA Sequence
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Coding sequence: 77..1372

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Seq ID NO: C113 DNA Sequence
Nucleic Acid Accession #: XM_087254.1
Coding sequence: 47..2332

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 Nucleic Acid Accession #: XM_087461.1
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55	TTGCTCTCAT	TTCAAGCAGA	TCTGCTTTTC	TGCATGTTTG	TCTGTGTGTC	TGCGTTGTGT	7260
	GTGATTTTCA	TGAAAAATA	AAATGCAAT	GCACTCATCA	CAAAAAA	AAAAA	7318

Seq ID NO: C117 DNA Sequence
Nucleic Acid Accession #: NM_006671.2
Coding sequence: 138..1820

60	1	11	21	31	41	51	
	GGCACGAGGC	TGGTGTTTAG	CAACTCCGAC	CACCTGCCTG	CTGAGGGGCT	AGAGCCCTCA	60
65	GCCCAGACCC	TGTGCCCCCG	GCCGGGCTCT	CATGCGTGGA	ATGGTGTGCT	GCCCCCTGCC	120
	AGCAGGCCAG	GCTCACCATG	GTGCGGCATG	CCATCTTGGC	ACGGGGGAGG	GACGTGTGCA	180
	GGCGGAATGG	ACTCCTCATC	CTGTCTGTGC	TGTCTGTGAT	CGTGGGCTGC	CTCCTCGGCT	240
	TCTTCTTGAG	GACCCGCGCG	CTCTCACAC	AGGAAATTAG	TTACTTCCAG	TTCCCTGGAG	300
	AGCTCCTGAT	GAGGATGCTG	AAGATGATGA	TCCTGCCACT	GGTGGTCTCC	AGCTTGATGT	360
70	CCGGACTTGC	CTCCCTGGAT	GCCAAGACCT	CTAGCCGCTT	GGGCGTCTCT	ACCGTGGCGT	420
	ACTACCTGTG	GACCACTTTC	ATGGCTGTCA	TCGTGGGCAT	CTTCATGGTC	TCCATCATCC	480
	ACCCAGGCAG	CGCGGCCAG	AAGGAGACCA	CGGAGCAGAG	TGGGAAGCCC	ATCATGAGCT	540
	CAGCCGATGC	CCTGTTGGAC	CTCATCCGGA	ACATGTTCCC	AGCCAACCTA	GTAGAAGCCA	600
	CATTCAAACA	GTACCGCACC	AAGACCAACC	CAGTTGTCAA	GTCCCCCAAG	GTGGCACCAG	660
75	AGGAGGCCCC	TCTCTGGCGG	ATCCTCATCT	ACGGGGTCCA	GGAGGAGAAT	GGCTCCCATG	720
	TGCAGAACTT	CGCCCTGGAC	CTGACCCCGC	CGCCGAGGT	CGTTTACAAG	TCAGAGCCGG	780
	GCACCAAGCA	TGGCATGAAT	GTGCTGGGCA	TCGTCTTCTT	CTCTGCCACC	ATGGGGCATCA	840
	TGCTGGGCGG	CATGGGTGAC	AGCGGGGCCC	CCCTGGTTCAG	CTTCTGCCAG	TGCTTCAATG	900
	AGTCGGTCAT	GAAGATGCTG	GCGGTGGCTG	TGTGGTATTT	CCCCTTCGGC	ATTGTGTTCC	960
80	TCAATGCGGG	TAAGATCCTG	GAGATGGACG	ACCCAGGGC	CGTCGGCAAG	AAGCTGGGCT	1020
	TCTACTCAGT	CACCGTGGTG	TGCGGGCTGG	TGCTCCACGG	GCTCTTTATC	CTGCCCTTGC	1080
	TCTACTTCTT	CATCACCAG	AAGAATCCCA	TCGTCTTCAT	CGCGGCATC	CTGCAGGCTC	1140
	TGCTCATCGC	GCTGGCCACC	TCTTCCAGCT	CAGCCACACT	GCCCCATACC	TTCAAGTGCC	1200
	TGCTGGAGAA	CAACCATC	GACCGGCGCA	TCGCTCGCTT	CGTGCTGCCC	GTGGGTGCCA	1260
	CCATCAACAT	GGACGGCACT	GCGCTCTACG	AGGCTGTGGC	CGCCATCTTC	ATCGCCACAG	1320

5 TCAACAACTA CGAGCTGGAC TTTGGCCAGA TCATACCAT CAGTATCACA GCCACTGCAG 1380
 CCAGCATTTGG GGCAGCTGGC ATCCCCCAGG CCGGCCTCGT CACCATGGTC ATCGTGCTCA 1440
 CCTCCGTGGG ACTGCCACC GATGACATCA CCTCATCAT TGCCGTGAC TGGGCTCTGG 1500
 ACCGTTTCCG CACCATGATT AACGTGCTGG GTGATGCGCT GGCAGCGGGG ATCATGGCCC 1560
 ATATATGTCG GAAGGATTTT GCCCGGGACA CAGGCACCGA GAAACTGCTG CCCTGCGAGA 1620
 CCAAGCCAGT GAGCCTCCAG GAGATCGTGG CAGCCACGCA GAATGGCTGT GTGAAGAGTG 1680
 TAGCCGAGGC CTCCGAGCTC ACCCTGGGCC CCACCTGCCC CCACCACGTC CCCGTCAAG 1740
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 AGCTGGAGAC CAATGTCTGA GCCTGCGGAG CTGCAGGGGC AGGCGAGGCC TCCAGGGGCA 1860
 10 GGGTCTTGAG GCAGGAACCT GACTCTCCA CCCTCTGAG CAGCCGGCAG GGGCCAGGAT 1920
 CACACATTCT TCTCACCCTT GAGAGGCTGG AATTAACCCC GCTTGACGGA AAATGTATCT 1980
 CAGAGAAGGG AAAGGCTGCA TGGGGGAGCC CCATCCAGGG AGTGTATGGC CCGGCATTGC 2040
 CTGAGGCCCC GCTGTGACAG TTTCCCGGT GTGAGCCCGG TGAGGGCGGC AGGCAGGGGT 2100
 TATCCGGCCC CACTTCTCTG ATGACAGACT TGAGGCTCTG AGAGCTGAAA ACACTTGTCT 2160
 15 AAGGTCTCAC GTTAAAGTCA AGACACTAAC TCAAATCTTT CAAGCCCGC CTCTCTCTT 2220
 GGAGGACAGG GCAGCTGCA GCTGTGTCCA GGGCCAGGCC CCACCCATA ACAGGTGGCC 2280
 TCAGCCACAC AGTTCTCCCC AAGGGGAGCA GCCCAGGGCC AAGCCCGCT GCCTTCCCCA 2340
 GGCCACAGTG CGTCCAGTCT CTTGTCTTGC CACGTGTCTT TTGCAAGCT CTTTGGATGT 2400
 20 GGAGACAGAT GTCTTTACTA GAGCTGAAAG GCCCCCTTGA CACATCCAGG CCAACTCCC 2460
 ATGGAATAGG TAGGCAAGCC AGGACTCCGG GAAGGAGGTG CAGCCAGGAT GCTCTGGTGG 2520
 AGCTGCCGAT GGGGCCCTGG TGTGAGAACT CCCCAGAGC CTGTGCTCC AAGTGGAGTG 2580
 AGGTTTTCTA TTCTTTCTG TGTTCGCAA TTCTAGTTTA ACTAATAAAA GGTATTTTGT 2640
 TTTTCAAAAA AAAAAAAAAA AAA 2663

25 Seq ID NO: C118 DNA Sequence
 Nucleic Acid Accession #: NM_005689
 Coding sequence: 278..2806

30 1 11 21 31 41 51
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 GTACGTGCCC TGCGTGAGTG CGTGGCGGCG GCGCGTGCGC TAGGGGAGTG GCGCGTGAGG 120
 CCTGGTCCAC GTGCGTCCCT TCCCGGGAGC CCGCAGCTT GGCGCCAGC GGCTACGTGA 180
 35 GCCAAGGCAC CCGGATGTCC GCGCCCTCT CCGAGTGACA AGTCCCGGCC TCCGGTCCCG 240
 CAGTGCCCGC AGCTCGGGC GCGTCCACG CATTGCCATG GTGACTGTGG GCAACTACTG 300
 CGAGGCCGAA GGGCCCGTGG GTCCGGCCTG GATGAGGAT GGCCTGAGTC CCGTCTCTT 360
 CTTACGCTC GTGCCCTCGA CGCGGATGGC TCTAGGACT CTGGCCTTGG TGCTGGCTCT 420
 TCCTTGAGCA CGCCGGGAGC GGGCCCGTGG TGCTGATTCG CTGTCTTGGG GGGCCGGCCC 480
 40 TCGCATCTCT CCTACGTGC TGCACTGCT TCTGGCCACA CTTAGGCGG CGCTGCCCT 540
 GGGCCGGCTG GCTGGCCGGG TGGCACTGCG CCGGGGGGCC CCACTGCCAA GCTATCTACT 600
 TCTGGCTTCC GTGCTGGAGA GTCTGGCCGG CGCTGTGGC CTGTGGCTGC TTGTCTGGA 660
 GCGGAGCCAG GCACGGCAGC GTCTGGCAAT GGGCATCTGG ATCAAGTTCA GGCACAGCCC 720
 TGGTCTCTCG CTCCTCTGGA CTGTGGCGTT TGCACTGAG AACTTGGCCC TGGTGTCTG 780
 45 GAACAGCCCA CAGTGGTGGT GGGCAAGGGC AGACTTGGGC CAACAGGTTA AGTTTACGCT 840
 GTGGGTGCTG CGGTATGTGG TCTCTGGAGG GCTGTTTGTG CTGGGTCTCT GGGCCCTGG 900
 ACTTCGTCCC CAGTCCCTATA CATTGCAGGT TCATGAAGAG GACCAAGATG TGGAAAGGAG 960
 CCAGGTTCCG TCAGCAGCCC AACAGTCTAC CTGGCGAGAT TTTGGCAGGA AGCTCCGCCT 1020
 CCTGAGTGGC TACCTGTGGC CTCGAGGGAG TCCAGCTCTG CAGCTGTGGG TGCTCATCTG 1080
 50 CCTGGGGCTC ATGGGTTTGG AACGGGCACT CAATGTGTTG GTGCCTATAT TCTATAGGAA 1140
 CATTGTGAAC TTGCTGACTG AGAAGGCACC TTGGAACCTC CTGGCCTGGA CTGTACCAG 1200
 TTACGTCTTC CTCAGTTTCC TCCAGGGGGG TGGCACTGGC AGTACAGGCT TCGTGAGCAA 1260
 CCTGCGCAC TTCCTGTGGA TCCGGGTGCA GCAGTTACG TCTCGCGGGG TGGAGCTGCT 1320
 CATCTTCTCC CACCTGCACG AGCTCTCACT GCGCTGGCAC CTGGGGCGCC GCACAGGGGA 1380
 55 GGTGCTGCGG ATCGCGGATC GGGGCACATC CAGTGTACCA GGGCTGTCTA GCTACCTGGT 1440
 GTTCAATGTC ATCCCCACGC TGGCCGACAT CATCATTTGG ATCATCTACT TCAGCATGTT 1500
 CTTCAACGCC TGGTTTGGCC TCATTGTGTT CCTGTGCATG AGTCTTTACC TCACCCTGAC 1560
 CATTGTGGTC ACTGAGTGGG GAACCAAGTT TCGTCGTGCT ATGAACACAC AGGAGAACGC 1620
 TACCCGGGCA CGAGCAGTGG ACTCTCTGCT AAACCTCGAG ACGGTGAAGT ATTACAACGC 1680
 CGAGAGTTAC GAAGTGGAAC GCTATCGAGA GGCCATCATC AAATATCAGG GTTTGGAGTG 1740
 60 GAAGTCGAGC GACTCACTGG TTTTACTAAA TCAGACCCAG AACCTGGTGA TTGGGCTCGG 1800
 GCTCCTCGCC GGCTCCCTGC TTTGCGCATA CTTTGTCACT GAGCAGAAGC TACAGGTTGG 1860
 GGACTATGTG CTCCTTGGCA CCTACATTAT CCAGCTGTAC ATGCCCTTCA ATTGGTTTGG 1920
 CACCTACTAC AGGATGATCC AGACCAACTT CATTGACATG GAGAACATGT TTGACTTGCT 1980
 65 GAAAGAGGAG ACAGAAGTGA AGGACCTTCC TGGAGCAGGG CCCCTTCGCT TTCAGAAGGG 2040
 CCGTATTGAG TTTGAGAACG TGCATTTCAG CTATGCCGAT GGGCGGGAGA CTCTGCAGGA 2100
 CGTGTCTTTC ACTGTGATGC CTGGACAGAC ACTTGCCCTG GTGGGCCCAT CTGGGGCAGG 2160
 GAAGAGCACA ATTTTGGCGC TGCTGTTTCG CTTCTACGAC ATCAGCTCTG GCTGCATCCG 2220
 AATAGATGGG CAGGACATT CACAGGTGAC CCAGGCCTCT CTCGGTCTC ACATTGGAGT 2280
 70 TGTGCCCCAA GACACTGTCC TCTTTAATGA CACCATCGCC GACAATATCC GTTACGGCCG 2340
 TGTACAGCT GGAATGATG AGGTGGAGGC TGCTGCTCAG GCTGCAGGCA TCCATGATGC 2400
 CATTATGGCT TTCTCTGAAG GGTACAGGAC ACAGGTGGGC GAGCGGGGAC TGAAGCTGAG 2460
 CGGCGGGGAG AAGCAGCGCG TCGCCATTGC CCGCACCATC CTCAGGCTC CGGGCATCAT 2520
 TCTGCTGGAT GAGGCAACGT CAGCGCTGGA TACATCTAAT GAGAGGGCCA TCCAGGCTTC 2580
 75 TCTGGCCAAA GTCTGTGCCA ACCGCACCAC CATCGTAGTG GCACACAGGC TCTCAACTGT 2640
 GGTCAATGCT GACCATGATC TCGTCAATCA GGATGGCTGC ATCGTGGAGA GGGGACGACA 2700
 CGAGGCTCTG TTGTCCCGAG GTGGGGTGTA TGCTGACATG TGGCAGCTGC AGCAGGGACA 2760
 GGAAGAAACC TCTGAAGACA CTAAGCCTCA GACCATGGAA CGGTGACAAA AGTTTGGCCA 2820
 CTTCCCTCTC AAAGACTAAC CCAGAAGGGA ATAAGATGTG TCTCCTTTCC CTGGCTTATT 2880
 80 TCATCTGGT CTGGGGTAT GGTGCTAGCT ATGGTAAGGG AAAGGAGCCT TTCCGAAAAA 2940
 CATCTTTTGG GGAATAAAAA ATGTGGACTG TGAAAAAAA AAAAAAAA AAA 2993

Seq ID NO: C119 DNA Sequence
 Nucleic Acid Accession #: NM_000676
 Coding sequence: 333..1331

1	11	21	31	41	51	
5	GGGCAATTG	TTAGTTATCC	GCCGCCACCA	AGACGCGGCA	CGGCGCCTGG	ACCGGAGGGG 60
	CCCCGCGCG	GCGCGAAGCT	TGGGCTCGGG	CGAGTGGGTG	GTGCTCCGCC	CAGCCCGAGA 120
	CGGGCGGGCG	CGCGGGCCAA	TGGGTGCGCG	CTCTTGCCCG	CGGGGGGGCC	CGACCCGTGG 180
	GTCCCGGCCA	CCAGCGCCCC	AGCCCCGAGG	CTCAGAAGCG	GCAGGCGGAG	GCGCGGTCCG 240
	GGCGCTATGG	CCATGCCCGG	CGGGTCTCAC	GCGGCTGCCC	CTCGCCCGGC	GCGCCTTCGG 300
10	TAGGGGGCGC	CCGGGGCCCA	GCTGGCCCCG	CCATGCTGCT	GGAGACACAG	GACGCGCTGT 360
	ACGTGGCGCT	GGAGCTGGTC	ATCGCCGCGC	TTTCGGTGCG	GGGCAACGTG	CTGGTGTGCG 420
	CCGCGGTGGG	CACGGCGAAC	ACTCTGCAGA	CGCCACCAAA	CTACTTCCTG	GTGTCCCTGG 480
	CTGCGGCCGA	CGTGGCCGTG	GGGCTCTTCG	CCATCCCTTT	TGCCATCACC	ATCAGCCTGG 540
	GCTTCTGCAC	TGACTTCTAC	GGTGCCTCT	TCCTCGCCTG	CTTCGTGCTG	GTGCTCACGC 600
	AGAGCTCCAT	CTTCAGCCTT	CTGGCCGTGG	CAGTCGACAG	ATACCTGGCC	ATCTGTGTCC 660
15	CGCTCAGGTA	TAAAAGTTTG	GTACCGGGGA	CCCAGACAAG	AGGGGTCAAT	GCTGTCTCT 720
	GGGTCTTGTC	CTTTGGCATC	GGATTGACTC	CATTCTCTGG	GTGGAACAGT	AAAGACAGTG 780
	CCACCAACAA	CTGCACAGAA	CCCTGGGATG	GAACCACGAA	TGAAAGCTGC	TGCCTTGTGA 840
	AGTGTCTCTT	TGAGAAATGTG	GTCCCATAGA	GCTACATGGT	ATATTTCAAT	TTCTTTGGGT 900
20	GTGTTCTGCC	CCCACTGCTT	ATAATGCTGG	TGATCTACAT	TAAGATCTTC	CTGGTGGCCT 960
	GCAGGCAGCT	TCAGCGCACT	GAGCTGATGG	ACCACCTGAG	GACCACCTTC	CAGCGGGAGA 1020
	TCCATGCAGC	CAAGTCACTG	GCCATGATTG	TGGGGATTTT	TGCCCTGTGC	TGGTTACCTG 1080
	TGCATGCTGT	TAACTGTGTC	ACTCTTTTCC	AGCCAGCTCA	GGGTAAAAAT	AAGCCCAAGT 1140
	GGCAATGAA	TATGGCCATT	CTTCTGTGAC	ATGCCAATTC	AGTTGTCAAT	CCCATGTGCT 1200
25	ATGCTTACCG	GAACCGAGAC	TTCCGCTACA	CTTTTCACAA	AATTATCTCC	AGGTATCTTC 1260
	TCTGCCAAGC	AGATGTCAAG	AGTGGGAATG	GTGAGGCTGG	GGTACAGCCT	GCTCTCGGTG 1320
	TGGGCTATG	ATCTAGGCTC	TCCCTCTTTC	CAGGAGAAGA	TACAAATCCA	CAAGAAACAA 1380
	AGAGGACACG	GCTGGTTTTC	ATTGTGAAAG	ATAGCTACAC	CTCACAAGGA	AATGGAAGTC 1440
	CTCTCTTGAG	CACCTTCCCT	GAGCTACCAC	GTATCTAGCT	AATATGTATG	TGTCAGTAGT 1500
30	AGGCTCCAAG	GATTGACAAA	TATATTTATG	ATCTATTTCAG	CTGCTTTTAC	TGTGTGGATT 1560
	ATGCCAACAG	CTTGAATGGA	TTCTAACAGA	CTCTTTTGTT	TTTAAAGTTC	TGCCTTGTGT 1620
	ATGGTGGAAA	ATTACTGAAA	CTATTTTACT	GTGAAACAGT	GTGAACATAT	ATAATGCAAA 1680
	TACTTTTAA	CTTAGAGGCA	ATGGAATAAT	AAAAGTTGAC	TGTACTAAAA	ATG 1733

Seq ID NO: C120 DNA Sequence
Nucleic Acid Accession #: NM_052932
Coding sequence: 217..786

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40	CCCAGCCCCG	CCCCGCCGCC	CCGGCTGCGC	ACGCGAGCGC	CCCTCCAGGC	CCCGCTCCTG 60
	CGCCCTATTT	GGTCATTTCG	GGGCAAGCG	GCGGGAGGGG	AAACGTGCGC	GGCCGAAGGG 120
	GAAGCGGAGC	CGCGCCCGGC	TGCGCAGAGG	AGCCGCTCTC	GCGCCGCCCA	CCTCGGCTGG 180
	GAGCCACAGA	GGCTGCCGCA	TCCTGCCCTC	GGAAACATGG	GACTCGGCGC	GCGAGGTGCT 240
45	TGGGCGCGCG	TGCTCTGGGG	GACGCTGCAG	GTGCTAGCGC	TGCTGGGGGC	CGCCCATGAA 300
	AGCGCAGCCA	TGGCGGAGAC	TCCTCAACAT	GTGCCCTCTG	ACCATACAAA	TGAAACTTCC 360
	AACAGTACTG	TGAAACCCAC	AACTTCAGTT	GCCTCAGACT	CCAGTAATAC	AACGGTCAAC 420
	ACCATGAAAC	CTACAGCGGC	ATCTAATAFA	ACAACCCAG	GGATGGTCTC	AACAATATG 480
	ACTTCTACCA	CCTTAAAGTC	TACACCCAAA	ACAACAAGTG	TTTCACAGAA	CACATCTCAG 540
50	ATATCAACAT	CCACAATGAC	CGTAACCCAC	AATAGTTCAG	TGACATCTGC	TGCTTCATCA 600
	GTAACAATCA	CAACAATAT	GCATTCTGAA	GCAAGAAAG	GATCAAAAT	TGATACTGGG 660
	AGCTTTGTTG	GTGGTATTGT	ATTAACGCTG	GGAGTTTAT	CTATTCTTTA	CATTGGATGC 720
	AAAATGTATT	ACTCAAGAAG	AGGCATTTCG	TATCGAACCA	TAGATGAACA	TGATGCCATC 780
	ATTTAAGGAA	ATCCATGGAC	CAAGGATGGA	ATACAGATTG	ATGCTGCCCT	ATCAATTAAT 840
55	TTTGGTTTAT	TAATAGTTTA	AAACAATATT	CTCTTTTGA	AAATAGTATA	AACAGGCCAT 900
	GCATATAATG	TACAGTGTAT	TACGTAAATA	TGTAAGATT	CTTCAAGGTA	ACAAGGGTTT 960
	GGGTTTGA	ATAAACATCT	GGATCTTATA	GACCGTTTAT	ACAATGGTTT	TAGCAAGTTC 1020
	ATAGTAAGAC	AAACAAGTCC	TATCTTTTTT	TTTTTGGCTG	GGGTGGGGGC	ATTGGTCACA 1080
	TATGACCAGT	AATTGAAAGA	CGTCATCACT	GAAAGACAGA	ATGCCATCTG	GGCATAACAA 1140
60	TAAGAAGTTT	GTACACGAC	TCAGGATTTT	GGGTATCTTT	TGTAGCTCAC	ATAAAGAACT 1200
	TCAGTGCTTT	TCAGAGCTGG	ATATATCTTA	ATTACTAATG	CCACACAGAA	ATTATACAAT 1260
	CAAAGTAGAT	CTGAAGCATA	ATTTAAGAAA	AACATCAACA	TTTTTTGTGC	TTTAACTGT 1320
	AGTAGTTGGT	CTAGAAACAA	AATACTCCAA	GAAAAAGAAA	ATTTTCAAAT	AAAACCCAAA 1380
	ATAATAGCTT	TGCTTAGCCC	TGTTAGGGAT	CCATTGGAGC	ATTAAGGAGC	ACATATTTTT 1440
65	ATTAACCTCT	TTTGAGCTTT	CAATGTTGAT	GTAATTTTTG	TTCTCTGTGT	AATTTAGGTA 1500
	AACCTGCAGT	TTTAAACATA	TAATGTTTAA	AAGACTTAGT	TGTCAGTATT	AAATAATCCT 1560
	GGCATTATAG	GGAAAAAACC	TCCTAGAAGT	TAGATTATTT	GCTACTGTGA	GAATATTGTC 1620
	ACCACTGGAA	GTTACTTTAG	TTTCAATTAAT	TTTAATTTTA	TATTTTGTGA	ATATTTTAAG 1680
	AACCTGTAGAG	CTGCTTTCAA	TATCTAGAAA	TTTTTAATTG	AGTGTAACAA	CACCTAACTT 1740
70	TAAGAAAAAG	AACCGCTGTG	ATGATTTTCA	AAAGAACATT	TAGAATTCTA	TAGAGTCAAA 1800
	ACTATAGCGT	AATGCTGTGT	TTATTAAGCC	AGGGATTGTG	GGACTTCCCC	CAGGCAACTA 1860
	AACCTGCAGG	ATGAAAATGC	TATATTTTCT	TTTCATGCACT	GTGCATATTA	CTCAGATTTG 1920
	GGGAAATGAC	ATTTTTATAC	TAAACCAAAC	ACCAAAATAT	TTTAGAATAA	ATTCTTAGAA 1980
	AGTTTTGAGA	GGAATTTTTA	GAGAGGACAT	TTCTCTCTTC	CTGATTGGGA	TATTCCTCA 2040
75	AATCCCTCCT	CTTACTCCAT	GCTGAAGGAG	AAGTACTCTC	AGATGCATTA	TGTTAATGGA 2100
	GAGAAAAAGC	ACAGTATTGT	AGAGACACCA	ATATTAGCTA	ATGTATTTTG	GAGTGTTTTC 2160
	CATTTTACAG	TTTATATTTCC	AGCACTCAAA	ACTCAGGGTC	AAGTTTAAAC	AAAAGAGGTA 2220
	TGTAGTCACA	GTAATACTA	AGATGGCATT	TCTATCTCAG	AGGGCCAAAG	TGAATCACAC 2280
	CAGTTTCTGA	AGGTCTTAAA	AATAGCTCAG	ATGTCTTAAT	GAACATGCAC	CTACATTTAA 2340
80	TAGGAGTACA	ATAAACTGT	TGTCAGCTTT	TGTTTTACAG	AGAACGCTAG	ATATTAAAGAA 2400
	TTTTGAAATG	GATCATTTCT	ACTTGCTGTG	CATTTTAAAC	AATAATCTGA	TGAATATAGA 2460
	AAAAAATGAT	CCAAAATATG	GATATGATTG	GATGTATGTA	ACACATACAT	GGAGTATGGA 2520
	GGAAATTTTC	TGAAAAATAC	ATTTAGATTA	GTTTAGTTTG	AAGGAGAGGT	GGGCTGATGG 2580
	CTGAGTTGTA	TGTTACTAAC	TGGGCCCTGA	CTGGTTGTGC	AACCATTGCT	TCATTTCTTT 2640
	GCAAAATGTA	GTTAAGATAT	ACTTTATTCT	AATGAAGGCC	TTTTAAATTT	GTCCAGTGCA 2700

TTCTTGGTAT TTCACTACTT CAAGTCAGTC AGAACTTCGT AGACCGACCT GAAGTTTCTT 2760
 TTTGAATACT TGTTCCTTTA GCACCTTGAA GATAGAAAAA CCACTTTTFA AGTACTAAGT 2820
 CATCATTTGC CTTGAAAGTT TCCTCTGCAT TGGGTTTGAA GTAGTTTAGT TATGCTTTTT 2880
 TCTCTGTATG TAAGTAGTAT AATTTGTTAC TTTCAAATAC CCGTACTTTG AATGTAGGTT 2940
 TTTTGTGTTG TGTATCTAT AAAAAATTGAG GGAAATGGTT ATGCAAAAAA ATATTTTGCT 3000
 TTGGACCATA TTTCTTAAGC ATAAAAAAT GCTCAGTTTT GCTTGCAATC CTTGAGAATG 3060
 TATTTATCTG AAGATCAAAA CAAACAATCC AGATGTATAA GTACTAGGCA GAAGCCAATT 3120
 TTAATAATTC CTTGAATAAT CCATGAAAGG AATAATTCAA ATACAGATAA ACAGAGTTGG 3180
 CAGTATATTA TAGTGATAAT TTTGTATTTT CAAMAAAAAA AAAGTTAAAC TCTTCTTTTC 3240
 TTTTATTAT AATGACCAGC TTTTGGTATT TCATTGTTAC CAAGTTCTAT TTTTAGATAA 3300
 AATTGTTCTC CTCTAAAAA AAAAAAATA AAAAAAAA 3338

Seq ID NO: C121 DNA Sequence
 Nucleic Acid Accession #: NM_004195
 Coding sequence: 1..726

1 11 21 31 41 51
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 GCGCTCAGCC TGGGTGAGCG CCCACCGGGG GGTCCCGGGT GCGGCCTGGG GCGCCTCCTG 120
 CTTGGGACGG GAACGGACGC GCGCTGCTGC CGGTTTACAC CGACGCGCTG CTGCCCGCAT 180
 TACCCGGGCG AGGAGTGCTG TTCGAGTGG GACTGCATGT GTGTCCAGCC TGAATTCAC 240
 TCGGAGAGCC CTTGCTGCAC GACCTGCCGG CACCACCCTT GTCCCCCAGG CCAGGGGGTA 300
 CAGTCCCAGG GGAATTCAG TTTTGGCTTC CAGTGTATCG ACTGTGCCCT GGGGACCTTC 360
 TCCGGGGGCG ACGAAGGCCA CTGCAACCTT TGGACAGACT GCACCCAGTT CGGGTTTCTC 420
 ACTGTGTTCC CTGGGACCAA GACCCACAAC GCTGTGTGCG TCCAGGGGTC CCGCCGGGCA 480
 GAGCCGCTTG GGTGGCTGAC CGTCGTCTC CTGGCGTGG CCGCTGCGT CCTCTCTCTG 540
 ACCTCGGCC AGCTTGGACT GCACATCTGG CAGCTGAGGA GTCACTGCAT GTGGCCCCGA 600
 GAGACCCAGC TGTGCTGGGA GGTGCGCGG TCGACCGAAG ACGCCAGAAG CTGCCAGTTC 660
 CCGAGGAAG AGCGGGGCGA GCGATCGGCA GAGGAGAAGG GCGGCTGGG AGACCTGTGG 720
 GTGTGA 726

Seq ID NO: C122 DNA Sequence
 Nucleic Acid Accession #: AK091896.1
 Coding sequence: 28..1572

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 ATCGCTTCTC TGGGGCCAC GCTGCTGGAC CTGCGCTGTC AGACGCACAG CTGCTGCCC 180
 CAGATCTCCT GGGTCTTCTT CTGCGACAG CTCTGCTCTC TGCTGGGCGA CGCCCTCGGG 240
 GGGCTCTTCA AAAGGACCTT GGGCCAGTCA CTATGGGCCC TGTTCACTCT CTCTCTGGCC 300
 ATCTCCCTGG TGTGTGCGT CATCCCTTC TGCCGCGACG TGAAGTGCT GGCCTCAGTC 360
 ATGGCGCTGG CGGGCTTGGC CATGGGCTGC ATCGACACCG TGGCCACAT GCAGCTGGTA 420
 AGGATGTACC AGAAGGACTT GGCCGTCTTC CTCCAGGTGC TCCATTCTT CTGTTGGCTT 480
 GGTGCTCTGC TGAAGCCCTT TATGCTGAC CCTTCTCTGT CTGAGGCCAA CTGCTTGCTT 540
 GCCAATAGCA CGGCCAACAC CACCTCCCGA GGCCACCTGT TCCATGTCTC CAGGGTGCTG 600
 GGCCAGCACC ACGTAGATGC CAAGCCCTTG TCCAACCAGA CGTTCCAGG GCTGACTCCA 660
 AAGGACGGGG CAGCGACCCG AGTGCTCTAT GCCTTCTGGA TCATGGCCCT CATCGATCTT 720
 CCAGTGCCCA TGGCTGTGCT GATGCTGCTG TCCAAGGAGC GGCTGTGAC CTGCTGTCCC 780
 CAGAGGAGG CCGTCTTCTT GTCTGCTGAT GAGCTTGCTT TGGAGACACA GCCTCCTGAG 840
 AAGGAAGATG CCTCTCACT GCCCCCAAG TTTCACTCAC ACCTAGGGCA TGAGGACCTG 900
 TTCAGCTGCT GCCAAAGGAA GAACCTCAGA GGAGCCCTT ATCTCTCTT TGCCATCCAC 960
 ATCACGGGCG CCTTGGTACT GTTCATGACG GATGGGTTGA CGGGTGCTTA TTCCGCTTTC 1020
 GTGTACAGCT ATGCTGTGGA GAAGCCCTTG TCTGTGGGAC ACAAGGTGGC TGGCTACTCT 1080
 CCCAGCTCTT TCTGGGGCTT CATCACTAG GGCCTGGTCC TCTCCATTCC CATATCTCTA 1140
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 GTGCTGCTTA TTTTCTCTTA CAACGTCGTC TTCCTGTTCG TGGGGACGGC AAGCCTGGGC 1260
 CTGTTTCTCA GCAGCACCTT CCCAGCATG CTGGCCTACA CGGAGGACTC GCTGCAGTAC 1320
 AAAGGCTGTG CAACACAGT GCTGGTGACA GGGGCAGGAG TTGGCGAGAT GGTGCTGCAG 1380
 ATGCTGGTTG GTTGTATATT CCAGGCTCAG GGCAGCTATA GTTTCTTGGT CTGTGGCGTG 1440
 ATCTTTGGTT GTCTGGCTTT TACCTTCTAT ATCTTGCTCC TGTTTTCCA CAGGATGCAC 1500
 CCTGGACTCC CATCAGTTCC TACCAGAGC AGATCAATTG GAATGGAAAA CTCTGAGTGC 1560
 TACCAGAGGT AAACTGGGT GAAGAAGGCA AGAGAAGACT TTCAGCTCTT TGATCACCAG 1620
 CACGACCATA CTGTTTCAGA AAGCTGGGTG GTGGTGGAGG CGCTCTCTCA ATGGCTATTC 1680
 AAGCTTCTCT CACTAAAACT TGGTTGGGTA GAGGAAATTA AATTGAGTCC TGGTACCTGG 1740
 TCAAAATCAT TAGAAGTTTA CTTGGCTTCT CAAGTTATCT TCTTCCCTGG TTCAGACTGT 1800
 TGGTAAGAGC TGTCAGATA CCCAGATGGG AAGGAAGGAG ACAGCCGCGC GCTTCACTCC 1860
 ATTTGTCACT TCATGCATGG ACCATACTCT GGGTTTGAGA TCATTCTTCA TTGAAGTTTG 1920
 TAAAAATAGG TTGAAATTGT AAAGCTCCAT GATCACTGCT ATATGTAGAT ATATTTCAAT 1980
 TTAAGCAAAA CAAAGCTGCA GTTATTCCTT GGCATGCTCA AAGGATTTTC GTGCTTTTCA 2040
 CTTAATAGTC AAGATCTCTT TAAATCTCTG CTGCAGATAT CAATAGCTTA TCTATATTCT 2100
 CAAACACCAA AAGGAAAAGT TGAATCTTGC TCTCTTTGGT ATACTAATGT AGTGGTATGC 2160
 TAAGCTGGCT CATACCACT TAGAAAAGCT GATTGTAAAA TTTTCATTTT GACAGCTGGT 2220
 TATTAAATGC AGCCATTATT AAAAATCAAA TCATACAAAC TTATAATTAA ATCAATTACA 2280
 TTTAAACAA AGGTAATAAA TATTCAAAGC ATATCACTTC CT 2322

Seq ID NO: C123 DNA Sequence
 Nucleic Acid Accession #: NM_002203.2
 Coding sequence: 43..3588

1 11 21 31 41 51
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	GGGGCCGCGC	CGCTGCCGCT	GCTGCTGGTG	TAGCGCTCA	GTCAGGGCAT	TTTAAATTGT	120
	TGTTTGGGCT	ACAAATGTTGG	TCTCCAGAA	GCAAAAATAT	TTTCCGGTCC	TTCAGTGAA	180
5	CAGTTTGGGT	ATGCAGTGCA	GCAGTTTATA	AATCCAAAAG	GCAACTGGTT	ACTGGTTGGT	240
	TCACCCCTGGA	GTGGCTTTCC	TGAGAACCGA	ATGGGAGATG	TGTATAAATG	TCCTGTTGAC	300
	CTATCCACTG	CCACATGTGA	AAAACTAAAT	TGCAAACTT	CAACAAGCAT	TCCAATGTT	360
	ACTGAGATGA	AAACCAACAT	GAGCCTCGGC	TTGATCCTCA	CCAGGAACAT	GGGAACCTGA	420
	GGTTTTCTCA	CATGTGGTCC	TCTGTGGGCA	CAGCAATGTG	GGAAATCAGTA	TTACACAACG	480
10	GGTGTTGTTT	CTGACATCAG	TCCCTGATTTT	CAGCTCTCAG	CCAGCTTCTC	ACCTGCAACT	540
	CAGCCCTGCC	CTTCCTCAT	AGATGTTGTG	GTTGTGTGTG	ATGAATCAAA	TAGTATTTAT	600
	CCTTGGGATG	CAGTAAAGAA	TTTTTTGGAA	AAATTGTATC	AAGGCCTTGA	TATAGGCCCC	660
	ACAAAGACAC	AGGTGGGGTT	AATTGAGTAT	GCCAATAATC	CAAGAGTTGT	GTTTAACTTG	720
	AACACATATA	AAACCAAGA	AGAAATGATT	GTAGCAACAT	CCCAGACATC	CCAATATGGT	780
15	GGGGACCTCA	CAAAACACAT	CGGAGCAATT	CAATATGCAA	GAAAATATGC	CTATTGACGA	840
	GCTTCTGGTG	CGGCACGAAG	TGCTACGAAA	GTAATGGTAG	TGTAACTGA	CGGTGAATCA	900
	CATGATGGTT	CAATGTTGAA	AGCTGTGATT	GATCAATGCA	ACCATGACAA	TATACTGAGG	960
	TTTGGCATAG	CAGTTCCTGG	GTACTTAAAC	AGAAAACGCC	TTGATACTAA	AAATTTAATA	1020
	AAAGAAATAA	AAGCGATCGC	TAGTATTTCA	ACAGAAAGAT	ACTTTTTCAA	TGTGTCTGAT	1080
20	GAAGCAGCTC	TACTAGAAAA	GGCTGGGACA	TTAGGAGAAC	AAATTTTCAG	CATTGAAGGT	1140
	ACTGTTCAAG	GAGGAGACAA	CTTTCAGATG	GAAATGTGAC	AAGTGGGATT	CAGTGCAGAT	1200
	TACTCTTCTC	AAAATGATAT	TCTGATGCTG	GGTGAGTGG	GAGCTTTTGG	CTGGAGTGGG	1260
	ACCATTTGCC	AGAAGACATC	TCAATGGCCAT	TTGATCTTTC	CTAAACAAGC	CTTTGACCAA	1320
	ATTCTGCAGG	ACAGAAATCA	CAGTTTCATAT	TTAGGTTACT	CTGTGGCTGC	AATTTCTACT	1380
25	GGAGAAAGCA	CTCATTGTTG	TGCTGGTGCT	CCTCGGGCAA	ATTATACCGG	CCAGATAGTG	1440
	CTATATAGTG	TGAATGAGAA	TGGCAATATC	ACGGTTATTC	AGGCTCACCG	AGGTGACCAG	1500
	ATTGGCTCCT	ATTTTGGTAG	TGTGCTGTGT	TCAGTTGATG	TGGATAAAGA	CACCATTACA	1560
	GACGTGCTCT	TGGTAGGTGC	ACCAATGTAC	ATGAGTGACC	TAAAGAAAGA	GGAGGAAGA	1620
	GTCCTACCTG	TTACTATCAA	AAAGGCCATT	TTGGGTCAGC	ACCAATTTCT	TGAAGGCCCC	1680
30	GAGGGCATTG	AAAACACTCG	ATTTGGTTCA	GCAATTGACG	CTCTTTCAGA	CATCAACATG	1740
	GATGGCTTTA	ATGATGTGAT	TGTTGGTTCA	CCACTAGAAA	ATCAGAATTC	TGGAGCTGTA	1800
	TACATTTTACA	ATGGTCTATC	GGGCACATATC	CGCACAAAGT	ATTCCCAGAA	AATCTTGGGA	1860
	TCCGATGGAG	CCTTTAGGAG	CCATCTCCAG	TACTTTGGGA	GGTCTCTGGA	TGGCTATGGA	1920
	GATTTAAATG	GGGATTCATC	CACCGATGTG	TCTATTGGTG	CCTTTGGACA	AGTGGTTCAA	1980
35	CTCTGGTCCAC	AAAGTATTGC	TGATGTAGCT	ATAGAAGCTT	CATTCAACCC	AGAAAAAATC	2040
	ACTTTGGTCA	ACAAGAAATG	TCAGATAAAT	CTCAAACTCT	GCTTCAGTGC	AAAGTTTACA	2100
	CCTACTAAGC	AAAACAATCA	AGTGGCCATT	GTATATAACA	TCACACTTGA	TGCAGATGGA	2160
	TTTTCATCCA	GAGTAACCTC	CAGGGGGTTA	TTTAAAGAAA	ACAATGAAAG	GTGCCTGCAG	2220
	AAGAATATGG	TAGTAATATC	AGCACAGAGT	TGCCCGGAGC	ACATCATTTA	TATACAGGAG	2280
40	CCCTCTGATG	TTGTCAACTC	TTTGGATTG	CGTGTGGACA	TCAGTCTGGA	AAACCTGGC	2340
	ACTAGCCCTG	CCCTTGAAGC	CTATTCTGAG	ACTGCCAAGG	TCTTCAGTAT	TCCTTCCAC	2400
	AAAGACTGTG	GTGAGGATGG	ACTTTGCATT	TCTGATCTAG	TCCTAGATGT	CCGACAAATA	2460
	CCAGCTGCTC	AAGAACAACC	CTTTATTGTC	AGCAACCAAA	ACAAAAGGTT	AACATTTTCA	2520
45	GTAACACTGA	AAAAATAAAG	GGAAAGTGCA	TACAACACTG	GAATTTGTTG	TGATTTTTC	2580
	GAAAACCTGT	TTTTTGCATC	ATTCTCCCTA	CCGGTTGATG	GGACAGAAAT	AACATGCCAG	2640
	GTGGCTGCAT	CTCAGAAGTC	TGTTGCCTGC	GATGTAGGCT	ACCCTGCTTT	AAAGAGAGAA	2700
	CAACAGGTGA	CTTTTACTAT	TAACTTTGAC	TTCAATCTTC	AAAACTTCA	GAATCAGGCG	2760
	TCTCTCAGTT	TCCAGCTCTT	AAGTGAAAGC	CAAGAAGAAA	ACAAGGCTGA	TAATTTGGTC	2820
	AACCTCAAAA	TTCCTCTCCT	GTATGATGCT	GAAATTCATC	TAAACAAGATC	TACCAACATA	2880
50	AATTTTATG	AAATCTCTTC	GGATGGGAAT	GTTCCTTCAA	TCGTGCACAG	TTTTGAAGAT	2940
	GTTGGTCCAA	AATTCATCTT	CTCCCTGAAG	GTAACAACAG	GAAGTGTTC	AGTAAGCATG	3000
	GCAACTGTAA	TCATCCACAT	CCCTCAGTAT	ACCAAGAAA	AGAACCCACT	GATGTACCTA	3060
	ACTGGGGTGC	AAACAGACAA	GGCTGGTGAC	ATCAGTTGTA	ATGCAGATAT	CAATCCACTG	3120
	AAAATAGGAC	AAACATCTTC	TCTGTATCT	TTCAAAGTG	AAAATTTTCA	GCACACCAAA	3180
55	GAATTGAAC	GCAGAATGTC	TTCTGTAGT	AATGTTACCT	GCTGGTTGAA	AGACGTTTCA	3240
	ATGAAGGAG	AATACTTTGT	TAATGTGACT	ACCAGAATTT	GGAAACGGGAC	TTTCGCATCA	3300
	TCACAGTTCC	AGACAGTACA	GCTAACGGCA	GCTGCAGAAA	TCAACACCTA	TAAACCTGAG	3360
	ATATATGTGA	TTGAAGATAA	CACCTGTTACG	ATTCCTCTGA	TGATAATGAA	ACCTGATGAG	3420
	AAAGCCGAAG	TACCAACAGG	AGTTATAATA	GGAAGTATAA	TTGCTGGAAT	CCTTTTGCTG	3480
60	TTAGCTCTGG	TTGCAATTTT	ATGGAAGCTC	GGCTTCTTCA	AAAGAAAATA	TGAAAAGATG	3540
	ACCAAAAATC	CAGATGAGAT	TGATGAGACC	ACAGAGCTCA	GTAGCTGAAC	CAGCAGACCT	3600
	ACCTGCAGTG	GGAAACCGCA	GCATCCAGC	CAGGGTTTGC	TGTTTGCCTG	CATGGATTTT	3660
	TTTTTAAATC	CATATTTTTT	TTTATCATGT	CGTAGGTAAA	CTAACCTGGT	ATTTTAAAGAT	3720
	AAAACCTGAC	GCTAGTTTGG	ATGAAGAAAT	TGTGGGGGGT	GGGGGAGGTG	CGGGGGGCAG	3780
65	GTAGGGAAAT	AATAGGAAAA	ATACCTATTT	TATATGATGG	GGGAAAAAAA	GTAATCTTTA	3840
	AACTGGCTGG	CCCAGAGTTT	ACATTCTAAT	TTGCATTGTG	TCAGAAACAT	GAAATGCTTC	3900
	CAAGCATGAC	AACTTTTAAA	GAAAAATATG	ATACTCTCAG	ATTTTAAAGG	GGAAAACTGT	3960
	TCTCTTTAAA	ATATTGTGCT	TTAAACAGCA	ACTACAGAAG	TGGAAGTGCT	TGATATGTAA	4020
	GTACTTCCAC	TTGTGTATAT	TTTAATGAAT	ATTGATGTTA	ACAAGAGGGG	AAAACAAAAC	4080
70	ACAGGTTTTT	TCAATTTATG	CTGCTCATCC	AAAGTTGCCA	CAGATGATAC	TTCCAAGTGA	4140
	TAATTTTATT	TATAAACTAG	GTAATAATTT	TGTTGGTTTC	CTTTTATACC	ACGGCTGCC	4200
	CTTCCACACC	CCATCTTGCT	CTAATGATCA	AAACATGCTT	GAATAACTGA	GCTTAGAGTA	4260
	TACCTCCTAT	ATGTCCATT	AAGTTAGGAG	AGGGGGCGAT	ATAGAGACTA	AGGCACAAAA	4320
	TTTTGTTTAA	AACTCAGAA	ATAACATTTA	TGTAATAATCC	CATCTGCTAG	AAGCCCATCC	4380
75	TGTGCCAGAG	GAAGGAAAAG	GAGGAAATTT	CCTTTCTCTT	TTAGGAGGCA	CAACAGTTCT	4440
	CTTCTAGGAT	TTGTTTGGCT	GACTGGCAGT	AACCTAGTGA	ATTTTGTGAA	GATGAGTAAT	4500
	TTCTTTGGCA	ACCTTCTCTC	TCCCTTACTG	AACCACTCTC	CCACCTCTCT	TGTTGATCAT	4560
	TATTATAGAA	GCCCTCTACA	GCCTGACTTT	CTCTCCAGCG	GTCCAAAGTT	ATCCCTCTCT	4620
	TTACCCCTCA	TCCAAAGTTT	CACTCTCTTC	AGGACAGCTG	CTGTGCATTA	GATATTAGGG	4680
80	GGGAAAGTCA	TCGTGTTAAT	TTACACACTT	GCATGAATTA	CTGTATATAA	ACTCCTTAAC	4740
	TTACAGGAGC	TATTTTCATT	TAGTGCTAAA	CAAGTAAGAA	AAATAAGCTA	GAGTGAATTT	4800
	CTAAATGTTG	GAATGTTATG	GGATGTAAAC	AATGTAAAGT	AAAACACTCT	CAGGATTTCA	4860
	CCAGAAAGTTA	CAGATGAGGC	ACTGGAACCC	ACCACCAAAT	TAGCAGGTGC	ACCTTCTGTG	4920
	GCTGTCTTGT	TTCTGAAGTA	CTTTTCTTTC	CACAAGAGTG	AATTTGACCT	AGGCAAGTTT	4980
	GTTCAAAAGG	TAGATCTTGA	GATGATTTTG	TCAGATTGGG	ATAAGGCCCA	GCAATCTGCA	5040

TTTTAAACAG CACCCAGTC ACTAGGATGC AGATGGACCA CACTTTGAGA AACACCACCC 5100
 ATTTCTACTT TTTGCACCTT ATTTTCTCTG TTCCTGAGCC CCCACATTCT CTAGGAGAAA 5160
 CTTAGATTAA AATTACAGAG CACTACATAT CTAAAGCTTT GACAAGTCTT TGACCTCTAT 5220
 AAACCTCAGA GTCCCTCATTA TAAATGGGA AGACTGAGCT GGAGTTCAGC AGTGATGCTT 5280
 TTTAGTTTAA AAAGTCTATG ATCTGATCTG GACTTCTCTAT AATACAAATA CACAATCCTC 5340
 CAAGAATTG ACTTGGAAAA G 5361

Seq ID NO: C124 DNA Sequence
 Nucleic Acid Accession #: NM_031460
 Coding sequence: 103..1101

1 11 21 31 41 51
 AGCAGGCGTT TGCGAGAGGA GATACGAGCT GGACGCCTGG CCCTTCCCTC CCACCGGGTC 60
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 CGGGCGGCTC CCGAGGGCAG GGTCCGGGGC TGCGCGGTGC CCAGCACCGT GCTCCTGCTG 180
 CTCGCTTACC TGGCTTACCT GGCCTGCGG ACCGCGGTGT TCTGGACGCT GGAGGGCCGC 240
 GCGGCGCAGG ACTCCAGCGG CAGCTTCCAG CGCGACAAGT GGGAGCTGTT GCAGAACTTC 300
 ACGTGTCTGG ACCGCCCGGC GCTGGACTCG CTGATCCGGG ATGTCTGTCCA AGCATAACAA 360
 AACGGAGCCA GCCTCCTCAG CAACACCACC AGCATGGGGC GCTGGGAGCT CGTGGGCTCC 420
 TTCTTCTTTT CTGTGTCCAC CATCACACC ATTGGCTATG GCAACCTGAG CCCCAACACG 480
 ATGGCTGCCC GCCTCTTCTG CATCTTCTTT GCCCTTGTGG GGATCCCACT CAACCTCGTG 540
 GTGCTCAACC GACTGGGGCA TCTCATGCAG CAGGGAGTAA ACCACTGGGC CAGCAGGCTG 600
 GGGGGCACCT GGCAGGATCC TGACAAGGCG CGGTGGCTGG CGGGCTCTGG CGCCCTCCTC 660
 TCGGGCTCTC TGCTCTTCTT GCTGCTGCCA CCGCTGCTCT TCTCCACAT GGAGGGCTGG 720
 AGCTACACAG AGGGCTTCTA CTTCGCTTC ATCACCTCA GCACCGTGGG CTTGCGGCAC 780
 TACGTGATTG GAATGAACCC CTCCAGAGG TACCACTGT GGTACAAGAA CATGTTGTCC 840
 CTGTGGATCC TCTTTGGGAT GGCATGGCTG GCCTTGATCA TCAAACATCAT CCTCTCCCAG 900
 CTGAGAGCGC CAGGGAGGGT ATGTTCTCTG TGCCACCACA GCTCTAAGGA AGACTTCAAG 960
 TCCCAAAGCT GGAGACAGGG ACCTGACCGG GAGCCAGAGT CCCACTCCCC ACAGCAAGGA 1020
 TGCTATCCAG AGGGACCCAT GGGAAATCATA CAGCATCTGG AACCTTCTGC TCACGTGCA 1080
 GGCTGTGGCA AGGACAGCTA GTTATACTCC ATTCTTTGGT CGTCTGCTC GGTAGCAAGA 1140
 CCCTGATT TAAAGCTTGC ACATGTCCAC CCAAATAAAA GACTACATT TCCATCCACC 1200
 CTAGAGGCTG GTGTCAGCTA TATGATTAAT TCTGCCAAT AGGGTATACA GAGACATGTC 1260
 CTGGGTGACA TGGGATGTGA CTTTCGGGTG TCGGGGCAGC ATGCCCTTCT CCCCACCTTC 1320
 CTTACTTTAG CGGGCTGCAA TGCCGCCGAT ATGATGGCTG GGAGCTCTGG CAGCCATACG 1380
 GCACCATGAA GTAGCGGCAA TGTTTGAGCG GCACAATTAG ATAGGAAGAG TCTGGATCTC 1440
 TGATGATCAC AGAGCCATCC TAACAAACGG AATATCACCG ACCCTCCTTT ATGTGAGAGA 1500
 GAAATAACA TCTATGAAA 1519

Seq ID NO: C125 DNA Sequence
 Nucleic Acid Accession #: NM_004154
 Coding sequence: 309..1295

1 11 21 31 41 51
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 TGGGGCTACC TCAGGGCCCC ACAGGATGAG GGGCTGGTTT TCAGATGAGT TTTCTGCTTG 180
 CCTGTCACTT GGATAGTGT TAAAAATTTG CAAACTGCCT TCTTGTCACT GTCTTGCTCA 240
 TTCTTCATGA CACTCTGTAT ATGTCTCTCA GTTCTCTCAT CTGCTGCCTC TCCAGACTTC 300
 TGCCAGAAC TTAGCAGCGA CAGTTTCAGG CACAGAAGT ACTGGCAGCA GGGGCTGCTC 360
 CACGAGTGGG AATTTGCTCC AGCACTTCAC GGACTGCAAG CGAGGCATT GCTAACTCTT 420
 GGATAACAAG ACCTCTGCCA GAAGAACCAT GGCTTTGGAA GGCGGAGTTC AGGCTGAGGA 480
 GATGGGTGCG TCCTCAGTG AGCCCTGCCC TCCTGAACA TAGGAAACCC ACCTGGGCAG 540
 CCATGGAATG GGACAATGGC ACAGGCCAGG CTCTGGGCTT GCCACCCACC ACCTGTGTCT 600
 ACCCGAGAA CTCAAGCAA CTGCTGCTGC CACCTGTGTA TTCGGCGGTG CTGGCGGCTG 660
 GCCTGCCGCT GAACATCTGT GTCAATTACC AGATCTGCAC GTCCCGCCGG GCCCTGACCC 720
 GCACGGCGGT GTACACCCCTA AACCTTGCTC TGGCTGACCT GCTATATGCC TGCTCCCTGC 780
 CCCTGTCTAT CTACAATAT GCCCAAGGTG ATCACTGGCC CTTTGGCGAC TTGCTCTGCC 840
 GCCTGGTCCG CTCTCTCTT TATGCCAACC TGCACGGCAG CATCTCTTTC CTCACCTGCA 900
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 TGCCACAGC CATCTTCTG GCCACAGGCA TCCAGCGTAA CCGCACTGTC TGCTATGACC 1080
 TCAGCCCGCC TGCCCTGGCC ACCCACTATA TGCCCTATGG CATGGCTCTC ACTGTCTATG 1140
 GCTTCTGCTT GCCCTTTGCT GCCCTGCTGG CTTGCTACTG TCTCTTGGCC TGCCGCTGT 1200
 GCGCCAGGGA TGGCCCGGCA GAGCCTGTGG CCCAGGAGCG GCGTGGCAAG GCGGCCGCGA 1260
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 CAGCGGCTTA CAAAGGCAGC CGGCCGTTTG CAGTGCCAA CAGCGTGTG GACCCCATCC 1440
 TCTTCTACTT CACCCAGAAG AAGTTCGCC GCGGACCACA TGAGCTCTTA CAGAACTCA 1500
 CAGCCAAATG GCAGAGGAG GGTGCTGAG TCCTCCAGGT CCTGGGCAGC CTTCTATATT 1560
 GCCATTGTGT CCGGGGCACC AGGAGCCCA CCAACCCCA ACCATGCGGA GAATTAGAGT 1620
 TCAGCTCAGC TGGGCATGGA GTTAAGATCC CTCACAGGAC CCAGAAGCTC ACCAAAACT 1680
 ATTTCTTACG CCCCTTCTCT GGCACAGACC CTGTGGGCAT GGAGATGGAC AGACCTGGGC 1740
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 AAAAAATAC AGTGTGACGT GTACTGTCAA AA 1832

Seq ID NO: C126 DNA Sequence
 Nucleic Acid Accession #: NM_007197
 Coding sequence: 18..1763

1 11 21 31 41 51
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	AGCCCATCGA	GATCCCGATG	TGCAAGGACA	TCCGCTACAA	CATGACTCGT	ATGCCCAAACC	180
5	TGATGGGCCA	CGAGAACCAG	CGCGAGGCAG	CCATCCAGTT	GCACGAGTTC	GCGCCGCTGG	240
	TGGAGTACGG	CTGCCACGGC	CACCTCCGCT	TCTTCTGTG	CTCGCTGTAC	GCGCCGATGT	300
	GCACCGAGCA	GGTCTCTACC	CCCATCCCGC	CCTGCCGGGT	CATGTGCGAG	CAGGCCCGGC	360
	TCAAGTGTCT	CCCGATTATG	GAGCAGTTCA	ACTTCAAGTG	GCCCGACTCC	CTGGAATGCC	420
	GGAAACTCCC	CAACAAGAAC	GACCCCAACT	ACCTGTGCAT	GGAGGCGCCC	AACAACGGCT	480
10	CGGACGAGCC	CACCCGGGGC	TCGGGCTGTG	TCCCGCCGCT	GTTCCGGCCG	CAGCGGCCCC	540
	ACAGCGCGCA	GGAGCACCGC	CTGAAGGACG	GGGGCCCCGG	GCGCGGCGGC	TGCGACAACC	600
	CGGGCAAGTT	CCACCACGTG	GAGAAGAGCG	CGTCGTGCGC	GCCGCTCTGC	ACGCCCGGCG	660
	TGGACGTGTA	CTGGAGCCGC	GAGGACAAGC	GCTTCGCACT	GGTCTGGCTG	GCCATCTGGG	720
	CGGTGCTGTG	CTTCTTCTCC	AGCGCCTTCA	CCGTGCTCAC	CTTCCTCATC	GACCCGGCCC	780
15	GCTTCCGCTG	CCCCGAGCGC	CCCATCATCT	TCCTCTCCAT	GTGCTACTGC	GTCTACTCCG	840
	TGGGCTACCT	CATCGCCTCG	TTCCGCGGCG	CCGAGAGCAT	CGCCTGCGAC	CGGGACAGCG	900
	GCCAGCTCTA	TGTCATCCAG	GAGGGACTGG	AGAGCACCGG	CTGCACGCTG	GTCTTCTCTG	960
	TCCTCTACTA	CTTCGGCATG	GCCAGCTCGC	TGTGGTGGGT	GGTCTCTCAG	CTCACCTGGT	1020
20	TCCTGGCCGC	CGGCAAGAAC	TGGGGCCACG	AGGCCATCGA	AGCCAAACAG	AGCTACTTCC	1080
	ACCTGGCAGC	CTGGGCCATC	CCGGCGGTGA	AGACCATCCT	GATCCTGGTC	ATGCGCAGGG	1140
	TGGCGGGGGA	CGAGCTCACC	GGGGTCTGCT	ACGTGGGCAG	CATGGACGTC	AACGCGCTCA	1200
	CGGCTTTCGT	GCTCATTTCC	CTGGCCTGCT	ACCTGGTCAT	CGGCACGTCC	TTTATCTCTT	1260
	CGGGCTTCGT	GGCCCTGTTC	CACATCCGGA	GGGTGATGAA	GACGGGCGGC	GAGAACACGG	1320
25	ACAAGCTGGA	GAAGCTCATG	GTGCGTATCG	GGCTCTTCTC	TGTGCTGTAC	ACCGTGGCGG	1380
	CCACCTGTGT	GATCGCCTGC	TACTTTTACG	AACGCCTCAA	CATGGATTAC	TGGAAGATCC	1440
	TGGCGGCGCA	GCACAAGTGC	AAAATGAACA	ACCAGACTAA	AACGCTGGAC	TGCCCTGATG	1500
	CCGCTCCAT	CCCCGCCGTG	GAGATCTTCA	TGGTGAAGAT	CTTTATGCTG	CTGGTGGTGG	1560
	GGATCACCAG	CGGATGTGGG	ATTGGGACCT	CCAAGACTCT	GCAGTCTCTG	CAGCAGGTGT	1620
	GCAGCCGTAG	GTTAAAGAAC	AAGAGCCGGA	GAAAACCGCG	CAGCGTGATC	ACCAGCGGTG	1680
30	GGATTACAA	AAAAGCCGAG	CATCCCCAGA	AAACTCACCA	CGGAAATAT	GAGATCCCTG	1740
	CCCAGTCGCC	CACCTGCGTG	TGAACAGGGC	TGGAGGGAAG	GGCACAGGGG	CGCCCGGAGC	1800
	TAAGATGTGG	TGCTTTTCTT	GGTGTGTGTT	TTCTTTCTTC	TTCTTTCTTT	TTTTTTTTTT	1860
	ATAAAGCAA	AAGAGAAATA	CATAAAAG	TGTTTACCCT	GAAATTCAGG	ATGCTGTGAT	1920
	ACACTGAAAG	GAAAAATGTA	CTTAAAGGGT	TTTGTTTTGT	TTTGGTTTTC	CAGCGAAGGG	1980
35	AAGCTCCTCC	AGTGAAGTAG	CCTCTGTGTG	AACTAATTGG	TGGTAAAGTA	GTTGATTCAG	2040
	CCCTCAGAA	AAAACCTTTG	TTTAGAGCCC	TCCGTAAATA	TACATCTGTG	TATTTGAGTT	2100
	GGCTTTGCTA	CCCATTTTCA	AATAAGAGGA	CAGATAACTG	CTTTGCAAA	TCAAGAGCCT	2160
	CCCCTGGGTT	AACAAATGAG	CCATCCCCAG	GGCCACCCCC	CAGGAAGGCC	ACAGTGTCTG	2220
	GCGGCATCCC	TGCAGAGGAA	AGACAGGACC	CGGGGCCCGC	CTCACACCCC	AGTGGATTGG	2280
40	GAGTTGCTTA	AAATGAGTCT	TGGCCTTCAC	CAATAGTCTC	TCTGCAAGAC	AGAAACCTCC	2340
	ATCAAACCTC	ACATTGTGTA	ACTCAAACGA	TGTGCAATAC	ATTTTCTTCT	CTTTCCTTGA	2400
	AAATAAAAG	AGAAACAAGT	ATTTTGCTAT	ATATAAGAC	AACAAAAGAA	ATCTCCTAAC	2460
	AAAAGAACTA	ATGAGACAAA	CCCTCAGAAA	CCCTCAGTGG	CTACATTTTG	TGGCTTTTTA	2520
	ATGGAACCA	AGCCAAATGT	ATAGACGTTT	GGACTGATTT	GTGAAAGGA	GGGGGGAAGA	2580
45	GGGAGAAGGA	TCATTCAAAA	GTTACCCAAA	GGGCTTATG	ACTCTTTCTA	TGTAAACAA	2640
	AATGATTTCC	ACAAACAGAT	CAGGAAGCAC	TAGGTTGGCA	GAGACACTTT	GTCTAGTGTG	2700
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	TTTTTCATGC	TCCACTATT	TATTAATAAT	AAAATATGTT	CTTTAAAAAA	A	2811

Seq ID NO: C127 DNA Sequence
Nucleic Acid Accession #: NM_005761.1
Coding sequence: 250..4956

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	GGATGGGGCG	GCCGCGGGAG	CCCGAGCGCG	CGCAGGAACC	GCCCGCGCCG	CCGCCCGCGT	180
	CTCCGTTGCC	GCGCGCCTGA	GCCGCGCTCG	CGGCCGCGCG	CCCTGCCCGG	GGGCGGCCCC	240
60	CCCAGCCCCA	TGGAGTCTTC	CCGGAGGAAG	GCGCCGCGCG	GCCCCCGCGG	CCCAGCAGCG	300
	CCACTGCCCC	TGCTCGCCTA	TCTGCTGGCA	CTGGCGGCTC	CGGCGCGGGG	CGCGGACGAG	360
	CCCGTGTGGC	GGTCGGAGCA	AGCCATCGGA	GCCATCGCGG	CGAGCCAGGA	GGACGCGCTG	420
	TTTGTGGCGA	GCGGCAGCTG	CCTGGACCAG	CTGGACTACA	GCCTGGAGCA	CAGCCTCTCG	480
	CGCCTGTACC	GGGACCAAGC	GGGCAACTGC	ACAGAGCCCG	TCTCGCTGGC	GCCCCCGCGG	540
65	CGGCCCGGCG	CCGGGAGCAG	CTTCAGCAAG	CTGCTGCTGC	CCTACCGCGA	GGGGGCGGCC	600
	GGCCTCGGGG	GGCTGCTGCT	CACCGGCTGG	ACCTTCGACC	GGGGCGCCTG	CGAGGTGCGG	660
	CCCCTGGGCA	ACCTGAGCCG	CAACTCCCTG	CGCAACGGCA	CCGAGGTGGT	GTCTGTCCAC	720
	CCGACGGGCT	CGACGGCCGG	CGTGGGTGAC	CGCGCGGGCC	GGAAACAACG	CTGGTACCTG	780
70	GCGGTGGCCG	CCACCTACGT	GCTGCCTGAG	CCGGAGACGG	CGAGCCGCTG	CAACCCCGCG	840
	GCATCCGAGC	ACGACACGGC	CATCGCGCTC	AAGGACAACG	AGGGGCGCAG	CCTGGCCACG	900
	CAGGAGCTGG	GGCGCCTCAA	GCTGTGCGAG	GGCGCGGGCA	GCCTGCACCT	CGTGGACGCC	960
	TTTCTCTGGA	ACGGCAGCAT	CTACTTCCCC	TACTACCCCT	ACAACATATC	GAGCGGCGCT	1020
	GCCACCGGCT	GGCCACGATC	GGCGCGCATC	GCGCAGAGCA	CCGAGGTGCT	GTTCCAGGGC	1080
75	GAGGCATCCC	TGCACTGCGG	CCACGGCCAC	CCGACGCGCC	CGCGCCTGCT	CCTCTCTCC	1140
	AGCCTAGTGG	AGGCCCTGGA	CGTCTGGGCG	GGAGTGTTC	GCGCGGCGCG	TGGAGAGGGC	1200
	CAGGAGCGGC	GCTCCCCCAC	CACCACGGCG	CTCTGCCTCT	TCAGAATGAG	TGAGATCCAG	1260
	GCGCGCGCCA	AGAGGGTCAG	CTGGGACTTC	AAGACGGCCG	AGAGCCACTG	CAAGAAGAGG	1320
	GATCAACCTG	AAAGAGTCCA	ACCAATCGCA	TCATCTACCT	TGATCCATTC	CGACCTGACA	1380
80	TCGCTTTATG	GCACCGTGGT	AATGAACAGG	ACTGTTTAT	TCTTGGGGAC	TGGAGATGGC	1440
	CAGTTACTTA	AGGTTATTCT	TGGTGAGAA	TTGACTTCAA	ATTGTCCAGA	GTTTATCTAT	1500
	GAAATTAAG	AAGAGACACC	TGTTTCTTAC	AAACTCGTTC	CTGATCCTGT	GAAGAATATC	1560
	TACATTATC	TACACTCTGG	GAAAGAGGTG	AGGAGAATTC	GTGTTGCAAA	CTGCAATAAA	1620
	CATAAATCCT	GTTCCGAGTG	TTTAACAGCC	ACAGACCCCT	ACTGCGGTTG	GTGCCATTCC	1680
	CTACAAAGGT	GCACCTTTTC	AGGAGATTGT	GTACATTCAG	AGAACTTAGA	AAACTGGCTG	1740
	GATATTTCTG	CTGGAGCAAA	AAAGTGCCCT	AAAATTCAGA	TAATTCGAAG	CAGTAAAGAA	1800

	AAGACTACAG	TGACTATGGT	GGGAAGCTTC	TCTCCAAGAC	ACTCAAAGTG	CATGGTGAAG	1860
	AATGTGGACT	CTAGCAGGGA	GCTCTGCCAG	AATAAAAGTC	AGCCCAACCG	GACCTGCACC	1920
	TGTAGCATCC	CAACCAGAGC	AACCTACAAA	GATGTTTCAG	TGTCAACGT	GATGTTCTCC	1980
5	TTCGGTTCTT	GGAA'TTTATC	AGACAGATTTC	AAC'TTTACCA	ACTGCTCATC	ATTAAAAGAA	2040
	TGCCCAGCAT	CGGTAGAAA	TGGCTGCGCG	TGGTGTAAAA	GTGCAAGAAG	GTGTATCCAC	2100
	CCCTTCACAG	CTTGCAGACC	TTCTGATTAT	GAGAGAAACC	AGGAACAGTG	TCCAGTGGCT	2160
	GTGAGAGAAG	CATCAGGAGG	AGGAAGACCC	AAGGAGAAC	AGGGGAACAG	AACCAACACG	2220
	GCTTTACAGG	TCTTCTACAT	TAAGTCCATT	GAGCCACAGA	AAGTATCGAC	ATTAGGGAAA	2280
	AGCAACGTGA	TAGTAACGGG	AGCAAACTTT	ACCCGGGCAT	CGAACATCAC	AATGATCCTG	2340
10	AAAGGAACCA	GTACCTGTGA	TAAGGATGTG	ATACAGGTTA	GCCATGTGCT	AAATGACACC	2400
	CACATGAAAT	TCTCTCTTCC	ATCAAGCCGG	AAAGAAATGA	AGGATGTGTG	TATCCAGTTT	2460
	GATGGTGGGA	ACTGCTCTTC	TGTGGGATCC	TTATCTTACA	TTGCTCTGCC	ACATTGTTCC	2520
	CTTATATTTT	CTGCTACCAC	CTGGATCAGT	GGTGGTCAAA	ATATAACCAT	GATGGGCAGA	2580
15	AATTTTGATG	TAATTGACAA	CTTAATCATT	TCACATGAAT	TAAAAGGAAA	CATAAATGTC	2640
	TCTGAATATT	GTGTGGCGAG	TTACTGCGGG	TTTTTAGCCC	CCAGTTTAAA	GAGTTCAAAA	2700
	GTGCGCACGA	ATGTCACCTG	GAAGCTGAGA	GTACAGACA	CCTACTTGGA	TGTGGGAACC	2760
	CTGCGATATC	GGGAGGACCC	CAGATTACCG	GGGTATCGGG	TGGAATCCGA	GGTGGACACA	2820
	GAACGTGAAG	TGAAAATTCA	AAAAGAAAAT	GACAACCTTC	ATATTTCCAA	AAAAGACATT	2880
20	GAAATTACTC	TCTTCCATGG	GGAAAATGGG	CAATTAAATT	GCAGTTTGA	AAATATTACT	2940
	AGAAATCAAG	ATCTTACCAC	CATCCTTTGC	AAAATTAAAG	GCATCAAGAC	TGCAAGCACC	3000
	ATTGCCAACT	CTTCTAAGAA	AGTTCGGGTC	AAGCTGGGAA	ACCTGGAGCT	CTACGTCAG	3060
	CAGGAGTCAG	TTCTTCCAC	ATGGTATTTT	CTGATTGTGC	TCCCTGTCTT	GCTAGTGATT	3120
	GTCAATTTTT	CGGCCGTGGG	GGTGACCAGG	CACAAATCGA	AGGAGCTGAG	TGCAAAACAG	3180
25	AGTCAACAAC	TAGAATTGCT	GGAAAAGCGA	CTCCGGAAG	AGATACGTGA	CGGCTTGTCT	3240
	GAGCTGCAGA	TGGATAAAT	GGATGTGGTT	GATAGTTTTG	GAACTGTTCC	CTTCTTGAC	3300
	TACAAACATT	TTGCTCTGAG	AAC'TTCTTC	CCTGAGTCAG	GTGGCTTCAC	CCACATCTTC	3360
	ACTGAAGATA	TGCATAACAG	AGACGCCAAC	GACAAGAATG	AAAGTCTCAC	AGCTTTGGAT	3420
	GCCTTAATCT	GTAATAAAG	CTTCTTGTGT	ACTGTCTATC	ACACCTTGA	AAAGCAGAAG	3480
30	AAC'TTTTCTG	TGAAGGACAG	GTGTCTGTTT	GCCTCTTCTC	TAACCATGTC	ACTGCAAAAC	3540
	AAGCTGGTCT	ACCTGACCAG	CATCCTAGAG	GTGCTGACCA	GGGACTTGAT	GGAACAGTGT	3600
	AGTAACATGC	AGCCGAAACT	CATGCTGAGA	CGCACGGAGT	CCGTCTGCGA	AAAACCTCTC	3660
	ACAAACCTGGA	TGTCCTGCTG	CCTTCTGGA	TTTCTCCGGG	AGACTGTCCG	AGAGCCCTTC	3720
	TATTTGCTGG	TGACGACTCT	GAACCCAGAA	ATTAACAAGG	GTCCCGTGGG	TGTAATCACT	3780
35	TGCAAAAGCC	TGACACACT	TAATGAAGAC	TGGCTGTTGT	GGCAGGTTCC	GGAATTCAGT	3840
	ACTGTGGCAT	TAAACGTCGT	CTTTGAAAAA	ATCCCGGAAA	ACGAGAGTGC	AGATGTCTGT	3900
	CGGAATATTT	CAGTCAATGT	TCTCGACTGT	GACACCATTG	GCCAGGCCAA	AGAAAAGATT	3960
	TTCCAAGCAT	TCTTAAGCAA	AAATGGCTCT	CCTTATGGAC	TTGAGCTTAA	TGAAATCTGT	4020
	CTTGAGCTTC	AAATGGGCGA	ACGACAGAAA	GAACTTCTGG	ACATCGACAG	TTCTCCGTG	4080
40	ATTCTTGAAG	ATGGAATCAC	CAAGCTAAAC	ACCATTGGCC	ACTATGAGAT	ATCAAATGGA	4140
	TCCAATAATA	AAGCTTTTAA	GAAGATAGCA	AATTTTACTT	CAGATGTGGA	GTACTCGGAT	4200
	GACCACTGCC	ATTGATTTTT	ACCAGATTCT	GAAGCATTC	AAGATGTGCA	AGGAAAGAGA	4260
	CATCGAGGGA	AGCACAGATT	CAAGTAAATA	GAAATGTATC	TGACAAAGCT	GCTGTGACAC	4320
	AAGGTGGCAA	TTCAATCTGT	GCTTGAAAAA	CTTTTGTAGAA	GCATTTGGAG	TTTACCCAAC	4380
45	AGCAGAGCTC	CATTGCTGAT	AAAATACTTT	TTTGACTTTT	TGGACGCCCA	GGCTGAAAAA	4440
	AAAAAAATCA	CAGATCCTGA	CGTCGTACAT	ATTGGGAAAA	CAAAACAGCT	TCCTCTTCGC	4500
	TTCTGGGTAA	ACATCCTGAA	GAACCCCTCAG	TTTGTCTTTG	ACATTAGAA	GACACACAT	4560
	ATAGACGGCT	GTTTGTCTAGT	GATTGCCAG	GCATTCATGG	ATGCATTTTC	TCTCACAGAG	4620
	CAGCAACTAG	GGAAAGGAGC	ACCAACTAAT	AAGCTTCTCT	ATGCCAAGGA	TATCCCAACC	4680
50	TACAAAGAA	AAGTAAATAT	TTATTACAAA	GCAATCAGGG	ATTGCTCTCC	ATTGTCATCC	4740
	TCAGAAATGC	AAGAAATTTT	AAC'TCAGGAA	TCTAAGAAAC	ATGAAATGTA	ATTTAATGAA	4800
	GAAGTGGCCT	TGACAGAAAT	TTACAAATAC	ATCGTAAAT	ATTTTGATGA	GATTCTAAAT	4860
	AAACTAGAAA	GAGAACGAGG	GCTGGAAGAA	GCTCAGAAAC	AACTCTTGCA	TGTAAAAGTC	4920
	TTATTGTAGT	AAAAGAAAGAA	ATGCAAGTGG	ATGTAAGCAC	TCTGGGCGCT	GGCTTAATCT	4980
55	GGCAAAAGTC	TTACAGACGAC	TTGGGAGCAA	AATGGCTGCT	TGAGCTACTC	TGTGTCGTTA	5040
	ATTTGTTGTT	TGCACATAGG	TTCCACTTTG	GGCACTGTCT	TTTTAAGAGA	CCAAGGCACA	5100
	TGCACAGCTT	TTAGAAAGCA	A				5121

Seq ID NO: C128 DNA Sequence
 Nucleic Acid Accession #: NM_002185.1
 Coding sequence: 23..1402

	1	11	21	31	41	51	
65	CTCTCTCTCT	ATCTCTCTCA	GAATGACAAT	TCTAGGTACA	ACTTTTGGCA	TGGTTTTTTC	60
	TTTACTTCAA	GTCGTTTCTG	GAGAAAGTGG	CTATGCTCAA	AATGGAGACT	TGGAAGATGC	120
	AGAACTGGAT	GACTACTCAT	TCTCATGCTA	TAGCCAGTTG	GAAGTGAATG	GATCGCAGCA	180
	TTCACTGACC	TGTGCTTTTG	AGGACCCAGA	TGTCAACACC	ACCAATCTGG	AATTTGAAAT	240
	ATGTGGGGCC	TCGTGGGAG	TAAAGTGCCT	GAATTTACAG	AAACTACAAG	AGATATATTT	300
70	CATCGAGACA	AAGAAATCT	TACTGATTGG	AAAGAGCAAT	ATATGTGTGA	AGGTTGGAGA	360
	AAAGAGTCTA	ACCTGCAAAA	AAATAGACCT	AACCACTATA	GTTAAACCTG	AGGCTCCTTT	420
	TGACCTGAGT	GTCTATCTAT	GGGAAGGAGC	CAATGACTTT	GTGGTGACAT	TTAATACATC	480
	ACACTTGCAA	AAGAAGTATG	TAAAAGTTTT	AATGCATGAT	GTAGCTTACC	GCCAGGAAAA	540
	GGATGAAAA	AAATGGACGC	ATGTGAATTT	ATCCAGCACA	AAGCTGACAC	TCCTGCAGAG	600
75	AAAGCTCCAA	CCGCGACGAA	TGTATGAGAT	TAAAGTTTGA	TCCATCCCTG	ATCACTATTT	660
	TAAAGGCTTC	TGGAGTGAAT	GGAGTCCAAG	TTATTACTTC	AGAACTCCAG	AGATCAATAA	720
	TAGCTCAGGG	GAGATGGATC	CTATCTTACT	AACCATCAGC	ATTTTGAGTT	TTTTCTCTGT	780
	CGCTCTGTTG	GTCATCTTGG	CCTGTGTGTT	ATGGAAAAAA	AGGATTAAGC	CTATCGTATG	840
	GCCAGTCTCT	CCCGATCATAT	AGAAGACTCT	GGAACATCTT	TGTAAGAAAC	CAAGAAAAAA	900
80	TTTAAATGTG	AGTTTCAATC	CTGAAAGTTT	CCTGGACTGC	CAGATTTCATA	GGGTGGATGA	960
	CATTCAAGCT	AGAGATGAAG	TGGAAGGTTT	TCTGCAAGAT	ACGTTTCCCT	AGCAACTAGA	1020
	AGAATCTGAG	AAGCAGAGGC	TTGGAGGGGA	TGTGCAGAGC	CCCAACTGCC	CATCTGAGGA	1080
	TGTAGTCGTG	ACTCCAGAAA	GCTTTGGGAG	AGATTCAATC	CTCACATGCC	TGGCTGGGAA	1140
	TGTCAAGTGA	TGTGACGCCC	CTATTCTCTC	CTCTTCCAGG	TCCCTAGACT	GCAGGGAGAG	1200
	TGGCAAGAAT	GGGCTCATG	TGTACCAGGA	CCTCTGCTTT	AGCCTTGGGA	CTACAAAACG	1260

CACGCTGCCC CCTCCATTTT CTCTCCAATC TGGAATCCTG ACATTGAACC CAGTTGCTCA 1320
 GGGTCAGCCC ATTCTTACTT CCCTGGGATC AAATCAAGAA GAAGCATATG TCACCATGTC 1380
 CAGCTTCTAC CAAAACCACT GAAGTGTAAG AAACCCAGAC TGAACCTACC GTGAGCGACA 1440
 AAGATGATTT AAAAGGGGAG TCTAGAGTTC CTAGTCTCCC TCACAGCACA GAGAAGACAA 1500
 AATTAGCAAA ACCCCACTAC ACAGTCTGCA AGATTCTGAA ACATTGCTTT GACCACTCTT 1560
 CCTGAGTTCA GTGGCACTCA ACATGAGTCA AGAGCATCCT GCTTCTACCA TGTGGATTGT 1620
 GTCACAAGGT TTAAGGTGAC CCAATGATTC AGCTATTT 1658

Seq ID NO: C129 DNA Sequence
 Nucleic Acid Accession #: NM_002722.1
 Coding sequence: 15..302

1 11 21 31 41 51
 ACTCTGGACT CCGGATGGCT GCCGCACGCC TCTGCCTCTC CCTGCTGCTC CTGTCCACCT 60
 GCGTGGCTCT GTTACTACAG CCACCTGCTGG GTGCCCAGGG AGCCCCACTG GAGCCAGTGT 120
 ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCCAAGTA TGCAGCTGAT CTCCGTAGAT 180
 ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAAAGACA CAAAGAGGAC ACGCTGGCCT 240
 TCTCGGAGTG GGGGTCCCCG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGGACTTAT 300
 AATGCCACCT TCTGTCTCCT ACGACTCCAT GAGCAGCGCC AGCCCCAGCTC TCCCTCTGTC 360
 ACCCTTGGCT CTGGCCAAAG CTGTCTCCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420
 AAGCC 425

Seq ID NO: C130 DNA Sequence
 Nucleic Acid Accession #: NM_032545.1
 Coding sequence: 47..718

1 11 21 31 41 51
 AAATGATCT TCAATGCACT AAGAGAAGGA GACTCTCAAA CCAAAAATGA CCTGGAGGCA 60
 CCATGTCAGG CTTCGTGTTA CGGTCAAGTT GGCATTACAG ATCATCAATT TGGGAACACAG 120
 CTATCAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTTG CCACTCAGAA 180
 GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCAATTC GGAGAGGTGA CTGGGAGCGC 240
 CGAGGGCTGG GGGCCGAGG AGCCGCTCCC TACTCCCGG GCTTTCGGAG AGGGTGCCTC 300
 CGCGCGGCCG CGCTGCTGCA GGAACGGCGG TACCTGCGTG CTGGGCAGCT TCTGCGTGTG 360
 CCCGGCCAC TTCACGGGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC 420
 CCTGGAGCAC GGAGCCTGGA CCCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGGC 480
 CCTGCACTGC CTCCCCCTCC AGACGCTGTA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC 540
 CCACGCTCAC GGGCCGAGCG CCGGGGCGC GCCAGCCTG CTACTCTTGC TGCCCTGCGC 600
 ACTCTGTCAC CGCCTCTGTC GCCCGGATGC GCCCGCGCAC CTTGGTCCC TGGTCCCTTC 660
 CGTCTCCAG CGGGAGCGGC GCCCTGCGG AAGGCCGGA CTTGGGCATC GCCTTTAATT 720
 TTCTATGTTG TAAATAATAG ATGTGTTTAG TTACCGTAA GCTGAAGCAC TGGGTGAATA 780
 TTTTATTGTA GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAATA AAAAAAATA 840
 AAAAA 846

Seq ID NO: C131 DNA Sequence
 Nucleic Acid Accession #: NM_006533.1
 Coding sequence: 72..467

1 11 21 31 41 51
 AGGGAGAGAG GGAGGGGAGG AATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTGCT 60
 CACAGTCCAC GATGGCCCGG TCCTTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT 120
 TCTCCGGACC TGGTGTGAGG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180
 CGGACAGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240
 CCGACTGCCG ATTCTGTACC ATTACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300
 AGGGCCGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360
 CTGCTCGCCT GGGCTATTTT CCGAGTAGCA TTGTCCGAGA GGACCGAGCC CTGAAACCTG 420
 GCAAGTCTGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG 480
 CTGGCCCTGC CGTTTCCCTT CCTTGGGTTT ATGCAATAC AATCAGCCCA GTGCAAAAC 538

Seq ID NO: C132 DNA Sequence
 Nucleic Acid Accession #: AB064272
 Coding sequence: 1..708

1 11 21 31 41 51
 ATGACACAAG TCACAGAAAA GTCCACAGAA CACCCAGAAA AGACCAGTC AACCAAGAG 60
 AAAACCACAA GAACCCACAG AAAGCCTACG CTATACTCAG AGAAGACCAT ATGCACCAAA 120
 GGGAAAAACA CACCACTCCC AGAAAAGCCT ACAGAAAACC TGGGGAACAC CACACTGACC 180
 ACTGAGACCA TAAAGCCCC AGTAAAGTCC ACAGAAAACC CAGAAAAAAC AGCAGCAGTC 240
 ACAAGAGCTA TAAACCTTC AGTCAAGTTC ACAGGAGACA AATCTCTCAC TACTACCTCT 300
 TCTCATCTAA ATAAACTTGA AGTTACTCAT CAGGTGCCCA CTGGTTCTTT CACCCTCAT 360
 ACATCTAGAA CGAAGCTGAG TTCTATCACA TCAGAAGCCA CAGGAAACGA GAGCCATCCA 420
 TACCTCAATA AAGATGGCTC ACAGAAAGGT ATCCACGCTG GACAGATGGG AGAGAAATAT 480
 TCAATCCCTG CATGGCCAT AGTTATTGTG GTCTGGTGG CTGTGATTCT CCTCTGGTG 540
 TTCCTTGGCC TGATCTTCTT GGTCTCCTAT ATGATGCGGA CACGCCGCAC ACTAACCAG 600
 AACACCCAGT ACAATGATGC AGAGGATGAG GGTGGCCCA ATTCTACCC GGTCTACCTG 660
 ATGGAGCAGC AGAATCTTGG CATGGGCCAG ATCCCTTCCC CACGGTGA 708

Seq ID NO: C133 DNA Sequence
 Nucleic Acid Accession #: NM_080870.1
 Coding sequence: 3..710

	1	11	21	31	41	51	
5	AGATGACACA	AGTCACAGAA	AAGTCCACAG	AACACCCAGA	AAAGACCACG	TCAACCCACAG	60
	AGAAAACCCAC	AAGAACCCCA	GAAAAGCCCTA	CGCTATACTC	AGAGAAGACC	ATATGCACCA	120
	AAGGGAAAAA	CACACCAGTC	CCAGAAAAGC	CTACAGAAAA	CCTGGGGAAC	ACCACACTGA	180
	CCACTGAGAC	CATAAAGGCC	CCAGTAAAGT	CCACAGAAAA	CCCAGAAAAA	ACAGCAGCAG	240
	TCACAAAGAC	TATAAAACCT	TCAGTCAAGG	TCACAGGAGA	CAAATCTCTC	ACTACTACCT	300
10	CTTCTCATCT	AAATAAAACT	GAAGTTACTC	ATCAGGTGCC	CAGTGGTTCT	TTCACCCCTA	360
	TTACATCTAG	AACGAAGCTG	AGTTCTATCA	CATCAGAAGC	CACAGGAAAC	GAGAGCCATC	420
	CATACCTCAA	TAAAGATGGC	TCACAGAAAG	GTATCCACGC	TGGACAGATG	GGAGAGAATG	480
	ATTCAATCCC	TGCATGGGCC	ATAGTTATTG	TGGTCTGGT	GGCTGTGATT	CTCCTCCTGG	540
	TGTTCCCTGG	CTGATCTTTC	TTGGTCTCCT	ATATGATGCG	GACACGCCGC	ACACTAACCC	600
15	AGAACACCCA	GTACATGAT	GCAGAGGATG	AGGGTGGCCC	CAATTCCCTAC	CCGGTCTACC	660
	TGATGGAGCA	GCAGAATCTT	GGCATGGGCC	AGATCCCTTC	CCCACGGTGA	TCTTGGAGTA	720
	GGCGCCGAGC	CCTGGCTCTT	CCATGCTCTG	CCCCTTTCCT	GGATGAGGAA	CCGGACTCAC	780
	AAATTTCTATT	TCCGGGACTA	CAGGAAGGGC	AGAGAATACT	GACGGTTACC	AGTATTAAAC	840
	CTTCATCTGT	TCTTGAACCT	GGTTGGGGAA	TGAGGTGATA	AGCAAGGAGG	GTGTAAGTTT	900
20	AGGGGACAAA	GAGAAAGAA	TGAATAATAC	GAGCAGACAT	TCTCTGTAGA	AGGTAATGGT	960
	CTGAGAATGA	AAAGGTGTTT	GATGGACATG	TTGTGGGGGC	ACCAATGCAG	AACACTGCAC	1020
	TGAGTCCCTAA	AGGAAGGACA	GGAGCCTTAT	AGGCAATGCC	CCAGACTGAC	TTGTGAGTGG	1080
	GGTTTATGGG	GAAAGGGAGG	GACTGAGGGC	AGAGTCTCTG	GGTTTCAGGA	CAGCATTATG	1140
	TTATTTCCAT	TCACTATTAC	TTAAGAGTTT	GTGTGTAACC	AGGCTCATCT	CTGAGTTCTC	1200
25	AGGACCCTTG	CCCCACCCC	CATTTTCTTA	ATGAAAAAAA	AAAAACAAAA	AAACGGATCC	1260
	AGAGAAGAAA	GAGAAATTAT	TTCTTCTCTC	ACTCTCTCCA	TGCCCTGGAG	AAAAAAAAGT	1320
	CCAGAAGAAA	CATAAATAT	CTCTCATCTA	CATGGTTGCT	TCCTCTTCCT	CCCAAATCCC	1380
	TTAGTTTCTC	TAAATGTCTA	CAGTGGACGC	CCTGTTGGTT	TGGCTTGCTG	GGTTGTGGGT	1440
	GGACACGCAA	GGAGGGGATT	TTTATTGGC	CAGCAGTCTC	ACCCACTGAT	CTCCACCCCA	1500
30	GACCTTCCCT	GATTTGGTGC	TCAGCATTTA	TTTCTCTGTC	TCTTCCACCA	AAAGCCAGCT	1560
	GTAGCTTTAT	TCGTGAAAAG	TTACCCATCT	TCTCTACTGT	CCCCATTCTC	TCTCTCTCCA	1620
	CCTTCACCCC	AGATTCCAAG	TTTCTCCTT	GTAGGCATT	CATCTGTGTG	TGTTTCTCGG	1680
	ATTTTCTCTC	TCTCTCTTA	TGGCCATTTC	ACCTTATTAC	TGATTGGGTA	GAGGGGGAAA	1740
35	AGGAGAATGA	TGATGATAGT	TTCTTCTGT	CTATTGACCT	TTTTTATAAT	AAAGTATAAC	1800
	ATGTT						1805

Seq ID NO: C134 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..10674

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	ATGTGGCCTC	GCCTGGCCTT	TTGTTGCTGG	GGTCTGGCGC	TCGTTTCGGG	CTGGGCGACC	60
45	TTTCAGCAGA	TGTCCTCGTC	GCACAATTTC	AGCTTCCGCC	TCTTCCCGGA	GACCGCGCCC	120
	GGGGCCCCCG	GGAGTATCCC	CGCGCCGCC	GCTCCTGGCG	ACGAAGCGGC	GGGGAGCAGA	180
	GTGGAGCGGC	TGGGCCAGGC	GTTCCGCGCA	CGCGTGCGGC	TGCTGCGGGA	GCTCAGCGAG	240
	CGCTCGGAGC	TTGTCTTCCT	GGTGGATGAT	TCGTCCAGCG	TGGGCGAAGT	CAACTTCCGC	300
	AGCGAGCTCA	TGTTCTGTCG	CAAGCTGCTG	TCCGACITCC	CCGTGGTGCC	CACGGCCACG	360
50	CGCGTGGCCA	TCGTGACCTT	CTCGTCCAAG	AACTACGTGG	TGCCGCGCGT	CGATTACATC	420
	TCCACCGGCC	CGCGCGGCCA	GCACAAGTGC	CGCTGTCTCC	TCCAAGAGAT	CCCTGCCATC	480
	TCCTACCGAG	GTGGCGGCAC	CTACACCAAG	GGCGCCTTCC	AGCAAGCCGC	GCAAAATCTT	540
	CTTCATGCTA	GAGAAAACCT	AACAAAAGTT	GTATTTCTCA	TCACTGATGG	ATATTCCAAT	600
	GGGGGAGACC	CTAGACCAAT	TGCAGCGTCA	CTGCGAGATT	CAGGAGTGA	GATCTTCACT	660
55	TTTGGCATAT	GGCAAGGGAA	CATTTCGAGAG	CTGAATGACA	TGGCTTCCAC	CCCAAAGGAG	720
	GAGCACTGTT	ACCTGCTACA	CAGTTTGA	GAATTTGAGG	CTTTAGCTCG	CCGGGCATTG	780
	CATGAAGATC	TACCTTCTGG	GAGTTTATT	CAAGATGATA	TGGTCCACTG	CTCATATCTT	840
	TGTGATGAAG	GCAAGGACTG	CTGTGACCSA	ATGGGAAGCT	GCAAAATGTGG	GACACACACA	900
	GGCCATTTTG	AGTGCATCTG	TGAAAAGGGG	TATTACGGGA	AAAGGTCTGCA	GTATGAATGC	960
60	ACAGCTTGCC	CATCGGGGAC	ATACAAACCT	GAAGGCTCAC	CAGGAGGAAT	CAGCAGTTGC	1020
	ATTCCATGTC	CTGATGAAA	TCACACCTCT	CCACCTGGAA	GCACATCCCC	TGAAGACTGT	1080
	GTCTGCAGAG	AGGGATACAG	GGCATCTGGC	CAGACCTGTG	AACCTTGCCA	CTGCCCTGCC	1140
	CTGAAGCCTC	CCGAAAATGG	TTACTTTATC	CAAAACACTT	GCAACRACCA	CTTCAATGCA	1200
	GCCTGTGGGG	TCCGATGTCA	CCCTGGATTT	GATCTTGTGG	GAAGCAGCAT	CATCTTATGT	1260
65	CTACCCAAATG	TTTGTGGTCC	CGGTTCAAGG	AGCTACTGCA	GAGTAAGAAC	ATGTCTCAT	1320
	CTCCGCCAGC	GTAACACATG	CCACATCAGC	TGTTCTACAA	GGGAATGTGT	ATATAAGACA	1380
	ACATGTTTGG	TTGCCTGTGA	TGAAGGGTAC	AGACTAGAAG	GCAGTGATAA	GCTTACTTGT	1440
	CAAGGAACA	GCCAGTGGGA	TGGGCCAGAA	CCCCGGTGTG	TGGAGCGCCA	CTGTTCCACC	1500
	TTTCAGATGC	CCAAAGATGT	CATCATATCC	CCCCACAAC	GTGGCAAGCA	GCCAGCCAAA	1560
70	TTTGGGACGA	TCTGCTATGT	AAGTTGCCGC	CAAGGGTTCA	TTTATCTGCG	AGTCAAAGAA	1620
	ATGCTGAGAT	GTACCACTTC	TGGAATAATG	AATGTCGGAG	TTCAGGCAGC	TGTGTGTAAA	1680
	GACGTGGAGG	CTCCTCAAA	CACTGTCCCT	AAGGACATAG	AGGCTAAGAC	TCTGGAAACAG	1740
	CAAGATTCTG	CCAATGTTAC	CTGGCAGATT	CCAACAGCTA	AAGACAACCT	TGGTGAAGAA	1800
	GTGTCACTGC	AGTTTCAACC	AGCTTTCACC	CCACCTTACC	TTTCCCAAT	TGGAGATGTT	1860
75	GCTATCGTAT	ACACGGCAAC	TGACCTATCC	GGCAACCAGG	CCAGCTGCAT	TTTCCATATC	1920
	AAGGTTATTG	ATGCAGAAGC	ACCTGTGATA	GACTGGTGCA	GATCTCCACC	TCCCGTCCAG	1980
	GTCTCGGAGA	AGGTACATGC	CGCAAGCTGG	GATGAGCCTC	AGTCTCTAGA	CAACTCAGGG	2040
	GCTGAATTGG	TCAATACACG	AAGTCATACA	CAAGGAGACC	TTTCCCTTCA	AGGGGAGACT	2100
	ATAGTACAGT	ATACAGCCAC	TGACCCCTCA	GGCAATAACA	GGACATGTGA	TATCCATATT	2160
80	GTCTATAAAG	GTTCTCCCTG	TGAAATTTCCA	TTACACCTTG	TAAATGGGGA	TTTTATATGC	2220
	ACTCCAGATA	ATACTGGAGT	CAACTGTACA	TTAACTTGCT	TGGAGGGGCTA	TGATTTTACA	2280
	GAAGGGTCTA	CTGACAGAGT	TTATTGTGCT	TATGAAGATG	GCGTCTGGAA	ACCAACATAT	2340
	ACCACTGAAT	GGCCAGACTG	TGCCAAAAAA	CGTTTTGCAA	ACCACGGGTT	CAAGTCTCTT	2400
	GAGATGTTCT	ACAAAGCAGC	TCGTTGTGAT	GACACAGATC	TGATGAAGAA	GTTTTCTGAA	2460
	GCATTTGAGA	GACCCCTGGG	AAAAATGGTC	CCATCATTTT	GTAGTGATGC	AGAGGACATT	2520

	GACTGCAGAC	TGGAGGAGAA	CCTGACCAAA	AAATATTGCC	TAGAATATAA	TTATGACTAT	2580
	GAAAATGGCT	TTGCAATTGG	ACCAGGTGGC	TGGGGTGCAG	CTAATAGGCT	GGATTACTCT	2640
	TACGATGACT	TCCTGGACAC	TGTGCAAGAA	ACAGCCACAA	GCATCGGCAG	TGCCAAGTCC	2700
5	TCACGGATTA	AAAGAAGTGC	CCCATTATCT	GACTATAAAA	TTAAGTTAAT	TTTTAACATC	2760
	ACAGCTAGTG	TGCATTAGCC	CGATGAAAGA	AATGATACCC	TTGAATGGGA	AAATCAGCAA	2820
	CGACTCCTTC	AGACATTGGA	AACTATCACA	AATAAATCTA	AAAGGACTCT	CAACAAAGAC	2880
	CCCATGTATT	CCTTTCAGCT	TGCATCAGAA	ATACTTATAG	CCGACAGCAA	TTTATTAGAA	2940
	ACAAAAAAGG	CTTCCCCCTT	CTGCAGACCA	GGCTCAGTGC	TGAGAGGGCG	TATGTGTGTC	3000
10	AATTGCCCTT	TGGGAACCTA	TTATAATCTG	GAACATTTC	CCTGTGAAAG	CTGCCGGATC	3060
	GGATCCTATC	AAGATGAAGA	AGGGCAACTT	GAGTGCAAGC	TTTGCCCTCT	TGGGATGTAC	3120
	ACGGAATATA	TCCATTCAAG	AAACATCTCT	GATTGTAAAG	CTCAGTGTAA	ACAAGGCACC	3180
	TACTCATACA	GTGGACTTGA	GACTTGTGAA	TCGTGTCCAC	TGGGCACCTA	TCAGCCAAAA	3240
	TTTGGTTCCC	GGAGCTGCCT	CTCGTGTCCA	GAAAACACCT	CAACTGTGAA	AAGAGGAGCC	3300
15	GTGAACATTT	CTGCATGTGG	AGTTCCCTGT	CCAGAAGGAA	AATTCTCGCG	TTCTGGGTTA	3360
	ATGCCCTGTC	ACCCATGTCC	TCGTGACTAT	TACCAACCTA	ATGCAGGGAA	GGCCTTCTGC	3420
	CTGGCCTGTC	CCTTTATGGG	AACTACCCCA	TTCTGTGTTT	CCAGATCCAT	CACAGAATGT	3480
	TCAACTTCAG	TTCTGAATAT	TACTATTTTC	GGTGGATTGG	GGCATCTGGA	GTTGTTAAAT	3540
	TGTCCTCTCG	AGGTTTCCCA	TGAATGCTTC	TTTAACCTTT	GCCACAATAG	TGGAACCTGC	3600
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	GAAACAGACA	TCGATGAGTG	CAGCCCACTG	CCTTGCCCTA	ACAATGGAGT	TTGTAAAGAC	3720
	CTAGTTGGGG	AATTCAATTG	TGAGTGCCCA	TCAGGTTACA	CAGGTGAGCG	GTGTGAAGAA	3780
	AATATAAATG	AGTGTAGCTC	CAGTCCTTGT	TAAATAAAG	GAATCTGTGT	TGATGGTGTG	3840
	GCTGGCTATC	GTTCACATG	TGTGAAAGGA	TTTGTAGGCC	TGCATTGTGA	AACAGAAGTC	3900
25	AATGAATGCC	AGTCAAAACC	ATGCTTAAAT	AATGCAGTCT	GTGAAGACCA	GGTTGGGGGA	3960
	TTCTTGTGCA	AATGCCCAAC	TGGATTTTGT	GGTACCCGAT	GTGGAAAGAA	CGTCGATGAG	4020
	TGTCCTAGTC	AGCCATGCAA	AAATGGAGCT	ACCTGTAAG	ACGGTGCCAA	TAGCTTCAGA	4080
	TGCCCTGTGT	CAGCTGGCTT	CACAGGATCA	CACTGTGAAT	TGAACATCAA	TGAATGTGAG	4140
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30	TGTCAGCCAG	GATTTTTCAGG	CAAAAGGTGT	GAAACAGAAC	AGTCTACAGG	CTTTAACTGT	4260
	GATTTTGAAG	TTCTTGGCAT	CTATGGATAT	GTCTAGCTAG	ATGGCATGCT	CCCATCTCTC	4320
	CATGCTCTAA	CTGTACCTTT	CTGGATGAAA	TCCTCTGACG	ACATGAACTA	TGGAACACCA	4380
	ATCTCCTATG	CAGTTGATAA	CGGCAGCGAC	AATACCTTGC	TCCTGACTGA	TTATAACGGC	4440
	TGGGTTCTTT	ATGTGAATGG	CAGGGAAAAAG	ATAACAAACT	GTCCCTCGGT	GAATGATGGC	4500
35	AGATGGCATC	ATATTGCAAT	CACCTTGGACA	AGTGCCAAATG	GCATCTGAAA	AGTCTATATC	4560
	GATGGGAAAT	TATCTGACGG	TGGTGTCTGG	CTCTCTGTGT	GTTCGCCCAT	ACCTGGTGGT	4620
	GGTGCGTTAG	TTCTGGGGCA	AGAGCAGAC	AAAAAAGGAG	AGGGATTGAG	CCCAGCTGAG	4680
	TCCTTTGTGG	GCTCCATAAG	CCAGCTCAAC	CTCTGGGACT	ATGTCTGTGC	TCCACAGCAG	4740
40	GTGAAGTCA	TGGCTACCTC	CTGCCCAGAG	GAACCTCAGT	AAGGAAACGT	GTTAGCATGG	4800
	CCTGATTTCT	TGTCAGGAAT	TGTGGGGAAG	GTGAAGATCG	ATTCTAAGAG	CATATTTTGT	4860
	TCTGATTGCC	CACGCTTAGG	AGGGTCAGTG	CCTCATCTGA	GAACCTGCATC	TGAAGATTTA	4920
	AAGCCAGGTT	CCAAAGTCAA	TCTGTTCTGT	GATCCAGGCT	TCCAGCTGGT	CGGGAAACCT	4980
	GTGCAGTACT	GTCTGAATCA	AGGACAGTGG	ACACAACCA	TTCCCTACTG	TGAACGCATT	5040
	AGCTGTGGGG	TGCCACCTCC	TTTGAGAGAA	GGCTTCCATT	CAGCCGATGA	CTTCTATGCT	5100
45	GGCAGCACAG	TAACTACCA	GTGCAACAAT	GGCTACTATC	TATTGGGTGA	CTCAAGGATG	5160
	TTCTGTACAG	ATAATGGGAG	CTGGAAACGG	GTTTCACCAT	CCTGCCTTGA	TGTCGATGAG	5220
	TGTGCAAGTG	GATCAGATTG	TAGTGAGCAT	GCTTCTTGCC	TGAACGTAGA	TGGATCCTAC	5280
	ATATGTTTAT	GTGTCCCAAC	GTACACAGGA	GATGGGAAAA	ACTGTGCAGA	ACCTATAAAA	5340
	TGTAAGGCTC	CAGGAAATCC	GGAAAAATGG	CACCTCCTCAG	GTGAGATTTA	TACAGTAGGT	5400
50	GCCGGAGTCA	CATTTTCTGT	TCAGGAAGGA	TACCAGTTGA	TGGGAGTAAC	CAAAATCACA	5460
	TGTTTGGAGT	TCGGAGAATG	GAATCATCTA	ATACCATATT	GTAAGAGCTGT	TTCATGTGGT	5520
	AAACCCGGCTA	TTCCAGAAAA	TGGTTGCATT	GAGGAGTTAG	CATTTACTTT	TGGCAGCAAA	5580
	GTGACATATA	GGTGTAAATA	AGGATATACT	CTGGCCGGTG	ATAAAGAATC	ATCCTGTCTT	5640
	GCTAACAGTT	CTTGGAGTCA	TTCCCTCCTC	GTGTGTGAAC	CAGTGAAGTG	TTCTAGTCCG	5700
55	GAAATATATA	ATAATGGAAA	ATATATTTTG	AGTGGGCTTA	CCTACCTTTC	TACTGCATCA	5760
	TATTCATGCG	ATACAGGATA	CAGCTTACAG	GGCCCTTCCA	TTATTGAATG	CACGGCTTCT	5820
	GGCATCTGGG	ACAGAGCGCC	ACCTGCCTGT	CACCTGCTCT	TCTGTGGAGA	ACCACCTGCC	5880
	ATCAAGAGAT	CTGTCAATAC	GGGGAATAAC	TTCACTTTCA	GGAAACCCGT	CACCTACACT	5940
	TGCAAGAAGG	GCTATACTCT	TGCTGGTCTT	GACACCATGG	AATGCCTGGC	CGACGGCAAG	6000
60	TGGAGTAGAA	GTGACCAGCA	GTGCTGGGCT	GTCTCTGTGT	ATGAGCCACC	CATTGTGGAC	6060
	CACGCCCTCT	CAGAGACTGC	CCATCGGCTC	TTTGGAGACA	TTGCATTCTA	CTACTGCTCT	6120
	GATGGTTACA	GCCTAGCAGA	CAATTCCTCAG	CTTCTCTGCA	ATGCCCAGGG	CAAGTGGGTA	6180
	CCCCCAGAA	GTCAAGACAT	GGCCCGTTGT	ATAGCTCATT	TCTGTGAAAA	ACCTCCATCG	6240
	GTTTCTCTATA	GCATCTTGGG	ATCTGTGAGC	AAAGCAAAAT	TTGCAGCTGG	CTCAGTTGTG	6300
65	AGCTTTAAAT	GCATGGAAGG	CTTGTACTG	AACACCTCAG	CAAAGATTGA	ATGTATGAGA	6360
	GGTGGGCACT	GGAAACCTTC	CCCCATGTCC	ATCCAGTGCA	TCCCTGTGCG	GTGTGGAGAG	6420
	CCACCAAGCA	TCATGAATGG	CTATGCAAGT	GGATCAAACT	ACAGTTTGGG	AGCCATGGTG	6480
	GCTTACAGCT	GCAACAAGGG	GTTCTACATC	AAAGGGGAAA	AGAAGAGCAC	CTGCGAAGCC	6540
	ACAGGGCAGT	GGAGTAGTCC	TATACCGACG	TGCCACCCGG	TATCTTGTGG	TGAACCACTT	6600
70	AAGTTGAGA	ATGGCTTTCT	GGAGCATACA	ACTGGCAGGA	TCTTTGAGAG	TGAAGTGAGG	6660
	TATCAGTGTA	ACCCGGGCTA	TAAGTCAGTC	GGAAGTCTCT	TATTTGTCTG	CCAAGCCAAT	6720
	CGCCACTGGC	ACAGTGAATC	CCCTCTGATG	TGTGTTCTCT	TCGACTGTGG	AAAACCTCCC	6780
	CCGATCCAGA	ATGGCTTCAT	GAAAGGAGAA	AACTTTGAAG	TAGGGTCCAA	GGTTCAAGTT	6840
	TTCTGTAAAT	AGGGTTATGA	GCTTGTGGT	GACAGTTCTT	GGACATGTCA	GAATCTGGC	6900
75	AAATGGAATA	AGAAAGTCAA	TCCAAGTGGC	ATGCCTGCCA	AGTGCCGAGA	GCCGCCCTCT	6960
	TTGAAAAACC	AGCTAGTATT	AAAGGAGTTG	ACCACCGAGG	TAGGAGTTGT	GACATTTTCC	7020
	TGTAAAGAGG	GGCATGTCTT	GCAAGGCCCC	TCTGTCTGTA	AATGCTTGCC	ATCCAGCAAA	7080
	TGGAATGACT	CTTTCCCTGT	TTGTAAGATT	GTTCTTTGTA	CCCCACCTCC	CCTAATTTCC	7140
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80	GTAGGTGGGT	TTTTCTTAAG	AGGAAATCT	ACCACCTCT	GCCAACTGTA	TGGCACCTGG	7260
	AGCTCTCCAC	TGCCAGAATG	TGTTCCAGTA	GAATGTCCCC	AACTGTAGGA	AATCCCAAT	7320
	GGAATCAATT	ATGTGCAAGG	CCTTGCCTAT	CTCAGCACAG	CTCTCTATAC	CTGCAAGCCA	7380
	GGCTTTGAAT	TGGTGGGAAA	TACTACCACC	CTTTGTGGAG	AAAATGGTCA	CTGGCTTGGG	7440
	GGAAAAACCA	CATGTAAAGC	CATTGAGTGC	CTGAAACCCA	AGGAGATTCT	GAATGGCAAA	7500
	TTCTCTTACA	CGGACCTACA	CTATGGACAG	ACCGTTACCT	ACTCTGCAA	CCGAGGCTTT	7560

	CGGCTCGAAG	GTCCCACTGC	CTTGACCTGT	TTAGAGACAG	GTGATTGGGA	TGTAGATGCC	7620
	CCATCTTGCA	ATGCCATCCA	CTGTGATTCC	CCACAACCCA	TTGAAAATGG	TTTTGTAGAA	7680
	GGTGCCAGATT	ACAGCATATGG	TGCCATAATC	ATCTACAGTT	GCTTCCCTGG	GTTCACAGTG	7740
5	GCTGGTCAATG	CCATGCAGAC	CTGTGAAGAG	TCAGGATGGT	CAAGTTCCAT	CCCAACATGT	7800
	ATGCCAATAG	ACTGTGGCCT	CCCTCCTCAT	ATAGATTTTG	GAGACTGTAC	TAAACTCAAA	7860
	GATGACCAGG	GATATTTTGA	GCAAGAAGAC	GACATGATGG	AAGTTCCATA	TGTGACTCCT	7920
	CACCCCTCCTT	ATCATTTGGG	AGCAGTGGCT	AAAACCTGGG	AAAATACAAA	GGAGTCTCCT	7980
	GCTACACATT	CATCAAACTT	TCTGTATGGT	ACCATGGTTT	CATACACCTG	TAATCCAGGA	8040
10	TATGAACCTC	TGGGGAACCC	TGTGCTGATC	TGCCAGGAAG	ATGGAACCTG	GAATGGCAGT	8100
	GCACCATCCT	GCAATTCAT	TGAATGTGAC	TTGCCTACTG	CTCCTGAAAA	TGGCTTTTTG	8160
	CGTTTTACAG	AGACTAGCAT	GGGAAGTGCT	GTGCAGTATA	GCTGTAAACC	TGGACACATT	8220
	CTAGCAGGCT	CTGACTTAAG	GCTTTGTCTA	GAGAATAGAA	AGTGGAGTGG	TGCCCTCCCA	8280
	CGCTGTGAAG	CCATTTCAATG	CAAAAAGCCA	AATCCAGTCA	TGAATGGATC	CATCAAAAGGA	8340
15	AGCAACTACA	CATACCTGAG	CACGTGTGAC	TATGAGTGTG	ACCCCGGATA	TGTGCTGAAT	8400
	GGCACTGAGA	GGAGAACATG	CCAGGATGAC	AAAACTGGG	ATGAGGATGA	GCCCATTTCG	8460
	ATTCCTGTGG	ACTCGAGTTC	ACCCCCAGTC	TCAGCCAATG	GCCAGGTGAG	AGGAGACGAG	8520
	TACACATTCC	AAAAAGAGAT	TGAATACACT	TGCAATGAAG	GGTTCCTGCT	TGAGGGAGCC	8580
	AGGAGTCGGG	TTGTCTTTGC	CAATGGAAAT	TGGAGTGGAG	CCACTCCCGA	CTGTGTGCCT	8640
20	GTCAGATGTG	CCACCCCGCC	ACAACCTGGC	AATGGGGTGA	CGGAAGGCCT	GGACTATGGC	8700
	TTCATGAAGG	AAGTAACATT	CCACTGTGAC	GAGGGCTACA	TCTTGACGGG	TGCTCCAAAA	8760
	CTCACCTGTC	AGTCAGATGC	CAACTGGGAT	GCAGAGATTC	CTCTCTGTAA	ACCACTCAAC	8820
	TGTGGACCTC	CTGAAGATCT	TGCCCATGGT	TTCCCTAATG	GTTCCTCCTT	TATTATGGG	8880
	GGCCATATAC	AGTATCAGTG	CTTTCCTGGT	TATAAGCTCC	ATGGAATTC	ATCAAGAAGG	8940
25	TGCTCTCTCA	TGGGCTCCTG	GAGTGGCAGC	TCACCTTCCT	GCCTGCCTTG	CAGATGTTCC	9000
	ACACCAAGTAA	TTGAATATGG	AACGTGCAAT	GGGACAGATT	TTGACTGTGG	AAAGGCAGCC	9060
	CGGATTTCAG	GCTTCAAGG	CTTCAAGCTC	CTAGGACTTT	CTGAATCAC	CTGTGAAGCC	9120
	GATGGCCAGT	GGAGCTCTGG	GTTCCTCCAC	TGTGAACACA	CTTCTGTGG	TTCTCTTCCA	9180
	ATGATACCAA	ATGCGTTTAT	CAGTGAGACC	AGCTCTTGGA	AGGAAAATGT	GATAACTTAC	9240
	AGCTGCAGGT	CTGGATATGT	CATACAAGGC	AGTTCAGATC	TGATTTGTAC	AGAGAAAGGG	9300
30	GTATGGAGCC	AGCCTTATCC	AGTCTGTGAG	CCCTTGTCCT	GTGGGTCCCC	ACCGTCTGTC	9360
	GCCAAATGCAG	TGGCAACTGG	AGAGGCACAC	ACCTATGAAA	GTGAAGTGAA	ACTCAGATGT	9420
	CTGGAAGGTT	ATACGATGGA	TACAGATACA	GATACATTCA	CCTGTGAGAA	AGATGGTCGC	9480
	TGTTTCCCTG	AGAGAATCTC	CTGCAGTCCT	AAAAAATGTC	CTCTCCCGGA	AAACATAACA	9540
	CATATACTTG	TACATGGGGA	CGATTTTCAAT	GTGAATAGGC	AAGTTTCTGT	GTCTATGTGA	9600
35	GAAGGGTATA	CTTTTGGAGG	AGTTAACATA	TCAGTATGTC	AGCTTGATGG	AACCTGGGAG	9660
	CCACCATTCT	CCGATGAATC	TTGCAGTCCA	GTTCCTTGTG	GGAAACCTGA	AAGTCCAGAA	9720
	CATGGATTTG	TGTTTGGCAG	TAAATACACC	TTTGAAGACA	CAATTATTTA	TCAGTGTGAG	9780
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40	GGAGGGGTGG	CAATATGCAA	AGAGACCAGG	TGTGAACTC	CACCTTGAAAT	TCTCAATGGG	9900
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	TACAGCTCTG	AAGGGCCATC	TGAGGCACAC	TGCACAGAAA	ATGGAACCTG	GAGCCACCCA	10020
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	CTGTCTGAAA	AGGAGTTTAA	TGTTGATCAG	AATGTGTCCA	TCAATGTAG	GGAAGGTTTT	10140
45	CTGCTGCAGG	GCCACGGCAT	CATTACCTGC	AACCCCGACG	AGACGTGGAC	ACAGACAAGC	10200
	GCCAAATGTG	AAAAAATCTC	ATGTGGTCCA	CCAGCTCACG	TAGAAAATGC	AATTGCTCGA	10260
	GGCGTACATT	ATCAATATGG	AGACATGATC	ACCTACTCAT	GTTCACAGTG	ATACATGTTG	10320
	GAGGGTTTCC	TGAGGAGTGT	TTGTTTAGAA	AATGGAACAT	GGACATCACC	TCTTATTTCG	10380
	AGAGCTGTCT	GTGATTTTCC	ATGTGAGAAT	GGGGGCATCT	GCCAACGCCC	AAATGCTTGT	10440
50	TCCTGTCCAG	AGGGCTGGAT	GGGGCGCCTC	TGTGAAGAAC	CAATCTGCAT	TCTTCCTCTG	10500
	CTGAACGGAG	GTGCTGTGTG	GGCCCTTATC	CAGTGTGACT	GCCTGCTGGG	CTGGACGGGG	10560
	TCTCGCTGTC	ATACAGCTGT	TTGCCAGTCT	CCCTGCTTAA	ATGGTGGAAA	ATGTGTGAAG	10620
	CCAAACCGAT	GTCACTGTCT	TTCTTCTTGG	ACGGGACATA	ACTGTTCCAG	GTAA	10674

Seq ID NO: C135 DNA Sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..390

	1	11	21	31	41	51	
60	ATGAGGTTCA	GTGCTCAGG	CATGAGGACC	GACTACCCCA	GGAGTGTGCT	GGCTCTGCT	60
	TATGTGTGAG	TCTGTCTCCT	CCTCTTGTGT	CCAAGGGGAG	TCATCGCTCC	CGCTGGCTCA	120
	GAACCATGGC	TGTGCCAGCC	GGCACCCAGG	TGTGGAGACA	AGATCTACAA	CCCCTTGGAG	180
	CAGTGTCTGT	ACAAATGACG	CATCGTGTCC	CTGAGCGAGA	CCCGCCAATG	TGGTCCCCCC	240
65	TGCACCTTCT	GGCCCTGCTT	TGAGCTCTGC	TGTCTTGATT	CCTTTGGCCT	CACAAACGAT	300
	TTTGTGTGTA	AGCTGAAGGT	TCAGGGTGTG	AATTTCCAGT	GCCACTCATC	TCCCATCTCC	360
	AGTAAATGTG	AAAGAGGCCG	GATATGTTAG				390

Seq ID NO: C136 DNA Sequence

Nucleic Acid Accession #: BC035671.1

Coding sequence: 126..1745

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75	GGCAGCGACT	GCGCCCCGTC	CCGGCGCCGC	GCTCGTCCGC	AGAGGAGGCG	GCCCGGCCCG	60
	GGCAGCTGCG	GCTCGGGATC	CGTCGAGGGG	AGGCCGAGCT	TGCCAAGCTG	GCGCCAGCG	120
	GGGTCAATGGT	GCCCGCGGCC	CGCGCGCGCG	GCGCACTGGC	GCGGGCTGCC	GGGCGGGGCC	180
	TCCTGGCTTT	GCTGCTCGCG	GTCTCCGCCC	CGCTCCGGCT	GCAGGCGGAG	GAGCTGGGTG	240
80	ATGGCTGTGG	ACACCTAGTG	ACTTATCAGG	ATAGTGGCAC	AATGACATCT	AAGAATTATC	300
	CCGGGACCTA	CCCCAATCAC	ACTGTTTGCG	AAAAGACAAT	TACAGTACCA	AAGGGGAAAA	360
	GACTGATTCT	GAGGTGTTGA	GATTTGGATA	TGGAATCCCA	GACCTGTGCT	TCTGACTATC	420
	TTCTCTTAC	CAGCTTCTCA	GATCAATATG	GTCCATACTG	TGGAAGTATG	ACTGTTCCCA	480
	AAGAACTCTE	GTGTAACACA	AGTGAAGTAA	CCGTCCGCTT	TGAGAGTGA	TCCCAATTTT	540
	CTGGCCGGGG	TTTTTTGCTG	ACCTATGCGA	GCAGCGACCA	TCCAGATTGA	ATAACATGTT	600

)

5 TGGAACGAGC TAGCCATTAT TTGAAGACAG AATACAGCAA ATTCTGCCCA GCTGGTTGTA 660
 GAGACGTAGC AGGAGACATT TCTGGGAATA TGGTAGATGG ATATAGAGAT ACCTCTTTAT 720
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 GGGAGAAAAA GAAATAAACA GGAATTAGGA CCACAGGATC TACACAGTCG AACTTCAACT 1140
 10 TTTATGTTAA GAGTTTGTG ATGAACCTCA AAAACAATAA TTCTAAGTGG AAGACCTATA 1200
 AAGGAATTGT GAATAATGAA GAAAAGGTGT TTCAGGGTAA CTCTAACTTT CGGGACCCAG 1260
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 15 ATTCATTGGT GTGGCGCAAG ACAAGTCAA GCACCAGTGT TTCAACTAAG AAAGAAGATG 1440
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 CCTTTAGAAA GAGAAGAAAG AAAGGAAGTC CGTATGGATC AGCAGAGGCT CAGAAAACAG 1620
 ACTGTTGGAA GCAGATTAAA TATCCCTTTG CCAGACATCA GTCAGCTGAG TTTACCATCA 1680
 20 GCTATGATAA TGAGAAGGAG ATGACACAAA AGTTAGATCT CATCACAGT GATATGGCAG 1740
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 AGGTGCCCCC GGTGCGATCT CAGAGATGAG GATCGGAACA CCATGTTCTT TCCCACCCTA 1860
 ACAACAACAA AGGCGAGTAA ATTAAGTAC TCTTTGTAAG GTACAGTTAC CGATTAATCT 1920
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 25 AAAAAA AAAA AAAA AAAA AAAA AAAA 2010

Seq ID NO: C137 DNA Sequence
 Nucleic Acid Accession #: Bos sequence
 Coding sequence: 1..1761

30 1 11 21 31 41 51
 ATGGGATTTC GTGCGGGGCA GCGACTGCGC CCCGTCCCGG CGCGCGGCTC GTCCGCAGAG 60
 GAGGCGGGCC GGCCCGGGCA GCTGCGGCTC GGGATCCGTC GAGGGGAGGC CGAGCTTGCC 120
 AAGCTGGGCG CCAGCGGGGT CATGGTGCCC GGGCGCCGCG CGCGCGGCGC ACTGGCGCGG 180
 35 GCTGCGGGGC GGGGCTTCTT GGTCTTGCTG CTCGCGGTCT CGGCCCGCT CCGGCTGCAG 240
 GCGGAGGAGC TGGGTGATGG CTGTGGACAC CTAGTGACTT ATCAGGATAG TGGCACAATG 300
 ACATCTAAGA ATTATCCCGG GACCTACCCC AATCACACTG TTTGCGAAAA GACAATTACA 360
 GTACCAAGAG GGAAAGAGCT GATTCTGAGG TTGGGAGATT TGGATATCGA ATCCCAGACC 420
 40 TGTGCTTCTG ACTATCTTCT CTTACCAGC TCTTCAGATC AATATGGTCC ATACTGTGGA 480
 AGTATGACTG TTCCCAAGA ACTCTTGTG AACACAAGTG AAGTAACCGT CCGCTTTGAG 540
 AGTGGATCCC ACATTTCTGG CCGGGGTTTT TTGCTGACCT ATGCGAGCAG CGACCATCCA 600
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 TGCCAGCTG GTTGTAGAGA CGTAGCAGGA GACATTTCTG GGAATATGGT AGATGGATAT 720
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 CAGTCGGTCA ATGAGAGTGG AGACCAAGTT CACTGGTCTC CTGGCCAAGC CCGACTTCAG 1020
 50 GACCAAGGCC CATCATGGGC TTCGGGCGAC AGTAGCAACA ACCACAAACC ACGAGAGTGG 1080
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 CAGTCGAAC TCAACTTTTA TGTAAAGAGT TTTGTGATGA ACTTCAAAAA CAATAATTCT 1200
 AAGTGAAGA CCTATAAAGG AATTGTGAAT AATGAAGAAA AGGTGTTTCA GGGTAACCTCT 1260
 AACTTTCCGG ACCCAGTGCA AAACAATTTC ATCCCTCCCA TCGTGGCCAG ATATGTGCGG 1320
 GTTGTCCCCC AGACATGGCA CCAGAGGATA GCCTTGAAGG TGGAGCTCAT TGGTTGCCAG 1380
 55 ATTACACAG GTAATGATT CATTGTTGCG CCAAGACAAA GTCAAGACAC CAGTGTTCAT 1440
 ACTAAGAAAG AAGATGAGAC AATCACAAGG CCCATCCCT CGGAAGAAAC ATCCACAGGA 1500
 ATAAACATTA CAACGGTGGC TATTCCATTG GTGCTCCTTG TTGTCCTGGT GTTTGCTGGA 1560
 ATGGGGATCT TTGCGACCTT TAGAAGAAAG AAGAAGAAAG GAAGTCCGTA TGGATCAGCA 1620
 60 GAGGCTCAGA AACACAGACT TTGGAAGCAG ATTAATATC CTTTGCCAG ACATCAGTCA 1680
 GCTGAGTTTA CCATCAGCTA TGATAATGAG AAGGAGATGA CACAAAAGTT AGATCTCATC 1740
 ACAAGTGATA TGGCAGGTTA A 1761

Seq ID NO: C138 DNA Sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..2310

65 1 11 21 31 41 51
 ATGTTCCAGC GGCAGGAAAG ATTTCTTGAC TTATCTTCAG CTGAAGCAGT GGCAGCTTGG 60
 ATATTACATC AACATCCTGA CATTATTAAC AAAGGTGATG GCTGTGGACA CCTAGTGACT 120
 TATCAGGATA GTGGCACAAAT GACATCTAAG AATTATCCCG GGACCTACCC CAATCACACT 180
 GTTTGCGAAA AGACAATTAC AGTACCAAAG GGGAAAAGAC TGATTCTGAG GTTGGGAGAT 240
 70 TTGGATATCG AATCCAGAC CTGTGCTTCT GACTATCTTC TCTTCACCAG CTCTTCAGAT 300
 CAATATGGAA TGCAGAAAGG GAGAGGAGACA GAAGTGCTTT GTCTTTCAGT GGCTGGCGCT 360
 CAGAGAGTGG ACATTCCTGT GCAGCTGTTG CCCAGCTTCC TGGAAAGGTTG GAAGGGTCAT 420
 75 GCTGATGCAA GAGGTCCATA CTGTGGAAGT ATGACTGTTT CCAAGAACT CTTGTTGAAC 480
 ACAAGTGAAG TAACGTCCTG CTTTGAGAGT GGATCCACCA TTTCTGGCCG GGGTTTTTTG 540
 CTGACCTATG CGAGCAGCGA CCATCCAGAT TTAATAACAT GTTTGGAACG AGCTAGCCAT 600
 TATTTGAAGA CAGAATACAG CAAATTCTGC CCAGCTGGTT GTAGAGACGT AGCAGGAGAC 660
 80 ATTTCTGGGA ATATGTGATA TGGATATAGA GATACCTCTT TATTGTGCAA AGCTGCCATC 720
 CATGCAGGAA TAATTGCTGA TGAACTAGGT GGCCAGATCA GTGTGCTTCA GCGCAAAGGG 780
 ATCAGTCGAT ATGAAGGGAT TCTGGCCAAAT GGTGTTCTTT CGAGGGATGG TTCCCTGTCA 840
 GACAAGCGAT TTCTGTTTAC CTCCAATGGT TGCAGCAGAT CCTGAGTTT TGAACCTGAC 900
 GGGCAATACA GAGCTTTCTT CTCATGGCAG TCGGTCAATG AGAGTGGAGA CCAAGTTTCA 960

TGGTCTCCTG GCCAAGCCCG ACTTCAGGAC CAAGGCCCAT CATGGGCTTC GGGCGACAGT 1020
 AGCAACAACC ACAAACCACG AGAGTGGCTG GAGATCGATT TGGGGGAGAA AAAGAAAATA 1080
 ACAGGAATTA GGACCACAGG ATCTACACAG TCGAATTCA ACTTTTATGT TAAGAGTTT 1140
 GTGATGAATC TCAAAAACAA TAATTCTAAG TGAAGACCT ATAAAGGAAT TGTGAATAAT 1200
 GAAGAAAAGG TGTTCAGGG TAACTCTAAC TTTCGGGACC CAGTGCAAAA CAATTTTCATC 1260
 CCTCCCATCG TGGCCAGATA TGTGCGGTT GTCCCCAGA CATGGCACC AAGGATAGCC 1320
 TTGAAGGTGG AGCTCATTGG TTGCCAGATT ACACAAGGTA ATGATTCATT GGTGTGGCGC 1380
 AAGACAAGTC AAAGCACCAG TGTTCAACT AAGAAAGAAG ATGAGACAAT CACAAGGCC 1440
 ATCCCCTCGG AAGAAACATC CACAGATGCC ATGCCAGTGC AGATTGTCCG AGACCATAAC 1500
 CAGATGATCT CACAAAGGGA GAATCTGGGA CCTGATGAGG GCAAAATACC TTTTAAAGGC 1560
 ACAGCGGAAA GCATGGTTAG AGTAGTGTTC GCTGTGTGG TTAATGACCT TGGCATGCTG 1620
 TTCTTAGCAC ACACACTGA GAGGACATT GATCACTACT GTTGGAGCA GATTAAATAT 1680
 CCCTTTGCCA GACATCAGTC AGCTGAGTTT ACCATCAGCT ATGATAATGA GAAGGAGATG 1740
 ACACAAAGT TAGATCTCAT CACAAGTGAT ATGGCAGATT ACCAGCAGCC CCTCATGATT 1800
 GGCACCGGGA CAGTCACGAG GAAGGGCTCC ACCTTCCGGC CCATGGACAC GGATGCCGAG 1860
 GAGGACGGGG TGACAGCCGA TGCCGGCGGC CACTATGACT GCCCGCAGCG GGCCGGCGCG 1920
 CAGGAGTACG CGCTGCCCTT GCGCGCCCGG GAGCCCGAGT ACGCCACGCC CATCGTGGAG 1980
 CGGCACGTGC TGGCGGCCCA CACGTTCTCT GCGCAGAGCG GCTACCGCGT CCCAGGGCCC 2040
 CAGCCCGGCC ACAAACTC CTCTCTCTCG GCGCGCTTCT CCCCCGTAGC GGGTGTGGGC 2100
 GCCCAGGACG GAGACTATCA AAGGCCACAC AGCGCACAGC CTGCGGACAG GGGCTACGAC 2160
 CGGCCCAAAG CTGTACGCGC CCTCGCCACC GAAAGCGGGC ACCCTGACTC TCAGAAGCCC 2220
 CCAACGCATC CCGGACGAG TGACAGCTAT TCTGCCCCA GAGACTGCCT CACACCCCTC 2280
 AACCAGACGG CCATGACTGC CCTTTTGTGA 2310

Seq ID NO: C139 DNA Sequence
 Nucleic Acid Accession #: NM_004616.2
 Coding sequence: 180..893

1 11 21 31 41 51
 AGTGCCCCAG GAGCTATGAC AAGCAAAGGA ACATACTTGC CTGGAGATAG CCTTTGCGAT 60
 ATTTAAATGT CCGTGGATAC AGAAATCTCT GCAGGCAAGT TGCTCCAGAG CATATTGCAG 120
 GACAAGCCTG TAACGAATAG TTAATTCAC GGCATCTGGA TTCTTAATCC TTTTCCGAAA 180
 TGGCAGGTGT GAGTGCCTGT ATAAAATATT CTATGTTTAC CTTCAACTTC TTGTTCTGGC 240
 TATGTGGTAT CTTGATCCTA GCATTAGCAA TATGGGTACG AGTAAGCAAT GACTCTCAAG 300
 CAATTTTGG TTCTGAAGAT GTAGGCTCTA GCTCCTACGT TGCTGTGGAC ATATTGATTG 360
 CTGTAGGTGT CATCATCATG ATTCTGGGCT TCCTGGGATG CTGCGGTGCT ATAAAAGAAA 420
 GTCGCTGCAT GCTTCTGTTG TTTTTCATAG GCTTGCTTCT GATCCTGCTC CTGCAAGTGG 480
 CGACAGGTAT CCTAGGAGCT GTTTTCAAAT CTAAGTCTGA TCGCATTGTG AATGAAACTC 540
 TCTATGAAA CACAAAGCTT TTGAGCGCCA CAGGGGAAAG TGA AAAACAA TTCCAGGAAG 600
 CCATAATGT GTTTCAAGAA GAGTTTAAAT GCTGCGGTTT GGTCAATGGA GCTGCTGATT 660
 GGGGAAATAA TTTTCAACAC TATCTGAAT TATGTGCTGT TCTAGATAAG CAGAGACCAT 720
 GCCAAAGCTA TAATGGAAAA CAAGTTTACA AAGAGACCTG TATTTCTTTC ATAAAAGACT 780
 TCTTGGCAAA AATTTGATTG ATAGTTATTG GAATATCATT TGGACTGGCA GTTATTGAGA 840
 TACTGGGTTT GGTGTTTTCT ATGGTCTGTG ATTGCCAGAT CGGGAACAAA TGAATCTGTG 900
 GATGCATCAA CCTATCGTCA GTCAAACCCC TTTAAATGTG TGCTTTGGCT TTGTAAATTT 960
 AAATATGTA GTGCTATATA AGTCAGGAGC AGCTGTCTTT TTAATATGTC TCGGCTAGCT 1020
 AGACCACAGA TATCTTCTAG ACATATTGAA CACATTTAAG ATTTGAGGGA TATAAGGGAA 1080
 AATGATATGA ATGTGTAATT TTACTCAAAA TAAAAGTAAC TGTTTACGTT AAAAAAATA 1140
 AAAAAAATA AAAAAAATA 1159

Seq ID NO: C140 DNA Sequence
 Nucleic Acid Accession #: NM_004617.2
 Coding sequence: 232..840

1 11 21 31 41 51
 CTTCAAGTCA GGGAGAATGT ATAAATGTCC ATTGCCATCG AGGTTCTGCT ATTTTGTAGA 60
 AGCTGAAGCA ACTCCAAGGA CACAGTTTCA AGAAATTTGG TTCTCAGCCC CAAAATACTG 120
 ATTGAATTGG AGACAATTAC AAGGACTCTC TGGCCAAAAA CCCTTGAAGA GGCCCGTGA 180
 AGGAGGCAGT GAGGAGCTTT TGATGTCTGA CCTGTGCTGT ACCACCCAG AATGTGCACT 240
 GGGGGCTGTG CCAGATGCCCT GGGGGGGACC CTCATTCCTT TGCTTTTTT TGGCTTCCTG 300
 GCTAACATCC TGTATTTTTT TCCTGGAGGA AAAGTGATAG ATGACAAAGA CCACCTTTCC 360
 CAAGAGATCT GGTTTTTTCG AGGAATATTA GGAAGCGGTG TCTTGATGAT CTTCCCTGCG 420
 CTGGTGTCTT TGGGCTGAA GAACAATGAC TGCTGTGGGT GCTGCGGCAA CGAGGGCTGT 480
 GGGAAAGCGAT TTGCGATGTT CACCTCCACG ATATTGTCTG TGGTTGGATT CTTGGGAGCT 540
 GGATACTCGT TTATCATCTC AGCCATTTCA ATCAACAAGG GTCCTAAATG CCTCATGGCC 600
 AATAGTACAT GGGGCTACCC CTTCCACGAC GGGGATTATC TCAATGATGA GGCCTTATGG 660
 AACAAGTGCC GAGAGCCTCT CAATGTGGTT CCCTGGAATC TGACCCTCTT CTCCATCCTG 720
 CTGGTGTGAG GAGGAATCCA GATGGTTCTC TGCGCCATCC AGGTGGTCAA TGGCCTCCTG 780
 GGGACCCCTCT GTGGGGAGCT GCAAGTGTGT GGTGCTGTG GGGGAGATGG ACCCGTTTAA 840
 ACCTCCGAGA TGAGCTGCTC AGACTCTACA GCATGACGAC TACAATTTCT TTTCAATAAA 900
 CTTCTTCTCT TCTTGGAAAT ATTAATTCCT ATCTGCTTCC TAGCTGATAA AGCTTAGAAA 960
 AGGCAGTTAT TCCTTCTTTC CAACCAGCTT TGCTCGAGTT AGAATTTTGT TATTTTCAAA 1020
 TAAAAAATAG TTTGGCCACT TAACAAATTT GATTTATAAA TCTTTCAAAT TAGTTCCTTT 1080
 TTGAATTTA CCAACAGGTT CAAAGCATACT TTTTCATGAT TTTTATTA CAAATGTAAA 1140
 ATGTATAAAG TCACATGTAC TGCCATACTA CTTCTTTGTA TATAAAGATG TTTATATCTT 1200
 TGAAGTTTT ACATAAATCA AAGGAAGAAA GCACATTTAA AATGAGAAAC TAAGACCAAT 1260
 TCTGTTTTT AAGAGGAAAA AGAATGATTG ATGTATCCTA AGTATTGTTA TTTGTGTCT 1320
 TTTTGTGCTG CTTGTCTTGA GTTGCTGTG ACTGATCTTT TGAGGCTGTC ATCATGGCTA 1380
 GGGTCTTTTT ATGTATGTTA AATTAAACC TGAATTCAGA GGTAACGT 1428

Seq ID NO: C141 DNA Sequence
 Nucleic Acid Accession #: NM_002381.2

Coding sequence: 64..1524

	1	11	21	31	41	51	
5	AAATCCGAGC	CTCGCGTGGG	CTCCTGGCCC	CCGACGGACA	CCACCAGGCC	CACGGAGCCC	60
	ACCATGCCGC	GCCCGGCCCC	CGCGCGCCGC	CTCCCGGGAC	TCCTCTCTGCT	GCTCTGGCCG	120
	CTGCTGCTGC	TGCCCTCCGC	CGCCCCCGAC	CCCGTGGCCC	GCCCGGGCTT	CCGGAGGCTG	180
	GAGACCCGAG	GTCCCGGGGG	CAGCCCTGGA	CGCGCCCTCT	CTCCTGCGGC	TCCCGACGGC	240
	CGCGCCGCTT	CCGGGACGAG	CGAGCCTGGC	CGCGCCCGCG	GTGCAGGTGT	TTGCAAGAGC	300
10	AGACCTTGG	ACCTGGTGT	TATCATTGAT	AGTTCTCGTA	GCGTACGGCC	CCTGGAATTC	360
	ACCAAAGTGA	AAACTTTTGT	CTCCCGGATA	ATCGACACTC	TGGACATTGG	GCCAGCCGAC	420
	ACCGGGGTGG	CAGTGGTGAA	CTATGCTAGC	ACTGTGAAGA	TCGAGTTCCA	ACTCCAGGCC	480
	TACACAGATA	AGCAGTCCCT	GAAGCAGGCT	GTGGGTCGAA	TCACACCCTT	GTCAACAGGC	540
	ACCATGTGAG	GCCTAGCCAT	CCAGACAGCA	ATGGACGAAG	CCTTCACAGT	GGAGGCAGGG	600
15	GCTCGAGAGC	CCTCTTCTAA	CATCCCTAAG	GTGGCCATCA	TTGTTACAGA	TGGGAGGCC	660
	CAGGACCAAG	TGAATGAAGT	GGCGGCTCGG	GCCCAAGCAT	CTGGTATTGA	GCTCTATGCT	720
	GTGGGCGTGG	ACCGGGCAGA	CATGGCGTCC	CTCAAGATGA	TGGCCAGTGA	GCCCTAGAG	780
	GAGCATGTTT	TCTACGTGGA	GACCTATGGG	GTCTATTGAG	AACTTTCCTC	TAGATTCCAG	840
20	GAAACCTTCT	GTGCGCTGGA	CCCCTGTGTG	CTTGAACAC	ACCAGTGCCA	GCACGTCTGC	900
	ATCAGTGATG	GGGAAGGCCA	GCACCACTGT	GAGTGTAGCC	AAGGATACAC	CTTGAATGCC	960
	GACAAGAAAA	CGTGTTCAGC	TCTTGATAGG	TGTGCTCTTA	ACACCCACGG	ATGTGAGCAC	1020
	ATCTGTGTGA	ATGACAGAAG	TGGCTCTTAT	CATTGTGAGT	GCTATGAAGG	TTATACCTTG	1080
	AATGAAGACA	GGAAAACTTG	TTCAGCTCAA	GATAAATGTG	CTTTGGGTAC	CCATGGGTGT	1140
25	CAGCACTTTT	GTGTGAATGA	CAGAACAGGG	TCCCATCATT	GTGAATGCTA	TGAGGGCTAC	1200
	ACTCTGAATG	CAGATAAAAA	AACATGTTCA	GTCCGTGACA	AGTGTGCCCT	AGGCTCTCAT	1260
	GGTTGCCAGC	ACATTGTGTG	GAGTGATGGG	GCCGCATCCT	ACCACTGTGA	TTGCTATCCT	1320
	GGCTACACCT	TAAATGAGGA	CAAGAAAAACA	TGTTAGCCCA	CTGAGGAAGC	ACGAAGACTT	1380
	GTTTCCACTG	AAGATGCTTG	TGGATGTGAA	GCTACACTGG	CATTCCAGGA	CAAGGTCAGC	1440
30	TCGTATCTTC	AAAGACTGAA	CACATAAATT	GATGACATTT	TGGAGAAAGT	GAAAAATAAT	1500
	GAATATGGAC	AAATACATCG	TAAATTTGCT	CCAATTTCTC	ACCTGAAAAA	GTGGACAGCT	1560
	TGTTGTACTT	AATACTCATG	CATTCTTTTG	CACACCTGTT	ATTGCCAATG	TTCCTGTCAA	1620
	TAATTTGCCA	TTATCTGTAT	TAATGCTTGA	ATATTACTGG	ATAAATTGTA	TGAAGATCTT	1680
	CTGCAGAATC	AGCATGATTT	TTCCAAGGAA	ATACATATGC	AGATACTTAT	TAAGAGCAAA	1740
35	CTTTAGTGTC	TCTAAGTTAT	GACTGTGAAA	TGATTGGTAG	GAAATAGAAAT	GAAAAAGTTA	1800
	GTGTTTCTTT	ATCTACTAAT	TGAGCCATTT	AATTTTAAAT	TGTTTATATT	AGATAACCAT	1860
	ATTCACAATG	GAAACTTTAG	GTCTAGTTTC	TTTTGATAGT	ATTTATAATA	TAAATCAATC	1920
	TTATTACTGA	GAGTGCAAAAT	TGTACAAAGT	ATTTACACAT	ACAACCTCAT	ATAACTGAGA	1980
	TGAATGTAAT	TTTGAAGTGT	TTAACACTTT	TTGTTTTTTG	CTTATTTTGT	TGGAGTATTA	2040
40	TTGAAGATGT	GATCAATAGA	TTGTAATACA	CATATCTAAA	AATAGTTAAC	ACAGATCAAG	2100
	TGAACATTAC	ATTGCCATTT	TTAATTTCAT	CTGGTCTTTG	AAAGAAATGT	ACTACTAAAG	2160
	AGCACTAGTT	GTGAATTTAG	GGTGTTAAC	TTTTTACCAA	GTACAAAAAT	CCCAATTCA	2220
	CTTTATTATT	TTGCTTCAGG	ATCCAAGTGA	CAAAGTTATA	TATTTATAAA	ATTGCTATAA	2280
	ATCGACAAAA	TCTAATGTTG	TCTTTTTAAT	GTAGTGATC	CACCTGCCCT	AGCCTCCCAA	2340
45	AGTGCTGGGA	TTACAGGCTT	GAAAGTCTAA	CTTTTTTTTA	CTTATATATT	TGATACATAT	2400
	AATTTCTTTG	TTGCAACTTT	TGCAAACTTT	GAGAACAAAA	CAGTCCCTTA	AATTTTGAC	2460
	TGCTCAATTC	TGTTTTTCGT	TTGCATTTGC	TTTAATATAA	TAAAGTTTAT	TACCTTTACA	2520
	TATTATCATG	TCTATTTTGT	ATGACTCATC	AATTTTGTCT	ATTAAAGATA	TTTCTTTAAA	2580
	TTAAAAAAA	AAAAAAA					2599

Seq ID NO: C142 DNA Sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

	1	11	21	31	41	51	
55	GCGGCGGGCG	CAGACAGCGG	CGGGCGCAGG	ACGTGCACTA	TGGCTCGGGG	CTCGCTGCGC	60
	CGGTTGCTGC	GGCTCCCTCGT	GCTGGGGCTC	TGGCTGGCGT	TGCTGCGCTC	CGTGGCCGGG	120
	GAGCAAGCGC	CAGGCACCGC	CCCCTGCTCC	CGCGGCAGCT	CCTGGAGCGC	GGACCTGGAC	180
60	AAGTGCAATG	ACTTGGCGTC	TTGCAGGGCG	CGACCGCACA	GCGACTTCTG	CCTGGGCTGC	240
	GCTGCAGCAC	CTCCTGCCCC	CTTCCGGCTG	CTTTGGCCCA	TCCTTGGGGG	CGCTCTGAGC	300
	CTGACCTTCG	TGCTGGGGCT	GCTTCTGTCG	TTTTTGGTCT	GGAGACGATG	CCGCAGGAGA	360
	GAGAAGTTCA	CCACCCCAT	AGAGGAGACC	GGCGGAGAGG	GCTGCCCAGC	TGTGGCGCTG	420
	ATCCAGTGAC	AATGTGCCCC	CTGCCAGCCG	GGGCTCGCCC	ACTCATCATT	CATTCAATCA	480
65	TTCTAGAGCC	AGTCTCTGCC	TCCCAGACGC	GGCGGGAGCC	AAGCTCCTCC	AACCACAAGG	540
	GGGGTGGGGG	GCGGTGAATG	ACCTCTGAGG	CCTGGGGCCA	GGGTTGAGGG	GAACCTTCCA	600
	AGGTGTCTGG	TTGCCCTGCC	TCTGGCTCCA	GAACAGAAAG	GGAGCCTCAC	GCTGGCTCAC	660
	ACAAAACAGC	TGACACTGAC	TAAGGAATG	CAGCATTGTC	ACAGGGGAGG	GGGGTGCCTT	720
70	CCTTCCTTAG	GACCTGGGGG	CCAGGCTGAC	TTGGGGGGCA	GACTTGACAC	TAGGCCCCAC	780
	TCACCTAGAT	GTCTGAAAT	TCCACCACGG	GGGTCAACCT	GGGGGGTTAG	GGACCTATTT	840
	TTAACTAGT	GGGCTGGCCC	ACTAGGAGGG	CTGGCCCTAA	GATACAGACC	CCCCCACTC	900
	CCCAAAGCGG	GGAGGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAATTTATT	960
	AATAAAGAA	TCTTTAATCT	TAAAAAATAA	AAAAAATAA			998

Seq ID NO: C143 DNA Sequence
Nucleic Acid Accession #: NM_001819
Coding sequence: 113..2146

	1	11	21	31	41	51	
80	CCAGGAGGCA	CGCTGGTTT	CCGGGGCCGC	TCCATCGCGC	CTTCTCTCTG	CGCCTCGCTT	60
	CTCCGGTCCA	GCCGCCATCT	TCCTTTCCGC	ACAGGGGCGG	CCGAGCGGGG	CCATGCAGCC	120
	AACGCTGCTT	CTCAGCCTCC	TGGGAGCCGT	GGGGCTGGCG	GCTGTCAATT	CCATGCCAGT	180
	GGATAACAGG	AACCAACAATG	AAGGAATGGT	GACTCGCTGC	ATCATTGAGG	TCCTCTCAAA	240

5 TGCTTGTGCG AAGTCCAGCG CTCACCCCAT CACCCCTGAG TGCCGCCAAG TCCTGAAGAC 300
 GAGTAGAAAA GACGTCAAAG ACAAGAGAGC AACTGAAAAAT GAAAAACACAA AGTTTGAAGT 360
 AAGATTGTTA AGAGACCCAG CTGATGCCTC GGAAGCCCAC GAGTCTCTCA GCAGGGGAGA 420
 GGCAGGAGCC CCAGGGGAGG AGGACATCCA AGGCCCAACA AAGGCAGACA CAGAGAAATG 480
 GGCAGAGGGA GGCGGGCACA GCCGAGAGCG AGCGGATGAG CCCAGTGGGA GCCTCTATCC 540
 CTCCGACAGC CAAGTCTCTG AAGAAGTGAA GACACGCCAT TCTGAGAAGA GCCAGAGAGA 600
 GGATGAGGAG GAGGAGGAGG GAGAGAACTA TCAAAAAGGG GAGCGAGGGG AAGATAGCAG 660
 TGAAGAGAAA CACCTTGAAG AGCCAGGAGA GACACAAAAC GCTTTTCTCA ATGAAAGAAA 720
 GCAGGCTTCA GCTATAAAAA AAGAGGAGTT AGTGGCCAGA TCGGAAACAC ATGCTGCCCG 780
 GCATTCTCAG GAGAAGACAC ATAGCCGAGA GAAGAGTAGC CAGGAGAGTG GAGAGGAGGC 840
 AGGGAGCCAG GAGAATCACC CCCAGGAGTC TAAAGGCCAA CCCCAGAGCC AGGAAGAATC 900
 TGAGGAAGGT GAGGAAGATG CCACCTCTGA GGTGGACAAA CGACGCACGA GGCCACAGCA 960
 CCACCACGGG AGGAGCAGGC CCGACAGGTC CTCTCAAGGA GGGAGTCTTC CCTCTGAGGA 1020
 AAAGGGACAC CCCCAGGAGG AATCTGAGGA GTCAAACTGC AGCATGGCCA GTTTAGGGGA 1080
 15 AAAGAGGGAC CACCATTCOA CCCACTACAG GCCTTCAGAG GAAGAACCCTG AATATGGAGA 1140
 AGAAATAAAG GGTATTCAG CGGTCCAGGC CCTTGAGGAC CTGGAGTGGG AGCGCTATAG 1200
 GGGCAGAGGA AGTGAAGAAT ACAGGGCTCC AAGACCTCAG AGTGAGGAGA GTTGGGATGA 1260
 GGAGGACAAG AGAACTACC CAGCTTAGA GCTTGATAAG ATGGCACATG GATATGGTGA 1320
 20 AGAAAGTGAG GAAGAGAGGG GCCTTGAGCC GGGAAAGGGA CGCCATCACA GAGGCAGGGG 1380
 AGGGGAGCCA CGTGCTTATT TCATGTCTGA CACCAGAGAA GAGAAAAGGT TCTTGGGTGA 1440
 AGGACACCAAC CGTGTCCAAG AAAACCAGAT GGACAAAGGA AGGAGGCATC CACAAGGTGC 1500
 GTGGAAAGAG CTGGACAGAA ATTATCTCAA CTACGGTGAG GAAGGAGCCC CAGGGAAGTG 1560
 GCAGCAGCAG GGAGACCTGC AGGACACTAA AGAAACAGG GAGGAAGCTA GGTTCOAAGA 1620
 25 TAAACAATAT AGCTCCCATC ACACAGCTGA AAAGAGGAAG AGATTAGGGG AACTGTTCAA 1680
 CCCATACCTAC GACCCCTCTCC AGTGGAAAGAG CAGCCATTTT GAAAGAAAGAG ACAACATGAA 1740
 TGACAATTTT CTCGAGGGTG AGGAGGAAAA TGAGCTGACC TTGAAACGAGA AGAATTTCTT 1800
 CCCAGAATAC AACTATGACT GGTGGGAGAA AAAGCCCTTC TCTGAGSATG TGAATGCGG 1860
 GTATGAGAAG AGAAACCTCG CCAGGGTCCC CAAGCTGGAC CTGAAAAGGC AATATGACAG 1920
 30 GGTGGCCCAA CTGGACCACTA TCCTTCACTA CAGGAAGAAG TCAGCTGAGT TTCCAGACTT 1980
 CTATGATTCT GAGGAGCCCG TGAGCACCCA CCAGGAGGCA GAAATGAAA AGGACAGGGC 2040
 TGACCAGACA GTCTCTGACG AGGACGAGAA AAAAGAACTC GAAAACTTGG CTGCAATGGA 2100
 TTTGGAACCTA CAGAAGATAG CTGAGAAATT CAGCCAAAGG GGTCTGACTGT CATTGGAGCG 2160
 GTGGGCACTG TTAAGAAGCA GCCATCACAT GATCTGTTTT TCACCCTTC ACTGAAAGAC 2220
 35 ACCATTATTA TACCCAAAGG CAGAAAGTAG AACTTACTAT TCATTAAATG TTTGACACAA 2280
 TTGGAATTGT CTTTAATTTT TGTCAGAAAT CTATTGAAAA TGTGAATTGC ATGACTTGTA 2340
 GCATATTCTT TTTGCAAAA TAGACATATT AACATGCTTA TGACAATGAC TGTGCTACTG 2400
 TCTTTGGAAA AATGTTTGTG TCAGTTGGAA ATAATAAAGG ATTCACCTGA GACC 2454

Seq ID NO: C144 DNA Sequence
 Nucleic Acid Accession #: XM_093082.1
 Coding sequence: 93..1988

45 1 11 21 31 41 51
 CTCTCTGTGG TAGGGACCTC TCCTCAGTAT TTGAAACTAA CCAGCATCTG ACAGATTTCG 60
 AATTTGTAAG AAATACCCCTC GAAGATTTCAG GAATGAAGCT TCTGTGTGAA GGATTAAGAA 120
 AGCCCAACTG TGTATTACAG ACATTGAGGT GGTACCGGTG CCTATCTCT TCTGCTTCTT 180
 GTGGGGCTCT AGCAGCTGTT CTTAGCACCA GTCAGTGGCT CACTGAACTG GAATTTAGTG 240
 50 AGACAAAATC GGAAGCTTCA GCTTTGAAAT TGCTCTATGG AGGCTTAAAA GATCCAAATT 300
 GCAAAATTACA GAAGCTCAAC TTGCAGTTTT CTTTATCTGT AACCGCTGCA AAACCTCCAG 360
 TTGGAATGGT TGAAGATTGT TCTGGTTTCT CGGATCATT GGTGCAATCT CATTTTGGCT 420
 ACTGTCAAGA CAGTTCTTCT AAATGTGATC TTTGTAAGCT GCTCTGGCTT TCCACCAGAG 480
 TTGCTGTCTG AAAGGATTGT GGGAGTCTTA AGTCCCTCCT ATCAGAAGGG CTGAACTGGG 540
 55 CAGGAAGACT TGAGGCACTG GAGGAGGTTT TGGGGTTGGG GGTGCTTGTA CAGCCCGGTG 600
 ACCCAGCATC TCAGGGTGGG GGGCATTGTG AAAACTATGG GTCTTTTAGA GACTTGGTGG 660
 ACTTAGAAGT CAAGGCAGAA CCAAGCCTGA GAAAGGTGG TATGGATCTC CAGAGACCCA 720
 CCTTACAAGT TGTCCTCCTT TGCAAAATCT TCTCCCTCAA ACTATTCTC TTTATTGCAT 780
 TGCTTAATTC TCCTGGTCAG GTTAGTGTGG TGCAAGTGAC CATCCCAGAC GGTTCGTGTA 840
 60 ACGTGACTGT TGGATCTAAT GTCACTCTCA TCTGCATCTA CACCACCACT GTGGCCCTCC 900
 GAGAAGCAGT TTCCATCCAG TGGTCTTCT TCCATAAGAA GGAGATGGAG CCAATTCTT 960
 CTCCTTGGGA GGAGGGGAAG TGGCCAGATG TTGAGGCTGT GAAGGGCACT CTTGATGGAC 1020
 AGCAGGCTGA ACTCCAGATT TACTTTTCTC AAGGTGGACA AGCTGTAGCC ATCGGGCAAT 1080
 TTAAGATCG AATTACAGG TCCAACGATC CAGGTAATGC ATCTATCACT ATCTCGCATA 1140
 65 TGCAAGCAGC AGACAGTGGG ATTTACATCT GCGATGTTAA CAACCCCCCA GACTTTCTCG 1200
 GCCAAAACCA AGGCATCTCT AACGTCACTG TGTAGTGAA ACCTTCTAAG CCCCTTTGTA 1260
 GCGTTCAAGG AAGACCAGAA ACTGGCCACA CTATTTCCCT TTCTGTCTC TCTGCGCTTG 1320
 GAACACCTTC CCCTGTGTAC TACTGGCATA AACTTGAGGG AAGAGACATC GTGCCAGTGA 1380
 AAGAAAACCT CAACCCCAAC ACCGGGATTT TGGTCATTGG AAATCTGACA AATTTTGAAC 1440
 70 AAGGTTATTA CAGTGTACT GCCATCAACA GACTTGGCAA TAGTCTCTGC GAAATCGATC 1500
 TCACCTCTTC ACATCCAGAA GTTGAATCA TTGTTGGGGC CTGATTGGT AGCCTGGTAG 1560
 GTGCCGCCAT CATCATCTCT GTTGTGTGCT TCGCAAGGAA TAAGGCCAAA GCAAGGCCAA 1620
 AAGAAAGAAA TTCTAAGACC ATCGCGGAAC TTGAGCCAAT GACAAAGATA AACCCAAGGG 1680
 GAGAAAGCGA AGCAATGCCA AGAGAAGACG CTACCCAACT AGAAGTAACT CTACCATCTT 1740
 75 CCATTCTATG GACTGGCCCT GATACCATCC AAGAACCAGA CTATGAGCCA AAGCCTACTC 1800
 AGGAGCCTGC CCCAGACCTT GCCCCAGGAT CAGAGCCTAT GGCAGTGCCT GACCTTGACA 1860
 TCGAGCTGGA GCTGGAGCCA GAAACGAGT CGGAATTGGA GCCAGAGCCA GAGCCAGAGC 1920
 CAGAGTCAGA GCCTGGGGTT GTAGTTGAGC CCTTAAGTGA AGATGAAAAG GGAGTGGTTA 1980
 AGGCATAG 1988

Seq ID NO: C145 DNA Sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1242

1 11 21 31 41 51
 1290

	ATGGTGTTCG	CATTTTGGAA	GGTCTTCTG	ATCCTAAGCT	GCCTTGCAGG	TCAGGTAGT	60
	GTGGTGCAG	TGACCATCCC	AGACGGTTTC	GTGAACGTGA	CTGTTGGATC	TAATGTCACT	120
5	CTCATCTGCA	TCTACACCAC	CACCTGTGGC	TCCCGAGAAC	AGCTTTCCAT	CCAGTGGTCT	180
	TTCTTCCATA	AGAAGGAGAT	GGAGCCAATT	TCTTCTCCTT	GGGAGGAGGG	GAAGTGGCCA	240
	GATGTTGAGG	CTGTGAAGGG	CACCTCTGAT	GGACAGCAGG	CTGAACCTCA	GATTTACTTT	300
	TCTCAAGGTG	GACAAGCTGT	AGCCATCGGG	CAATTTAAAG	ATCGAATTAC	AGGGTCCAAC	360
	GATCCAGGTA	ATGCATCTAT	CACATCTCG	CATATGCAGC	CAGCAGACAG	TGGAATTAC	420
	ATCTGCGATG	TTAACAACCC	CCCAGACTTT	CTCGGCCAAA	ACCAAGGCAT	CCTCAACGTC	480
10	AGTGTGTTAG	TGAACCTTC	TAAGCCCCTT	TGTAGCGTTC	AAGGAAGACC	AGAACTGGC	540
	CACACTATTT	CCCTTTCTCG	TCTCTCTGCG	CTTGAACAC	CTTCCCCTGT	GTACTACTGG	600
	CATAAACTTG	AGGGAAGAGA	CATCGTGCCA	GTGAAAGAAA	ACTTCAACCC	AACCACCGGG	660
	ATTTTGGTCA	TTGGAATCT	GACAAATTTT	GAACAAGGTT	ATTACCACTG	TACTGCCATC	720
	AACAGACTTG	GCAATAGTTC	CTGCGAAATC	GATCTCACTT	CTTCACATCC	AGAAGTTGGA	780
15	ATCATTGTTG	GGGCCTTGAT	TGGTAGCCTG	GTAGGTGCCG	CCATCATCAT	CTCTGTTGTG	840
	TGCTTCGCAA	GGAATAAGGC	AAAAGCAAAG	GCAAAAGAAA	GAAATTCTAA	GACCATCGCG	900
	GAACCTGAGC	CAATGACAAA	GATAAACCCA	AGGGGAGAAA	GCGAAGCAAT	GCCAAGAGAA	960
	GACGCTACCC	AACCTAGAAT	AACTCTACCA	TCTTCCATTC	ATGAGACTGG	CCCTGATACC	1020
20	ATCCAAGAAC	CAGACTATGA	GCCAAAGCCT	ACTCAGGAGC	CTGCCCCAGA	GCCTGCCCCA	1080
	GGATCAGAGC	CTATGGCAGT	GCCTGACCTT	GACATCGAGC	TGGAGCTGGA	GCCAGAAACG	1140
	CAGTCGGAAT	TGGAGCCAGA	GCCAGAGCCA	GAGCCAGAGT	CAGAGCCTGG	GGTTGTAGTT	1200
	GAGCCCTTAA	GTGAAGATGA	AAAGGGAGTG	GTTAAGGCAT	AG		1242

Seq ID NO: C146 DNA Sequence

Nucleic Acid Accession #: NM_003020.1

Coding sequence: 29..664

	1	11	21	31	41	51	
30	CGCTCCTCGG	GCTGCCCTCG	GGTTGACAAT	GGTCTCCAGG	ATGGTCTCTA	CCATGCTATC	60
	TGGCCTACTG	TTTGGGCTGG	CATCTGGATG	GACTCCAGCA	TTTGCTTACA	GCCCCCGGAC	120
	CCCTGACCGG	GTCTCAGAA	CAGATATCCA	GAGGCTGCTT	CATGGTGTTA	TGGAGCAATT	180
	GGGCATTGCC	AGGCCCGGAG	TGGAATATCC	AGCTCACCAG	GCCATGAATC	TTGTGGGCCC	240
35	CCAGAGCATT	GAAGGTGGAG	CTCATGAAGG	ACTTCAGCAT	TTGGGTCTCT	TTGGCAACAT	300
	CCCCAACATC	GTGCGAGAGT	TGACTGGAGA	CAACATTCTT	AAGGACTTTA	GTGAGGATCA	360
	GGGGTACCCA	GACCTCCCAA	ATCCCTGTCC	TGTTGGAAAA	ACAGATGATG	GATGTCTAGA	420
	AAACACCCCT	GACACTGCAG	AGTTTCAGTCG	AGAGTTCAG	TTGCACCAGC	ATCTCTTTGA	480
	TCCGGAACAT	GACTATCCAG	GCTTGGGCAA	GTGGAACAAG	AAACTCCTTT	ACGAGAAGAT	540
40	GAAGGGAGGA	GAGAGACGAA	AGCGGAGGAG	TGTCAATCCA	TATCTACAAG	GACAGAGACT	600
	GGATAATGTT	GTTGCAAAGA	AGTCTGTCCC	CCATTTTTCA	GATGAGGATA	AGGATCCAGA	660
	GTAAAGAGAA	GATGCTAGAC	GAAAACCCAC	ATTACCTGTT	AGGCCTCAGC	ATGGCTTATG	720
	TGCAGTGTA	AATGGAGTCC	CTGTGAATGA	CAGCATGTTT	CTTACATAGA	TAATTATGGA	780
	TACAAAGCAG	CTGTATGTAG	ATAGTGTATT	GTCCTTACAC	CGATGATTCT	GCTTTTGTCT	840
45	AAATTAGAAT	AAGAGCTTTT	TTGTTTCTTG	GGTTTTTAAA	ATGTGAATCT	GCAATGATCA	900
	TAAAAAATTA	AATGTGAATG	TCAACAATAA	AAAGCAAGAG	TATGAAAGGC	TCAGATTTC	960
	TGCAGTTTAA	AATGTGTCT	GAGGTGTGAC	TATTTTGGCC	AAGTCTGTAG	AAAGCTGTCA	1020
	TTTGATTTTG	ATTATGTAGT	TCATCCAGCC	CTTGGGCATT	GTTATACACC	AGTAAAGAAG	1080
	GCTGTACTCA	AGAGGAGGAG	CTGACACATT	TCACTTGGCT	GCGTCTTAAT	AAACATGAAT	1140
50	GCAAGCATTG	GC					1152

Seq ID NO: C147 DNA Sequence

Nucleic Acid Accession #: NM_024021.2

Coding sequence: 144..806

	1	11	21	31	41	51	
60	AACATTCCTG	CAATGGTTT	CAATATATGC	AGATGTCTCG	ATATAGGAAT	GAAATTACGT	60
	CTTTGGAACA	ACTTAAATAA	GTCAATATAT	CTTGGAGCTT	TAAAAATTAA	AAGGAGAGAG	120
	ATTCGAGCAC	CTTTTCTGCT	GCCATGACAA	CCATGCAAGG	AATGGAACAG	GCCATGCCAG	180
	GGGCTGGCCC	TGGTGTGCCC	CAGCTGGGAA	ACATGGCTGT	CATACATTCA	CATCTGTGGA	240
	AAGGATTGCA	AGAGAAGTTC	TTGAAGGGAG	AACCCAAAGT	CCTTGGGGTT	GTGCAGATTC	300
	TGACTGCCCT	GATGAGCCTT	AGCATGGGAA	TAACATGAT	GTGTATGGCA	TCTAATACTT	360
65	ATGGAAAGTA	CCCTATTTC	GTGTATATCG	GGTACACAAT	TTGGGGGTCA	GTAATGTTTA	420
	TTATTTCAGG	ATCCTTGTCA	ATTGCAGCAG	GAATTAGAAC	TACAAAGGC	CTGGTCCGAG	480
	GTAGTCTAGG	AATGAATATC	ACCAGCTCTG	TACTGGCTGC	ATCAGGGATC	TTAATCAACA	540
	CATTTAGCTT	GGCGTTTAT	TCATTCCATC	ACCCTTACTG	TAACTACTAT	GGCAACTCAA	600
	ATAATTGTCA	TGGGACTATG	TCCATCTTAA	TGGGTCTGGA	TGGCATGGTG	CTCCTCTTAA	660
70	GTGTGCTGGA	ATTCTGCATT	GCTGTGTCCC	TCTCTGCCTT	TGGATGTAAA	GTGCTCTGTT	720
	GTACCCCTGG	TGGGGTTGTG	TTAATTCTGC	CATCACATTC	TCACATGGCA	GAAACAGCAT	780
	CTCCACACAC	ACTTAATGAG	GTTTGGAGCC	ACCAAAAGAT	CAACAGACAA	ATGCTCCAGA	840
	AATCTATGCT	GACTGTGACA	CAAGAGCCTC	ACATGAGAAA	TTACCAAGTAT	CCAACCTCGA	900
	TACTGATAGA	CTTGTGATA	TTATTATTAT	ATGTAATCCA	ATTATGAAC	GTGTGTGTAT	960
75	AGAGAGATAA	TAAATTCAAA	ATTATGTCT	CATTTTCTTC	CCTGGAAC	AATAACTCAT	1020
	TTCACTGGCT	CTTATCTGAG	AGTACTAGAA	GTTAAATTAA	TAAATAATGC	ATTTAATGAG	1080
	GCAACAGCAC	TTGAAAGTTT	TTCACTCATC	ATAAGAACTT	TATATAAAGG	CATTACATTG	1140
	GCAAAATAGG	TTTGAAGCAA	GAAGAGCAAA	AAAAAGATAT	TGTTAAATG	AGGCCTCCAT	1200
	GCAAAACACA	TACTTCCCTC	CCATTTATTT	AACTTTTCTT	TTCTCCTACC	TATGGGGACC	1260
80	AAAGTGCTTT	TTCCCTCAGG	AAGTGGAGAT	GCATGGCCAT	CTCCCTCTCC	TTTCTTCTCT	1320
	CTCTCTGCTT	TTCTTCCCCA	TAGAAAGTAC	CTTGAAGTAG	CACAGTCCGT	CCTTGCTATG	1380
	GCAAGAGTAT	TCATTTGAGT	AAAAGTATAC	ATGGAGTAAA	AATCATATTA	AGCATCAGAT	1440
	TCAACTTATA	TTTTCTATTT	CATCTTCTTC	CTTCCCTTTC	TCCCACCTTC	TACTGGGCAT	1500
	AAATTATATCT	TAATCATATA	TGGAAATGTG	CAACATATGG	TATTTGTATA	ATACGTTTGT	1560
	TTTTATATGCA	GAGCAAAATT	AAATCAAAAT	AGAAGCAATA	AAAAAATAAA	AAAAAATAAA	1619

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CCCCCAACGA TTGGTAAACT GCAGGTGTTT CCCGCAGGCC GCAGTGCTC CAAGGTGGAA 300
 GTGGTAGCCT CCCTGAAGAA CGGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTCTA 360
 AAGAAAGTCA TCCAGAAAAT TTTGGACAGT GGAAACAAGA AAAACTGAGT AACAAAAAAG 420
 ACCATGCATC ATAAATATGC CCAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC 480
 CAGTAAGAAT AAGAGGAAG GGTGGTTT TTTCCATTTT CTACATGGAT TCCCTACTTT 540
 GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CCTGAAGTTT ACAGCTCAGC TAATGAAGTA 600
 CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCTTTGG 660
 CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCTTCAATG AATATTGAAT 720
 TGAAGATAAC TATTGTATTT CTATCATACA TTCTTAAAG TCTTACCAGG AAGGCTGTGG 780
 ATTTCTGTATG GAAAATATGT TTTATTAGTG TGCTGTGAG GGAGGTATCC TGTGTCTT 840
 ACTCACTCTT CTCATAAAAT AGGAAATATT TTAGTTCTGT TTTCTGGGG AATATGTTAC 900
 TCTTTACCCCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACATGGGGTG TGTCAATCCG 960
 TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG 1020
 CTAATATATT CTCTTCTTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT 1080
 CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCACTATAG GATGACTATA 1140
 ATTTCTGGTCA CTAAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC 1200
 TGATTGCTAA TTTACATAGA AATGTATTCT CTGGTTTTTT TAAATAAAG CAAAATTAAC 1260
 AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTGAA CAATTGAAAT ATAAATTCAT 1320
 CATTTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
 TTTAAAGGTT TTGACCATTT TGTTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
 AAATTGCACCT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TGGTACTTGT TATTGTCATT 1500
 TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAA AAAA 1547

Seq ID NO: C152 DNA Sequence

Nucleic Acid Accession #: NM_005242.2

Coding sequence: 148..1341

1 11 21 31 41 51
 CGGCCCGCCC TGGGGAGGCG CGCAGCAGAG GCTCCGATTC GGGGCAGGTG AGAGGCTGAC 60
 TTCTCTCGG TCGCTCCAGT GGAGCTCTGA GTTTCGAATC GGTGGCGGCG GATTCCCCGC 120
 GCGCCCGGCG TCGGGGCTTC CAGGAGGATG CCGAGCCCCA GCGGCGCGTG GCTGCTGGGG 180
 CGCGCCATCC TGCTAGCAGC CTCTCTCTCC TGCAGTGGCA CCATCCAAGG AACCAATAGA 240
 TCCTCTAAG GAAGAAGCCT TATTGGTAAG GTTGATGGCA CATCCACAGT CACTGGAAAA 300
 GGAGTTACAG TTGAAACAGT CTTTTCTGTG GATGAGTTTT CTGCATCTGT CCTCACTGGA 360
 AAACAGACCA CGGTCTTCTT TCCAATTGTC TACACAATTG TGTTTGTGGT GGGTTTGCCA 420
 AGTAACGGCA TGGCCCTGTG GGTCTTTCTT TTCCGAACCTA AGAAGAAGCA CCCTGCTGTG 480
 ATTTACATGG CCAATCTGGC CTGGCTGAC CTCTCTCTG TCATCTGGTT CCCCTTGAAG 540
 ATTGCCTATC ACATACATGC CAACAACCTGG ATTTATGGGG AAGCTCTTTG TAATGTGCTT 600
 ATTGGCTTTT TCATATGGCA CATGTACTGT TCATTTCTCT TCATGACCTG CCTCAGTGTG 660
 CAGAGGTATT GGGTCATCGT GAACCCCATG GGGCACTCCA GGAAGAAGGC AAACATTGCC 720
 ATTGCCATCT CCTTGGCAAT ATGGCTGTG ATTCTGCTGG TCACCATCCC TTTGTATGTC 780
 GTGAAGCAGA CCATCTTCAT TCCTGCCCTG AACATCACGA CTGTCTATGA TGTTTTGCCT 840
 GAGCAGCTCT TGGTGGGAGA CATGTTCAAT TACTTCTCT CTCTGGCCAT TGGGGTCTTT 900
 CTGTTCCGAC CTTTCTCTAC AGCCTCTGCC TATGTGCTGA TGATCAGAAT GCTGCGATCT 960
 TCTGCCATGG ATGAAAACCT AGAGAAGAAA AGGAAGAGGG CCATCAAACT CATTGTCACT 1020
 GTCTGGCCA TGTACCTGAT CTGCTTCACT CCTAGTAACC TTCTGCTTGT GGTGCATTAT 1080
 TTTCTGATTA AGAGCCAGGG CCAGAGGACAT GTCTATGCCC TGTACATTGT AGCCCTCTGC 1140
 CTCTCTACCC TTAACAGCTG CATCGACCCC TTTGTCTATT ACTTTGTTTC ACATGATTTT 1200
 AGGGATCATG CAAAGAAGCG TCTCCTTTGC CGAAGTGTC GCACTGTAAA GCAGATGCAA 1260
 GTATCCCTCA CCTCAAAGAA ACACCTCAGG AAATCCAGCT CTTACTCTTC AAGTTCAACC 1320
 ACTGTTAAGA CCTTCTAAG AGTTTCCAG GTCCCTCAGT GGGAAATGCA CAGTAGGATG 1380
 TGAACCTGT TTAATGTTAT GAGGACGTGT CTGTTATTTT CTAATCAAAA AGGTCTCACC 1440
 ACATACCACC G 1451

Seq ID NO: C153 DNA Sequence

Nucleic Acid Accession #: NM_003469.2

Coding sequence: 92..1945

1 11 21 31 41 51
 GAAACGGCCC GAGAAGCTCG CCCGAGAAC GGGGAGGAAT ATGCTGTGGA GTCCTCTGCG 60
 CATATAAACA AAAAGAGGAA ATCTTTCAAA CATGGCTGAA GCAAGACCC ACTGGCTTGG 120
 AGCAGCCCTG TCTCTTATCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180
 TCAGAGAAAC CAGCTGCTTC AGAAAGAACC AGACCTCAGG TTGGAATAATG TCCAAAAGTT 240
 TCCAGTCCCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACAAAGCTCA 300
 TAAGGAAGAA AGCAGCCGAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA 360
 AAAAGAAAAT GGCAGTGAAG GCCACTTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG 420
 GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAAT GAGCCTCAGT CTGCACCAAA 480
 AGAAAAAAG CCCTATGCCT TGAATTCAGA AAAGAACCTT CCAATGGACA TGAGTGATGA 540
 TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCTATGTA 600
 TGAAGAGAAT TCCAGGGATA ACCCTTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660
 TACTCTCAAA AGCCTTGCTA CATTGGAATC TGTCTTCAA GAGCTGGGGA AACTGCAGG 720
 ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACCTTATA CGGATGATGA 780
 AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTCCGGG GAGAAGACTG 840
 GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAGA 900
 GAATATAGGA AAAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT 960
 CCAGGAAGAA GATCTTCCGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT 1020
 AATTGCCTAT TTGAAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080
 AAATGGGGAA AGGGCCACCA GGCTTTTGA GAAACCTCTT GATTCTCAGT CTATTATCA 1140
 GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCAGAA GACTTAATGT AGATGCTCAA 1200
 AACTGGGAG AAGCCGAATG GATCAGTGA ACCGGAGCGG GAGCTTGACC TTCTGTTGA 1260
 CCTAGATGAC ATCTCAGAGG CTGACTTAGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT 1320

CTCCAAGAGT GGCTACCCCTA AAACACCTGG TCGTGCTGGG ACTGAGGCC TACCAGACGG 1380
 GCTCAGTGTT GAGGATATTT TAAATCTTT AGGGATGGAG AGTGCAGCAA ATCAGAAAAC 1440
 GTCGTATTTT CCCAATCCAT ATAACCAGGA GAAAGTTCTG CCAAGGCTCC CTTATGGTGC 1500
 TGGAGATCT AGATCGAACC AGCTTCCCAA AGCTGCCTGG ATTCCACATG TTGAAAACAG 1560
 ACAGATGGCA TATGAAAACC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG 1620
 GATGCTAGTT AAATACCCCTG AGATCATTAA TTCAAACCAA GTGAAGCGAG TTCCTGGTCA 1680
 AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAAT GAGCAGGCCA TCAAAGAGCA 1740
 TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGGTTCCT 1800
 TGTGGGGCCC CGAAGAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860
 AATGAAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGGAAGGG AGCATATTGC 1920
 TAAGAGAGCA ATGGAATAA TGTAAGCTGC TTTCATTAAT TACCCTACTT TCATTCCTCC 1980
 CACCCCAAGC AAATCCCAAC ATTCTCTTTC AGTGTGTTGA CTTCTATCCT GTTAACACTG 2040
 TAATATCTTT AAATGATGTA CAGGCAGATG AAACCAGGTC ACTGGGGAGT CTGCTTCATT 2100
 TCCTCTGAGC TGTATCTTGT TGTATGGATA TGTGTAATG TTATGACTCC TTGATAAAAA 2160
 ATTTATTATG TCCATTATTG AAGAAAGATA TCTATGACTG TGTTTAATAG TATATCTAAT 2220
 GGCTGTGGCA TTGTGATGTC TCACATATGA TAAAAAAGTG TCCTATAATT CTATTGAAAG 2280
 TTTTAAATAT TTATTGAATT ATTTTGTTC TGTCTGTAGC GTTTTGTGGA GTACTGGACC 2340
 AAAAAATAA AGCATTATAA ATATA 2365

Seq ID NO: C154 DNA Sequence
 Nucleic Acid Accession #: NM_030955
 Coding sequence: 327..5108

1 11 21 31 41 51
 GAATTCGGGG AGCGGGCGGG CTGCGAGGCC GCGGGGCATG CGGGAGGCGG AGGGGTGGGA 60
 CCGGGTGGCT GCGCCCATTC CACACCCGCC GAAAGCGGAC ACTGTCAGCT GAATCACTCC 120
 CCTTTTAGGA GGAGGGAGGG GGAAGAGGTG TCTAGCTAAT TTCTGCTTAA AAAAGCACAG 180
 GAGATCGCGG GTCAGCTTTG CAGTCGTGTC CTCTCGCGC CTGACCATGC ACCCCTGCAT 240
 CTTCTCTGCT GGCACAGGCG AGCGCTTTAT TTCTGAGGCT GAGGGCTAAA ACTTTTTTCA 300
 CTTTCTTCTT CCTCAACATC TGAATCATGC CATGTGCCCA GAGGAGCTGG CTGTCACACC 360
 TTTCCGTGGT GGCTCAGCTC CTTAAGTTTG GGGCGCTTTG CTATGGGAGA CAGCCTCAGC 420
 CAGGCCCGGT TCCTCTCCCG GACAGGAGGC AAGAGCATTT TATCAAGGGC CTGCCAGAAT 480
 ACCAGCTGGT GGGTCCAGTC CGAGTAGATG CCAGTGGGCA FTTTGTGTC TATGGCTTGC 540
 ACTATCCCAT CAGCAGCAGC AGGAGGAAGA GAGATTGGGA TGGCTCAGAG GACTGGGTGT 600
 ACTACAGAAT TTCTCAGGAG GAGAAGGACC TGTTTTTTAA CTGACGGTC AATCAAGGAT 660
 TTCTTTCCAA TAGCTACATC ATGGAGAAGA GATATGGGAA CCTCTCCAT GTTAAGATGA 720
 TGGCTTCTCT TGCCCCCTCT TGCCATCTCA GTGGCAGCGT TCTACAGCAG GGCACCAAG 780
 TTGGGACGGC AGCCCTCAGT GCCTGCCATG GACTGACTGG ATTTTTCCAA CTACCCATG 840
 GAGACTTTTT CATGTAACCC GTGAAGAAGC ATCCACTGGT TGAGGGAGGG TACCACCCGC 900
 ACATCGTTTA CAGGAGGCAG AAGGTTCCAG AAACCAAGGA GCCAACCTGT GGATTAAAGG 960
 ACAGTGTTAA CATCTCCCGA AAGCAAGAGC TATGGCGGGA GAAGTGGGAG AGGCACAACT 1020
 TGCCAAGCAG AAGCCTCTCT CGGCGTTCCA TCAGCAAGGA GAGATGGGTG GAGACACTGG 1080
 TGGTGGCCGA CACAAAGATG ATTGAATACC ATGGGAGTGA GAATGTGGAG TCCTACATCC 1140
 TCACCATCAT GAACATGGTC ACTGGGTGT TCCATAACCC AAGCATTGGC AATGCAATTG 1200
 ACATTGTGTG GGTTCGGCTC ATTCTACTCG AAGAAGAAGA GCAAGGACTG AAAATAGTTC 1260
 ACCATGCAGA AAGACACTG TCTAGCTTCT GCAAGTGGCA GAAGAGTATC AATCCCAAGA 1320
 GTGACCTCAA TCCTGTTCAT CACGACGTGG CTGTCTTCT CACCAGAAAG GACATCTGTG 1380
 CTGGTTTCAA TCGCCCTGTC GAGACCTTGG GCCTGTCTCA CCTTTCAGGA ATGTGTGAG 1440
 CTACCCGAGC TTGTAACATC AATGAAGATT CGGGACTCCC TCTGGCTTTC ACAATTGCC 1500
 ATGAGCTAGG ACACAGCTTC GGCATCCAGC ATGATGGGAA AGAAATGAC TGTGAGCCTG 1560
 TGGGCAGACA TCCGTACATC ATGTCCCGCC AGCTCCAGTA CGATCCCACT CCGCTGACAT 1620
 GGTCCAAGTG CAGCGAGGAG TACATCACCC GCCTTCTGGA CCGAGGCTGG GGGTTCTGTG 1680
 TTGATGACAT ACCTAAAAGG AAGGCTTGA AGTCCAAGGT CATGCCCCC GGAGTGATCT 1740
 ATGATGTTCA CCACAGTGC CAGCTACAAT ATGGACCCAA TGCTACCTTC TGCCAGGAAG 1800
 TAGAAAAGCT CTGCCAGACA CTGTGGTGCT CCGTGAAGGG CTTTGTGTCG TCTAAGCTGG 1860
 ACGCTGCTGC AGATGGAATC CAATGTGGTG AGAAGAAGTG GTGTATGGCA GGCAGGTGCA 1920
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 CCCACTGTTC CAGGACCTGT GGGGCTGGAG TCCAGAGCGC AGAGAGGCTC TGCAACCAAC 2040
 CCGAGCCRAA GTTTGGAGGG AAATATTGCA CTGGAGAAAG AAAACGCTAT CGCTTGTGCA 2100
 ACGTCCACCC CTGTCTGCTA GAGGCACCAA CATTTCTGCA GATGCAGTGC AGTGAATTG 2160
 ACATGTTTCC CTACAAGAAAT GAACCTTACC ACTGGTTTCC CATTTTAAAC CCAGCAGATC 2220
 CTTGTGAGCT CTACTGCCGA CCCATAGATG GCCAGTTTTC TGAGAAAATG CTGGATGCTG 2280
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 TGGAAATTGA GGGAGCTGGA AACTTCCTGG CCATCAGGAG TGAAGATCCT GAAAAATATT 2580
 ACCTGAATGG AGGGTTTATT ATCCAGTGGA ACGGGAACCTA TAAGCTGGCA GGGACTGTCT 2640
 TTCAGTATGA CAGGAAAAGG GACCTGGAAG AGCTGATGGC CACAGGTCCT ACCAATGAGT 2700
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 GACAGAAAGG GTGCCATGAA AAGGCTTGT CACCCAGGTG GTGGGCAGGG GAGTGGGAAG 3000
 CATGCTCGCG GACATGCGGG CCCCACGGGG AGAAGAAGCG AACCGTGCTG TGCATCCAGA 3060
 CCATGGTCTC TGACGAGCAG GCTCTCCCGC CCACAGACTG CCAGCACCTG CTGAAGCCCA 3120
 AGACCCTCCT TTCTGTCAAC AGAGACATCC TGTGCCCCCT GGCCTGGACA GTGGGCAACT 3180
 GGAGTGAATG TCTGTTTCC TGTGTGGTGT GAGTGGGAT TCGCAGTGTG ACATGTGCCA 3240
 AGAACCATGA TGAACCTTGC GATGTGACAA GGAACCCCAA CAGCCGAGCT CTGTGTGGCC 3300
 TCCAGCAATG CCCTTCTAGC CGGAGAGTTC TGAAACCCAA CAAAGGCACCT ATTTCCAATG 3360
 GAAAAAACCC ACCAACACTG AAGCCCGTCC CTCACCTTAC ATCCAGGCCG AGAATGCTGA 3420
 CCACCCACAG AGGGCCTGAG TCTATGAGCA CAAGCACTCC AGCAATCAGC AGCCCTAGTC 3480
 CTACCAACAG CTCCAAAGAA GGAGACCTGG GTGGGAAACA GTGGCAAGAT AGCTCAACCC 3540

AACCTGAGCT GAGCTCTGCG TATCTCATTT CCACTGGAAG CACTTCCCAG CCCATCCTCA 3600
 CTTCCTCAATC CTTGAGCATT CAGCCAAGTG AGGAAAATGT TTCCAGTTCA GATACTGGTC 3660
 CTACCTCGGA GGGAGGCTTT GTAGCTACAA CAACAAGTGG TTCTGGCTTG TCATCTTCCC 3720
 GCACCCCTAT CACTTGGCCT GTGACTCCAT TTTACAATAC CTTGACCAAA GGTCCAGAAA 3780
 TGGAGATTCA CAGTGGCTCA GGGGAAGAAA GAGAACAGCC TGAGGACAAA GATGAAAGCA 3840
 ATCTCTGAAT ATGGACCAAG ATCAGAGTAC CTGGAATGA CGCTCCAGTG GAAAGTACAG 3900
 AAATGCCACT TGCACCTCCA CTAACACCAG ATCTCAGCAG GGAGTCCCTGG TGGCCACCCT 3960
 TCAGCACAGT AATGGAAGGA CTGCTCCCCA GCCAAAGGCC CACTACTTCC GAAACTGGGA 4020
 CACCACAGT TGAGGGGATG GTTACTGAAA AGCCAGCCAA CACTCTGCTC CCTCTGGGAG 4080
 GAGACCACCA GCCAGAACC TCAGGAAAGA CGGCAACCCG TAACCACCTG AAACCTCCAA 4140
 ACAACATGAA CCAACAGAAA AGTTCTGAAC CAGTCTTGAC TGAGGAGGAT GCAACAAGTC 4200
 TGATTACTGA GGGCTTTTGT CTAATGTGCT CCAATTACAA GCAGCTCACA AACGGCCACG 4260
 GCTCTGCACA CTGGATCGTC GGAACCTGGA GCGAGTGTCT CACCACATGT GGCCTGGGGG 4320
 CCTACTGGAA AAGGGTGGAG TGCACCACCC AGATGGATTG TGAAGTGTGC GGCATCCAGA 4380
 GACCTGACCC TGCAAAAAGA TGCCACCTCC GTCCCTGTGC TGGCTGGAAA GTGGGAAACT 4440
 GGAGCAAGTG CTCAGAGAAC TGCAGTGGGG GCTTCAAGAT ACGCGAGATT CAGTGCCTGG 4500
 ACAGCCGGGA CCACCGGAAC CTGAGGCCAT TTCACTGCCA GTTCTGTGCC GGCATTCTCT 4560
 CCCCATTGAG CATGAGCTGT AACCCTGAGC CCTGTGAGGC GTGGCAGGTG GAGCCTTGA 4620
 GCCAGTGTCT CAGTCTCTGT GGAGGTGGAG TTCAGGAGAG AGGAGTGTTC TGTCCAGGAG 4680
 GCCTCTGTGA TTGGACAAAA AGACCCACAT CCACCATGTC TTGCAATGAG CACCTGTGCT 4740
 GTCACCTGGC CACTGGGAAC TGGGACCTGT GTTCCACTTC CTGTGGAGGT GGCTTTTACA 4800
 AGAGGATTGT CCAATGTGTG CCCTCAGAGG GCAATAAAAC TGAAGACCAA GACCAATGTC 4860
 TATGTGATCA CAAACCCAGA CCTCCAGAAT TCAAAAATG CAACCAGCAG GCCTGCAAGA 4920
 AAAGTGCCGA TTTACTTTGC ACTAAGGACA AACTGTGAGC CAGTTTCTGC CAGACACTGA 4980
 AAGCCATGAA GAAATGTTCT GTGCCACCG TGAGGGCTGA GTGTGTGCTC TCGTGTCCCC 5040
 AGACACACAT CACACACACC CAAAGGCAAA GAAGGCAACG GTTGCTCCAA AAGTCAAAAG 5100
 AACTCTAAGC CCAAA 5115

Seq ID NO: C155 DNA Sequence
 Nucleic Acid Accession #: NM_001062.1
 Coding sequence: 76..1380

1 11 21 31 41 51
 GCTCTCATT CTTCTGCCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG 60
 TACACTGTTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTTT 120
 TCTTTTATTC CAAGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180
 CTAAACCTTC TGTGAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC 240
 AATGTTGTGT TGTCCTCAA ACTTGTGGA ATCCAGATCC AAACCTGAT GCAAAAGATG 300
 ATCCAACAAA TCAAAATCAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACCGTG AGGAAAACTT AATATATGAT 420
 TACCACCTGA CTGACAAGCT AGAAAATAAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480
 CACAATGGCA CTCCCCTGAC TAACTACTAC CAGCTCAGCC TGGACGTTT GGCCTTGTGT 540
 CTGTTCAATG GGAACCTACT AACCCTGCGA GTTGTCAACC ACTTCACTCC TGAAAATAAA 600
 AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CTGGCTCTG 660
 ACCTGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAAG CAGATGAAGG CAGTTTAAAG 720
 AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATTG TGTCTGAGAA AAAAGAAAAT 780
 GGTCTCATTG GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840
 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAACTC TGAATACAGT GCTCACGGAA 900
 ATTTCTCAAG GAGCATTCAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960
 GGAAAGACCT TCTTGATAT TAACAAAGAC TCTTCTTGG TCTCTGCTTC AGGTAACCTC 1020
 AACATCTCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC 1080
 GTCAATTACT CTGTGAGAA CAATGAAACA TATTTACCA ATGTCACTGT GCTAAATGGT 1140
 TCTGTCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC 1200
 ACAAATGGAG AGCGCTCATG GGGGCCCTAT ATCACTGTGA TTCAGGGCCT ATGTGCCAAC 1260
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCCTGAG CCAAGGAGCT 1320
 GGTAGTTACG TTGTCCGCAA TGGAGAAAAC TTGGAGGTTG GCTGGAGCAA ATACTAATAA 1380
 GCCCAACTT TCCTCAGCTG CATAAAATCC ATTTGCAAGT GAGTTCATG TTTATTGTCC 1440
 TTAGCCCTTC TTCTCATTT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCCTTCTC 1500
 TCTCTACATG TTCAATAAAA GTTGTGAAA GATTAAC 1537

Seq ID NO: C156 DNA Sequence
 Nucleic Acid Accession #: NM_004591
 Coding sequence: 59..349

1 11 21 31 41 51
 CACTCCCAAA GAAGTGGGTA CTCACACTG AGCAGATCTG TTCTTTGAGC TAAAAACCAT 60
 GTGCTGTACC AAGAGTTTGC TCCTGGCTGC TTTGATGTCA GTGCTGCTAC TCCACCTCTG 120
 CGGCGAATCA GAAGCAGCAA GCAACTTTGA CTGCTGTCTT GGATACACAG ACCGTATTCT 180
 TCATCCTAAA TTATTGTGG GCTTCACACG GCAGCTGGCC AATGAAGGCT GTGACATCAA 240
 TGCTATCATC TTTACACAAA AGAAAAAGTT GTCTGTGTGC GCAAAATCAA AACAGACTTG 300
 GGTGAAATAT ATGTGCGCTC TCCTCAGTAA AAAAGTCAAG AACATGTAAA AACTGTGGCT 360
 TTTCTGGAAT GGAATTGGAC ATAGCCCAAG AACAGAAAAG ACCTTGCTGG GGTGGAGGTT 420
 TTCACTTGCA CATCATGGAG GGTTTAGTGC TTAATCAATT TGTGCTTAC TGGACTTGTC 480
 CAATTAATGA AGTTGATTC TATTGCATCA TAGTTTGCTT GTTTAAGCA TCACATTAAA 540
 GTTAAACTGT ATTTATGTT ATTTATAGCT GTAGGTTTTC TGTGTTTAGC TATTTAATAC 600
 TAATTTTCCA TAAGCTATTT TGGTTTAGTG CAAAGTATAA AATATATTT GGGGGGAAT 660
 AAGATTATAT GGACTTTCTT GCAAGCAACA AGCTATTTT TAAAAAACT ATTTAATCATT 720
 CTTTGTGTTA TATGTTTGTG TCTCTAAAT TGTGTAAATT GCATTATAAA ATAAGAAAAA 780
 CATTAATAAG ACAATATTT 799

Seq ID NO: C157 DNA Sequence
 Nucleic Acid Accession #: NM_013271.1

Coding sequence: 27..809

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1      11      21      31      41      51
5      |      |      |      |      |
TCCGGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTGCGC GCTGCTCTGG GGGCCGCGGG 60
CCGGGGGCGT CGGCCTTTTG GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCGCGC 120
TCTGCGCGCG GCCGTTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGCTCG 180
AGACTGGCGC TCCTCGCCGC TTCCGGCGGT CAGTGCCCGG AGGTGAGGCG GCGGGGGCGG 240
TGCAGGAGCT GGC CGGCGC GTCCGCGCATC TGCTGGAGGC CGAACGTCAG GAGCGGGCGC 300
10      GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG 360
TCTGGGGCGC CCCC CGCAAC TCTGATCOGG CTCTGGGCCT GGACGACGAC CCGACGCGC 420
CTGACGCGCA GCTCGCTCGC GCTCTGCTCC GCGCCCGCCT TGACCTTGCC GCCCTAGCAG 480
CCCAGCTTGT CCCC CGCGCC GTCCCGCGCG CGGCGCTCCG ACCCGGCGCC CCGGTCTACG 540
15      ACGACGGCCC CGCGGGCCCG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660
TGGCAGCCCC GCGCCGCGCTC GCGCGTGCCG CCGACCAAGA TGTGGGCTCT GAGCTGCCCC 720
CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAACGCCT AGAGACCCCG GCGCCCCAGG 780
TGCCTGCACG CCGCTCTTGT CCACCTTGAG CACTGCCCGG ATCCCGTGCA CCCTGGGACC 840
20      CAGAAGTGCC CCGGCATACC CGCCACCAGG ACTTCTCCCC GCCAGCAGT GCCAGGCAAC 900
TTACCCCGGC CAGCCAGCCC TCTACCCGA GGATCCCTAC CCCC TGCGCC ACAATAACAT 960
GATCTGAGC

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Seq ID NO: C158 DNA Sequence
Nucleic Acid Accession #: NM_002245.2
Coding sequence: 183..1193

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1      11      21      31      41      51
30      |      |      |      |      |
GGGCAGGAAG ACGGCGCTGC CCGGAGGAGC GGGGCGGGCG GGCGCGCGGG GGAGCGGGCG 60
GCGGGCGGGA GCCAGGCCCG GCGCGGGGCG GGGGCGGGCG GGCCAGAAGA GCGGCGGGCG 120
CGCGCTCCGG CCGGTCTGCG GCGTTGGCCT TGGCTTTGGC TTTGGCGCGG GCGGTGGAGA 180
AGATGCTGCA GTCCCTGGCC GGCAGCTCGT GCGTGCGCCT GGTGGAGCGG CACCGCTCGG 240
CCTGCTGCTT CCGCTTCTTG GTGCTGGGCT ACTTGCTCTA CCTGGTCTTC GGCAGCTGG 300
35      TCTTCTCCTC GGTGAGCTG CCCTATGAGG ACCTGCTGCG CCAGGAGCTG CGCAAGCTGA 360
AGCGACGCTT CTGAGGAGG CACGAGTGCC TGTCTGAGCA GCAGCTGGAG CAGTTCCTGG 420
GCCGGGTGCT GGAGGCCAGC AACTACGGCG TGTCTGGTGT CAGCAACGCC TCGGGCAACT 480
GGAACTGGGA CTTCACCTCC GCGCTCTTCT TCGCCAGCAC CGTGCTCTCC ACCACAGGTT 540
ATGGCCACAC CGTGCCCTTG TCAGATGGAG GTAAGGCCCT CTGCATCATC TACTCCGTCA 600
40      TTGGCATTCC CTTCACCTC CTGTTCTTGA CGGCTGTGGT CCAGCGCATC ACCGTGCACG 660
TCACCCGCGG CCGGCTCCTC TACTTCCACA TCCGCTGGGG CTCTCCCAAG CAGGTGGTGG 720
CCATCGTCCA TGCCGTGCTC CTGCGTTTGT TCACTGTGTC CTGCTTCTTC TTATCCCCGG 780
CGCTGTCTT CTACGTCCTG GAGGATGACT GGAACITCCT GGAATCCTTT TATTTTGT 840
TTATTTCCCT GAGCACCAAT GGCCTGGGGG ATTATGTGCC TGGGAAGGC TACAATCAAA 900
45      AATTGAGAGA GCTCTATAAG ATTGGGATCA CGTGTACCT GCTACTTGGC CTTATTGCCA 960
TGTTGGTAGT TCTGGAAACC TTCTGTGAAC TCCATGAGCT GAAAAAATTC AGAAAAATGT 1020
TCTATGTGAA GAAGGACAAG GACGAGGATC AGGTGCACAT CATAGAGCAT GACCAACTGT 1080
CCTTCTCCTC GATCACAGAC CAGGCAGCTG GCATGAAAGA GGACCAGAAG CAAAATGAGC 1140
CTTTTGTGGC CACCCAGTCA TCTGCCTGCG TGGATGGCCC TGCAAAACCAT TGAGCGTAGG 1200
50      ATTTGTGCA TTATGCTAGA GCACCAAGGT CAGGGTGCAA GGAAGAGGCT TAAGTATGTT 1260
CATTTTATC AGAATGCAAA AGCGAAAATT ATGTCACTTT AAGAAATAGC TACTGTTTGC 1320
AATGTCTTAT TAAAAACAA CAAAAAAGA CACATGGAAC AAAGAAGCTG TGACCCAGC 1380
AGGATGTCTA ATATGTGAGG AATGAGATG TCCACCTAAA ATTCTATATG GACAAAATTA 1440
TCTCGACCTT ACATAGGAGG AGAATACTTG AAGCAGTATG CTGCTGTGGT TAGAAGCAGA 1500
TTTATACTT TTAACGTGAA ACTTTGGGGT TTGCATTTAG ATCATTTAGC TGATGGCTAA 1560
55      ATAGCAAAAT TCTATTATG AAGCAAAAAA AAAAAAGATA GAGATGTGTT TTATAAATAG 1620
GTTTATGTGT ATCTGTTTGC ATGTACCCAC CAAAATGAT TATTTTGGGA GAATCTAAGT 1680
CAAACCTACT ATTTATAATG CATAGGTAAC CATTAACATAT GTACATATAA AGTATAAATA 1740
TGTTTATATT CTGTATATAT GGTTTAGGTC ACCAGATCCT AGTGTAGTTC TGAAACTAAG 1800
60      ACTATAGATA TTTGTTTCT TTTGATTCT CTTTATACTA AAGAAATCCAG AGTTGTCTACA 1860
ATAAAAAAG GGAATAAATA AACTTGAGAG TGAATAACCA T 1901

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Seq ID NO: C159 DNA Sequence
Nucleic Acid Accession #: NM_005472.1
Coding sequence: 93..404

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1      11      21      31      41      51
70      |      |      |      |      |
AAAGGGACTC CTTGAAACTG ATTGAGAGCC CAGTGGATT T GCCAGCAGTT TGAGCTTCTA 60
CCGAGTCTTC CCCCACCTCA ATCCCTGTTG CTATGGAGAC TACCAATGGA ACGGAGACCT 120
GGTATGAGAG CCTGCATGCC GTGCTGAAGG CTCTAAATGC CACTCTTCAC AGCAATTGTC 180
TCTGCGCGCC AGGGCCAGGG CTGGGGCCAG ACAACCAGAC TGAAGAGAGG CGGGCCAGCC 240
TACCTGGCCG TGATGACAAC TCCTACATGT ACATTCTCTT TGTCTATGTT CTATTTGCTG 300
TAACCTGTGG CAGCTCATC CTGGGATACA CCGCTCCCG CAAAGTGGAC AAGCGTAGTG 360
75      ACCCTATCA TGTGTATATC AAGAACCCTG TGTCTATGAT CTAACACGAG AGGGCTGGGA 420
CGGTGGAAGA CCAAGACACC TGGGGATTGC GTCTGGGGCC TCCAGAATCT TGCTGTGGAC 480
TGACATCAGG CT 492

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Seq ID NO: C160 DNA Sequence
Nucleic Acid Accession #: NM_005245.1
Coding sequence: 187..13959

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1      11      21      31      41      51
80      |      |      |      |      |
CTGGGCGGCC GGGCGCGGGG AGAGGGCGCG GGAGCGGCTC GTGCGGCAGG TACCATGCGG 60

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	ACGCGCGAGC	CCGCGGAGGC	CCCGGCAGGC	CCGTCCCTGC	TCGGGGGCGC	GCTGAGACGG	120
	CGGGTGAGCT	CCACGAGAGC	GCCGTGCGCA	CTTCGGGCGCA	ACTTTGCGAT	TCCGACAGT	180
	TAAGCAATGG	GGAGACATT	GGCTTTGCTC	CTGCTTCTGC	TCCTTCTCTT	CCAACATTTT	240
5	GGAGACAGTG	ATGGCAGCCA	ACGACTTGAA	CAGACTCCTC	TGCAGTTTAC	ACACCTCGAG	300
	TACAACGTCA	CCGTGCAGGA	GAACCTCTGA	GCTAAGACTT	ATGTGGGGCA	TCCTGTCAAG	360
	ATGGGTGTTT	ACATTACACA	TCCAGCGTGG	GAACTAAGGT	ACAAAATTTG	TCCCGGAGAC	420
	AGTGA AAAAC	TGTTCAAAGC	TGAAGAGTAC	ATTCTCGGAG	ACTTTTGCTT	TCTAAGAATA	480
	AGGACCAAG	GAGGAAATAC	AGCTATTCTT	AATAGAGAAG	TGAAGGATCA	CTACACATTG	540
10	ATAGTGAAAG	CAC TTGAAA	AAATACTAAT	GTGGAGGCGC	GAAACAAAGT	CAGGGTGCAG	600
	GTGCTGGATA	CAAAATGACTT	GAGACCGTTA	TTCTCACCCA	CCTCATACAG	CGTTTCTTTA	660
	CCTGAAAACA	CAGCTATAAG	GACCAGTATC	GCAAGAGTCA	GCGCCACGGA	TGCAGACATA	720
	GGAAACCAAG	GGGAATTTTA	CTACAGTTTT	AAAGATCGAA	CAGATATGTT	TGCTATTTCAC	780
	CCAACCAAGT	GTGTGATAGT	GTTAACTGGT	AGACTTGATT	ACCTAGAGAC	CAAGCTCTAT	840
15	GAGATGGA AA	TCCTCGCTGC	GGACCGTGGC	ATGAAGTTGT	ATGGGAGCAG	TGGCATCAGC	900
	AGCATGGCCA	AGCTAACGGT	GCACATCGAA	CAGGCCAATG	AATGTGCTCC	GGTGATAACA	960
	CGAGTGACAT	TGTCACCAT	AGAACTGGAC	AGGGACCCAG	CATATGCAAT	TGTGACAGTG	1020
	GATGATCGCG	ATCAGGGTGC	CAATGGTGAC	ATAGCATCTT	TAAGCATCGT	GGCAGGTGAC	1080
	CTTCTCCAGC	AGTTTAGAAC	AGTGAGGTCC	TTTCCAGGGA	GTAAGGAGTA	TAAAGTCAAA	1140
20	GCCATCGGTG	ACATTGATTG	GGACAGTCAT	CCTTTCCGGCT	ACAATCTCAC	ACTACAGGCT	1200
	AAAGATAAAG	GAAC TCCGCC	CCAGTTCTCT	TCTGTTAAAG	TCATTACAGT	GACTTCTCCA	1260
	CAGTTCAAAG	CCGGGCCAGT	CAAGTTTGAA	AAGGATGTTT	ACAGAGCAGA	AATAAGTGAA	1320
	TTTGCTCCTC	CCAACACACC	TGTGTCATG	GTAAGGCCA	TTCTGCTTTA	TTCCCATTTG	1380
	AGGTATGTTT	TTAAAAGGAC	ACCTGGAAAA	GCTAAATTCA	GTTTAAATTA	CAACACTGGT	1440
25	CTCATTTCTA	TTTTAGAACC	AGTTAAAAGA	CAGCAGGCAG	CCCATTTTGA	ACTTGAAGTA	1500
	ACAACAAGTG	ACAGAAAAGC	GTCCACCAAG	GTCTTGGTGA	AAGTCTTAGG	TGCAAAATAGC	1560
	AATCCCCCTG	AATTTACCCA	GACAGCGTAC	AAAGCTGCTT	TTGATGAGAA	CGTGCCCAT	1620
	GGTACTACTA	TCATGAGCCT	GAGTGCCTGA	GACCTTGATG	AGGGTGAGAA	TGGGTACGTG	1680
	ACATACAGTA	TGCAAAATTT	AAATCATGTG	CCGTTTGCGA	TTGACCATT	CACTGGTGCC	1740
30	GTGAGTACGT	CAGAAAACCT	GGACTACGAA	CTGATGCCCT	GGGTTTATAC	TCTGAGGATT	1800
	CGTGCAATCAG	ACTGGGGCTT	GCCGTACCGC	CGGGAAGTCG	AAGTCTCTGC	TACAATTACT	1860
	CTCAATAACT	TGAATGACAA	CACACCTTTG	TTTGAGAAAA	TAAATTGTGA	AGGGACAATT	1920
	CCGAGAGATC	TAGGCGTGGG	AGAGCAAATA	ACCAC TGT	CTGCTATTGA	TGCAGATGAA	1980
	CTTCAAGTTG	TACAGTATCA	GATTGAAGCT	GGAAATGAAC	TGGATTGTTT	TAGTTTAAAC	2040
35	CCCAACTCGG	GGGTATTGTC	ATTAAAGCGA	TCGCTAATGG	ATGGCTTAGG	TGCAAGGGTG	2100
	TCITTTCCACA	GTCTGAGAAT	CACAGCTACA	GATGGAGAAA	ATTTTGCCAC	ACCATTATAT	2160
	ATCAACATAA	CAGTGGCTGC	CAGTCACAAG	CTGGTAAACT	TGCAGTGTGA	AGAGACTGGT	2220
	GTTCGCAAAA	TGCTGGCAGA	GAAGCTCCTG	CAGGCAATA	AATTACACAA	CCAGGGAGAG	2280
	GTGGAGGATA	TTTTCTTCGA	TTCTCACTCT	GTCAATGCTC	ACATACCGCA	GTTTAGAAGC	2340
40	ACTCTTCCGA	CTGGTATTCA	GGTAAAGGAA	AACCAGCCTG	TGGGTTCCAG	TGTAATTTTC	2400
	ATGAAC TCCA	CTGACCTTGA	CACTGGCTTC	AATGGAAAAC	TGGTCTATGC	TGTTTCTGGA	2460
	GGAAATGAGG	ATAGTTGCTT	CATGATTGAT	ATGGAAACAG	GAATGCTGAA	AATTTTATCT	2520
	CCCTCTTGACC	GTCAAGCAAC	AGACAAATAC	ACCCTGAATA	TTACCCCTCTA	TGACCTTGGG	2580
	ATACCCGAGA	AGGCTCGGTG	GCGTCTTCTA	CATGTCGTGG	TTGTCGATGC	CAATGATAAT	2640
45	CCACCCGAGT	TTTTACAGGA	GAGCTATTTT	GTGGAAGTGA	GTGAAGACAA	GGAGGTACAT	2700
	AGTGAAATCA	TCCAGTTTGA	AGCCACAGAT	AAAGACCTGG	GGCCCAACGG	ACACGTGACG	2760
	TACTCAATCT	TTACAGACAC	AGACACATTT	TCAATTGACA	GCGTGACGGG	TGTTGTTAAC	2820
	ATCGCACGCC	CTCTGGATCG	AGAGCTGCAG	CATGAGCACT	CCTTAAAGAT	TGAGGCCAGG	2880
	GACCAAGCCA	GAGAAGAGCC	TCAGCTGTTC	TCCACTGTGC	TTGTGAAAGT	ATCACTAGAA	2940
50	GATGTTAATG	ACAACCCACC	TACATTTATT	CCACCTAATT	ATCGTGTGAA	AGTCCGAGAG	3000
	GATCTTCCAG	AAGGAACCGT	CATCATGTGG	TTAGAAGCCC	ACGATCCTGA	TTTAGGTTCAG	3060
	TCTGGTCAGG	TGAGATACAG	CCTTCTGGAC	CACGGAGAAG	GAAACTTCGA	TGTGGATAAA	3120
	CTCAGTGGAG	CAGTTAGGAT	CGTCCAGCAG	TTGGACTTTG	AGAAGAAGCA	AGTGTATAAT	3180
	CTCACTGTGA	GGGCCAAAGA	CAAGGGAAAG	CCAGTTTCTC	TGCTCTCTAC	TTGCTATGTT	3240
55	GAAGTGAGG	TGTTTGAATG	GAATGAGAAC	CTGCACCCAC	CCGTGTTTTC	CAGCTTTGTG	3300
	GAAAAGGGGA	CAGTGAAGAA	AGATGCACCT	GTTGGTTTCT	TGGTAATGAC	GGTGTCCGCT	3360
	CATGATGAGG	ACGCCGGAAG	AGATGGGGAG	ATCCGATACT	CCATTAGAGA	TGGCTCTGGC	3420
	GTTGGTGTTT	TCAAATAGG	TGAAGAGACA	GGTGTCTAG	AGACGTGAGA	TCGACTGGAG	3480
	CGTGAATCGA	CTCCCAATTA	TTGGCTAACA	GTCTTTGCAA	CCGATCAGGG	TGTCGTGCTC	3540
60	CTTTTCATCGT	TCATAGAGAT	CTACATAGAG	GTTGAGGATG	TCAATGACAA	TGCACCACAG	3600
	ACATCAGAGC	CTGTTTATTA	CCCAGAAATC	ATGGAAAATT	CTCCTAAAGA	TGTATCTGTG	3660
	GTCCAGATCG	AGGCATTTGA	TCCAGATTCTG	AGCTCTAATG	ACAAGCTCAT	GTACAAAATT	3720
	ACAAGTGGAA	ATCCACAAGG	ATTCTTTTCA	ATACATCCTA	AAACAGGTCT	CATCACAACT	3780
	ACGTCAAGGA	AGCTAGACCG	AGAACAGCAA	GATGAACACA	TATTAGAGGT	TACTGTGACA	3840
65	GACAAATGTA	GTCCCCCACA	ATCAACCAAT	GCAAGAGTCA	TTGTGAAAAT	CCTTGATGAA	3900
	AATGACAACA	AACCTCAGTT	TCTGCAAAAG	TTCTACAAAA	TCAGACTCCC	TGAGCGGGAA	3960
	AAGCCAGACC	GAGAAAGAAA	TGCCAGACGG	GAGCCGCTCT	ATCGCTCAT	AGCCACCAGC	4020
	AAGGATGAGG	GCCCCAATGC	AGAAATCTCC	TACAGCATCG	AAGACGGGAA	TGAGCATGGC	4080
	AAATTTTTC	GTCAACCGAA	AACTGGAGTG	GTTTCGTCCA	AGAGGTTTTC	AGCAGCTGGA	4140
70	GAATATGATA	TTCTTTCAAT	TAAGGCAATT	GACAAATGGT	GCCCCAAAA	GTCAATCAAC	4200
	ACCAGACTCC	ATATTGAATG	GATCTCCAAG	CCCAACAGT	CCCTGGAGCC	CATTTCTATT	4260
	GAAGAATCAT	TTTTTACCTT	TACTGTGATG	GAAAGTGACC	CCGTTGCTCA	CATGATTGGA	4320
	GTAATATCTG	TGGAGCCTCC	TGGCATACCC	CTTTGGTTTG	ACATCACTGG	TGGCAACTAC	4380
	GACAGTCACT	TCGATGTGGA	CAAGGGAAC	GGAACCATCA	TTGTTGCCAA	ACCTCTTGAT	4440
75	GCAGAACAGA	AGTCAAACTA	CAACCTCACA	GTCCGAGGCTA	CAGATGGAAC	CACCACTATC	4500
	CTCACTCAGG	TATTATCAAA	AGTAATAGAC	ACAAATGACC	ATCGTCTCTA	GTTTTCTACA	4560
	TCAAAGTATG	AAGTTGTTAT	TCCTGAAGAT	ACAGCGCCAG	AAACAGAAAT	TTTGCAAAATC	4620
	AGTGTCTGTG	ATCAGGATGA	GAAAAACAAA	CTAATCTACA	CTCTGCAGAG	CAGTAGAGAT	4680
	CCACTGAGTC	TCAAGAAAT	TGCTCTTGAT	CCTGCAACCG	GCTCTCTCTA	TACTTCTGAG	4740
80	AAACTGGATC	ATGAAGCTGT	TTCAACGACA	CACCTCACGG	TCAATGGTACG	AGATCAAGAT	4800
	GTGCCGTGTA	AACGCAACTT	TGCAAGGATT	GTGGTCAATG	TCAGCGACAC	GAATGACCAC	4860
	GCCCCGTGGT	TCACCGCTTC	CTCCTACAAA	GGGCGGGTTT	ATGAATCGGC	AGCCGTGGC	4920
	TCAGTTGTGT	TGCAGGTGAC	GGCTCTGGAC	AAGGACAAAG	GGAAAAATGC	TGAAGTGCTG	4980
	TACTCGATCG	AGTCAGGAAA	TATTGAAAT	ATTGGAAT	CTTTTATGAT	TGATCCTGTC	5040
	TTGGGCTCTA	TTAAAAGTGC	CAAAGAATTA	GATCGAAGTA	ACCAAGCGGA	GTATGATTTA	5100

	ATGGTAAAAG	CTACAGATAA	GGGCAGTCCA	CCAATGAGTG	AAATAACTTC	TGTGCGTATC	5160
	TTTGTACAAA	TTGCTGACAA	CGCCTCTCCG	AAGTTTACAT	CAAAAGAATA	TTCTGTTGAA	5220
	CTTAGTGAAA	CTGTGAGCAT	TGGGAGTTTC	GTGGGATGG	TTACAGCCCA	TAGTCAATCA	5280
5	TCAGTGGTGT	ATGAAATAAA	AGATGGAAT	ACAGGTGATG	CTTTTGATAT	TAATCCACAT	5340
	TCTGGAACCTA	TCATCACTCA	GAAAGCCCTG	GACTTTGAAA	CTTTGCCCAT	TTACACATTG	5400
	ATAATACAAG	GAACATAACAT	GGCTGGTTTG	TCCACTAATA	CAACGGTTCT	AGTTCACCTG	5460
	CAGGATGAGA	ATGACAACGC	GCCAGTTTTT	ATGCAGGCAG	AATATACAGG	ACTCATTAGT	5520
	GAATCAGCCT	CAATTAACAG	CGTGGTCCTA	ACAGACAGGA	ATGTCCCCT	GGTGATTGGA	5580
10	GCAGCTGATG	CTGATAAAGA	CTCAATAGCT	TTGCTTGAT	ATCAGATTGT	TGAACCATCT	5640
	GTACACACAT	ATTTTGCTAT	TGATTCTAGC	ACTGGTGCTA	TTCATACAGT	ACTAAGTCTG	5700
	GACTATGAAG	AAACAAGTAT	TTTTCACTTT	ACCGTCCAAG	TGCATGACAT	GGGAACCCCA	5760
	CGTTTATTGG	CTGAGTATGC	AGCGAATGTA	ACAGTACATG	TAATTGACAT	TAATGACTGC	5820
	CCCCCTGTGT	TTGCCAAGCC	ATTATATGAA	GCATCTCTTT	TGTTACCAAC	ATACAAAGGA	5880
15	GTAAAAGTCA	TCACAGTAAA	TGCTACAGAT	GCTGATTCAA	GTGCATTCTC	ACAGTTGATT	5940
	TACTCCATCA	CCGAAGGCCA	CATCGGGGAG	AAGTTTTCTA	TGGACTACAA	GACTGGTGCT	6000
	CTCACTGTCC	AAAAACAAC	TCAGTTAAGA	AGCCGCTACG	AGCTAACCGT	TAGAGCTTCC	6060
	GATGGCAGAT	TTGCCGGCCT	TACCTCTGTC	AAAAATTAATG	TGAAAGAAAG	CAAGAAAGAT	6120
	CACCTAAAGT	TATCCAGGTA	TGCTACTCT	CGCGTAGTGA	AAGAGAATT	CACCGAGGCC	6180
20	GAAACATTAG	CTGTCACTAC	TGCTATTGGG	AGTCCAATCA	ATGAGCCTTT	GTTTTATCAC	6240
	ATCCTCAACC	CAGATCGCAG	ATTAAAAATA	AGCCGCACTT	CAGGGGTTCT	GTCAACCACT	6300
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	TCACTGAAA	AGCAATTTGA	GCTTGACACC	TTAAATAAAG	AATATCTTGT	TACAGTGGTT	6660
	GCAAAAGATG	GAGGGAACCC	GGCCTTTTCA	GCGGAAGTTA	TCGTTCCGAT	CACCTGTCATG	6720
	AATAAAGCCA	TGCTCTGTTT	TGAAAAACCT	TTCTACAGTG	CAGAGATTGC	AGAGAGCATC	6780
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30	TACAGCATCA	CAGACGGAGA	CCCTTTCAGC	CAGTTCACTA	TTAACTTCAA	TACTGGAGTT	6900
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	GCAACTGACT	CCTTGACGGG	CGCTCATGCT	GAAGTATTTG	TGGACATCAT	AGTAGACGAC	7020
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35	TCGTGAATTG	GAACGTCTGT	TGTTCAAGTT	AGAGCCACCG	ATTCTGATT	AGAACCAAAAT	7140
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40	GAAGCCAGAA	TTAGCGAGCA	CGCCCTCAT	GGGCATTTCG	TGACCTGTGT	AAAAGCCTAT	7440
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45	GAATATGAAG	TGGAACTAGC	TGAAAAAGCT	CCCTACATA	CCCTGGTGAT	GGAGGTGAAA	7740
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	GCCAAAGACA	GATTTTACAT	AAATGAGAGA	GGACAGATAT	TTACTTTGGA	AAAACCTGAT	7860
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55	GATAATGGGT	CTTCATCAAA	AGAACTGTGT	GTCTTGTCT	ATGTTAAAT	CCTTCCACCG	8280
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	CCTGTTGAAA	CAGAGATAGA	TCTCATCCGA	GCAGAACATA	GTGGGACTGT	TCTTTACAGC	8400
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65	CATGAAAAGA	GAGACAAATTA	CCAGATTAAA	GTGGTTGCAT	CAGATCATGG	TGAAAAGATC	8880
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	AAACACAGAG	CGGGAACGCT	GCTGACAGA	GTGCAGGCCA	CAGATGCCGA	CGCAGGATTA	9660
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	GCCACCGTGT	CTGAGGACAT	TCTTGTGTTGA	ACTGAAGTTC	TTCAAGTGTA	TGCAGCAAGT	9960
	CGGGATATTG	AAGCAAAATG	AGAAATCAC	TACTCAATAA	TAAGTGGAAA	TGAACATGGG	10020
	AAATTGAGCA	TAGATTCTAA	AACAGGGGCC	GTATTATCA	TTGAGAATCT	GGATTATGAG	10080
	AGCTCTCATG	AGTATTACCT	AACAGTAGAG	GCCACTGATG	GAGGCACGCC	TTCACTGAGC	10140

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	GCGCCCGTCT	TCTCCAGGGG	AAACTACAGT	GTCAATTATCC	AGGAAAATAA	GCCAGTGGGC	10560
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	GAGATGTGTA	ACCAACACAT	CGCGATCCGC	TTTGCCAAAC	TCACTCCGGA	AGAATTCTGT	11160
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20	GACATACAGA	TTGTTAGTTT	GCAGTCTCTT	GAACCTCACC	CACATCTGGA	CGTCTTACTT	11280
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	TCCTCCAACC	CATGCCTCTA	TGGGGGCACG	TGTGTGTGTC	ACAACGGAGG	CTTTGTTTGC	12420
40	CAGTGTAGAG	GATTATATAC	TGGTCAGAGG	TGTCAGCTTA	GTCCATACTG	CAAAGATGAA	12480
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50	ACCCCGAGTA	TCCAAGTGA	CTCAAGAAAC	AATCTGGACC	GAAATTCCTT	CGAAGGATCT	13020
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55	AGTGGCCGGG	AAAGCCCTGC	TGAAGTGCAG	TCCCTGAGCT	CCTTCCAGTC	CGAATCGTGC	13320
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	GATATGTCTG	AACTCAAAC	AAAAGGCACT	GGTGAGAATA	GTACTTGTAG	AGAACCCCAT	13740
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	CCTGACTTTA	GTGAACCTAG	AGGTGATGTG	AGTAATCCGC	GCTGTTCTTT	GCAGCAGTGC	14040
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	GTCTCTTTTT	TTTGTAATAT	TTATGTACAG	ATTTGATTTT	TCATAGTTTT	AACTAGATTT	14340
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	CCATGACACA	GTTTTTATAG	TGTCGTGTATA	TTTGTGATGC	AATGGTCTTG	TAAAGGTTTT	14700
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Seq ID NO: C161 DNA Sequence
Nucleic Acid Accession #: NM_014220.1
Coding sequence: 102..710

1 11 21 31 41 51
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	TGTGGTCTT	TTCCTGCATC	GTAGGAGGTG	GCCTGCTGAT	GCTCCTGCCA	GCATTGTGCT	300
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	GATGTGCGAT	GCTTTCTTCT	GTATTGGCTG	CTCTCATTTG	AATTGCAGGA	TCTGGCTACT	420
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10	AGTGGAACTA	CACCTTTGCC	AGCACCAGAG	GCCAGTACCT	TCGGATACCT	TCCACATGGT	540
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20	AGTTGCTTTT	TATAAGACCA	AGAAGGAGAA	AATCCGACAA	CCTGGAAAGA	TTTTTGTGTT	1140
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	AACCTGCCTG	TGTTCTGTGA	GAAACAATA	TTTACTTAGA	GTGGAAGGAC	TGATTGAGAA	1260
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	AATAAGCAG	TTGATCAGCA	TCAATGGAAC	ATGGGGACGA	GTGACGGCAG	GAGGACCAAG	1500
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Seq ID NO: C162 DNA Sequence
Nucleic Acid Accession #: NM_003759.1
Coding sequence: 150..3257

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	GTAACCTTGG	GGAGAGAGGA	AGAGCCCGGA	GCTCCACTTT	CCTCAGGGTT	GTCCAGCCAA	240
40	TGTTTAAACA	CAGTATTTTC	ACTTCTGCAG	TCTCTCTGCG	TGCAGAACGC	ATCCGATTCA	300
	TCTTGGGAGA	GGAGGATGAC	AGCCGAGCTC	CCCCTCAGCT	CTTCAACGAA	CTGGATGAGC	360
	TGCTGGCCGT	GGATGGGCG	GAGATGGAGT	GGAAAGGAAAC	AGCCAGGTGG	ATCAAGTTTG	420
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45	TATTGAAACC	TGAACCTTAAG	GATAAGGTGA	CCTATACTTT	GCTCCGGAAG	CACCGGCATC	660
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	TAGGATGTTT	TACCAACCTT	GATAATGGTA	GCCCAGCCAT	GACCCATAGG	AATCTGACTT	780
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50	TGAAAAAATT	GCCACGTGAT	GCAGAAAGCT	CCAACGTGCT	TGTTGGGGAG	GTTGACTTTT	900
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	CTGAAGTTCC	TGTGCCACCA	AGGTTCTTGT	TCATTTCTCT	AGGTCCTAAG	GGGAAGCCCA	1020
	AGTCTCTACC	CGAGATTGGC	AGAGCCATTG	CCACCCTGAT	GTCTGATGAG	GTGTTCCATG	1080
	ACATTGCTTA	TAAAGCAAAA	GACAGGCAAG	ACCTGATTGC	TGGTATTGAT	GAGTTCCTAG	1140
	ATGAAGTCAT	CGTCTCTTCA	CCTGGGGAAT	GGGATCCAGC	AATTAGGATA	GAGCCTCCTA	1200
55	AGAGTCTTCC	ATCCTCTGAC	AAAAGAAAGA	ATATGTACTC	AGGTGGAGAG	AATGTTTCAA	1260
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60	TCATTATCTC	GGCACTGTGA	ACTAATGCTA	TCATTTTGGG	AGGACTGCTT	GGGGATGCCA	1500
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	TTTGCCCTTT	TGCTGGTCAA	CCACTCACTA	TTCTGAGCAG	CACCGGAACCT	GTCTAGTTT	1620
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65	TCTTGGTTCA	ATACTTCACA	CGTTTCACGG	AGGAGGGCTT	TTCTCTCTTG	ATTAGCTTCA	1800
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Seq ID NO: C163 DNA Sequence
 Nucleic Acid Accession #: NM_000958
 Coding sequence: 389..1855

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Seq ID NO: C164 DNA Sequence
Nucleic Acid Accession #: NM_002659.1
Coding sequence: 427..1434

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Seq ID NO: C165 DNA Sequence
Nucleic Acid Accession #: AK027843.1
Coding sequence: 193..1731

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Nucleic Acid Accession #: NM_000574.1
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70	CTACCACAGT	AAATGTTCCA	ACTACAGAAG	TCTCACCAC	TTCTCAGAAA	ACCACCACAA	1020
	AAACCACACC	ACCAAAATGCT	CAAGCAACAC	GGAGTACACC	TGTTTCCAGG	ACAACCAAGC	1080
	ATTTTCATGA	ACAACCCCCA	AATAAAGGAA	GTGGAACCC	TTCAAGTACT	ACCCGTTCTT	1140
	TATCTGGGCA	CAGTGTGTTT	ACGTTGACAG	GTTTGCTTGG	GACGCTAGTA	ACCATGGGCT	1200
	TGCTGACTTA	GCCAAAGAAG	AGTTAAGAAG	AAAATACACA	CAAGTATACA	GACTGTTCTT	1260
75	AGTTTCTTAG	ACTTATCTGC	ATATTGGATA	AAATAAATGC	AATTTGTGCT	TTCAATTAGG	1320
	ATGCTTTCAT	TGCTTTTAAG	ATGTGTTAGG	AATGTCAACA	GAGCAAGGAG	AAAAAAGGCA	1380
	GTCTGGGAAT	CACATTCCTTA	GCACACCTAC	ACCTCTTGAA	AATAGAACAA	CTTGAGAAT	1440
	TGAGAGTGAT	TCCTTTCCCTA	AAAGTGTAA	AAAGCATAGA	GATTTGTTTC	TATTTAGAA	1500
	GGGATCACGA	GGAAAAAGAGA	AGGAAAGTGA	TTTTTTTCCA	CAAGATCTGT	AATGTTATTT	1560
80	CCACTATATA	AGGAAATAAA	AAATGAAAAA	CATTATTGGA	ATATCAAAAG	CAAAATAAAA	1620
	CCCATTTCAG	TCCTTCTCAA	GCAAAATTGC	TAAAGAGAGA	TGAACCATAT	TATAAAGTAA	1680
	TCTTTGGCTG	TAAGGCATTT	TCATCTTTCC	TTGCGGTTGG	CAAAATATTT	TAAAGGTAAA	1740
	ACATGCTGGT	GAACCGGGG	TGTTGATGGT	GATAAGGGAG	GAATATAGAA	TGAAAGACTG	1800
	AATCTTCTCT	TGTTGACAAA	ATAGAGTTTG	GAAAAAGCCT	GTGAAAGGTG	TCTTCTTTGA	1860
	CTTAATGTCT	TAAAAAGTAT	CCAGAGATAC	TACAATATTA	ACATAAGAAA	AGATTATATA	1920

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Seq ID NO: C167 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..2651

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 CTGCTCCCGA ATCCCTGCC CAGTCTCCGC TTCCTGGAGG AGTTACGTCT TCGCGGAAAC 300
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Seq ID NO: C168 DNA Sequence
 Nucleic Acid Accession #: NM_003667.2
 Coding sequence: 49..2772

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Seq ID NO: C169 DNA Sequence
 Nucleic Acid Accession #: NM_003506.1
 Coding sequence: 259..2379

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Seq ID NO: C170 DNA Sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88...990

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Seq ID NO: C171 DNA Sequence
 Nucleic Acid Accession #: NM_002821
 Coding sequence: 150...3362

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 GAGGAGGGAG CCGCTCAGG ATGGCTGGG CAGGGGAGGA CATCTCTAGA GGGAGCTCA 3420
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 30 TGCAGCGTGG GGTGGGTGGG CATGGGAGGT AGGGGTGGGC CCTGGAGATG AGGAGGGTGG 4080
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Seq ID NO: C172 DNA Sequence
 Nucleic Acid Accession #: NM_002309.2
 Coding sequence: 65..673

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CAATGCCCTC	TTTATTCTCT	ATTACACAGC	CCAGGGGGAG	CCGTTCCCA	ACAACCTGGA	300
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CACCCGGGAC	CAGAAGATCC	TCAACCCAG	TGCCCTCAGC	CTCCACAGCA	AGCTCAACGC	480
CACCGCCGAC	ATCCTGCGAG	GCCTCCTTAG	CAACGTGCTG	TGCCCGCTGT	GCAGCAAGTA	540
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GGCCCTTTGC	TCACCTTTGTG	CAGTGAACAA	ACTACACAAG	TCATCTACAA	GAGCCCTGAC	1020
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CACGTGTTCT	GGGCGCCCCA	GCATTGTGTT	GTGAGGCGCA	CTGTTCTCTG	CAGATATTGT	2160
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GACACAGCAG	GGAAAGCTCCT	CCTGTGGCCC	GGACACCCAT	AGACGGTGGC	GGGGGCTCTG	2340
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TGAGCGGGCT	GCCGGCCTTC	AAGTTCCTCC	GACAAGATGA	TGGTACTAAT	TATGGTACTT	2700
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 5 CTGGCTGCAT TCCCCAGGA TGGGCTTCGA GAAAGACAAA CTTGTCTGGA AACCAGAGTT 3000
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 20 GAGAAATGAA TAAAGAACTT ACTCTTCG 3868

Seq ID NO: C173 DNA Sequence
 Nucleic Acid Accession #: XM_097508
 Coding sequence: 44..2788

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 30 CACAGAGCTT CAGCCTGGCC TCTTCCACCA CCTGCGCTTC TTGGAGGAGC TGCGTCTCTC 180
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 CCTGATGCTG CAGAACATC AGCTGGGAGG AATCCCCGCA GAGGCGCTGT GGGAGCTGCC 300
 GAGCCTGCAG TCGCTGCGCC TAGATGCCAA CCTCATCTCC CTGTCCCGG AGAGGAGCTT 360
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 35 TGTACGGGCC CTCAACAACC TCCCTGCCCT GCAGGCCATG ACCCTGGCCC TCAACCGCAT 480
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 45 AATCGGCCTC CAACACAACC GCATCTGGGA AATTGGAGCT GACACCTTCA GCCAGCTGAG 1080
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 70 GCTGGAGAAG AGCTCCTGTG ATTCTACCCA GGCCTGGTA GCCTTCTCTG ATGTGGATCT 2520
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Seq ID NO: C174 DNA Sequence
 Nucleic Acid Accession #: NM_130849

Coding sequence: 101..2044

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	TCTGCTGAGC	CTGCTCACCT	CTGGCCAGGG	CGCTCTGGAT	CAAGAGGCTC	TGGGCGGCCT	240
10	GTTAAATACG	CTGGCGGACC	GTGTGCACTG	CACCAACGGG	CCGTGTGGAA	AGTGCCCTGT	300
	TGTGGAGGAG	GCCCTGGGCC	TGGGCGAGCC	TGAGGGGTCA	GGGCTGCCCC	CGGGCCCGGT	360
	CCTGGAGGCC	AGGTACGTCG	CCGCGCTCAG	TGCGCGCGCC	GTCTGTATCC	TACGAACCC	420
	CGAGGGCACC	TGTGAGGACA	CTCGGGCTGG	CCTCTGGGCC	TCTCATGCAG	ACCACCTCCT	480
	GGCCCTGCTC	GAGAGCCCCA	AGGCCCTGAC	CCCGGGCCTG	AGCTGGCTGC	TGCAGAGGAT	540
15	GCAGGCCCGG	GCTGCCGGCC	AGACCCCAAA	GACGGCCTGC	GATAGATATC	CTCAGCTGCT	600
	GGAGGAGGCG	GTGGGGGCGG	GGGCTCCGGG	CAGTGCTGGC	GGCGTCTGGG	CTGCCCTGCT	660
	GGACCATGTC	AGGAGCGGGT	CTTGCTTCCA	CGCCTTGCCG	AGCCCTCAGT	ACTTCGTGGA	720
	CTTTGTGTTT	CAGCAGCACA	GCAGCGAGGT	CCCTATGACG	CTGGCCGAGC	TGTCAGCCTT	780
	GATGCAGCGC	CTGGGGGTGG	GCAGGGAGGC	CCACAGTGAC	CACAGTCATC	GGCACAGGGG	840
	AGCCAGCAGC	CGGACCCCTG	TGCCCTCAT	CAGCTCCAGC	AACAGCTCCA	GTGTGTGGGA	900
20	CACGGTATGC	CTGAGTGCCA	GGGACGTGAT	GGCTGCATAT	GGACTGTCGG	AACAGGCTGG	960
	GGTGACCCCG	GAGGCCCTGG	CCCAACTGAG	CCCTGCCCTG	CTCCAACAGC	AGCTGAGTGG	1020
	AGCCTGCACC	TCCAGTCCA	GGCCCCCGT	CCAGGACCAG	CTCAGCCAGT	CAGAGAGGTA	1080
	TCTGTACGGC	TCCCTGGCCA	CGCTGCTCAT	CTGCCCTCTG	CGGGTCTTTG	GCCTCCTGCT	1140
25	GCTGACCTGC	ACTGGCTGCA	GGGGGGTCCG	CCACTACATC	CTGCAGACCT	TCCTGAGCCT	1200
	GGCAGTGGGT	GCACTCACTG	GGGACGCTGT	CCTGCATCTG	ACGCCCAAGG	TGCTGGGGCT	1260
	GCATACACAC	AGCGAAGAGG	GCCTCAGCCC	ACAGCCCAAC	TGGCGCCTCC	TGGCTATGCT	1320
	GGCCGGGCTC	TAGCCCTTCT	TCCTGTTTGA	GAACCTCTTC	AATCTCCTGC	TGCCCAGGGA	1380
	CCCGGAGGAC	CTGGAGGACG	GGCCTGCGGG	CCACAGCAGC	CATAGCCACG	GGGGCCACAG	1440
30	CCACGGTGTG	TCCTTGCAGC	TGGCACCCAG	CGAGCTCCGG	CAGCCCAAGC	CCCCCACGA	1500
	GGGCTCCCGC	CCAGACCTGG	TGGCGGAGGA	GAGCCCGGAG	CTGTGAACCC	CTGAGCCGAG	1560
	GAGACTGAGC	CCAGAGTTGA	GGCTACTGCC	CTATATGATC	ACTCTGGGCG	ACGCCGTGCA	1620
	CAACTTCGCC	GACGGGCTGG	CCGTGGGCGC	CGCCTTCGCG	TCCTCCTGGA	AGACCGGGCT	1680
	GGCCACCTCG	CTGGCCGTGT	TCTGCCACGA	GTTGCCACAC	GAGCTGGGGG	ACTTCGCCGC	1740
35	CTTGTGTGAC	GCGGGGCTGT	CCGTGCGCCA	AGCACTGTCT	CTGAACCTGG	CCTCCGCGCT	1800
	CACGGCCTTC	GCTGGTCTCT	ACGTGGCACT	CGCGGTTGGA	GTCAGCGAGG	AGAGCGAGGC	1860
	CTGGATCCTG	CGAGTGGCCA	CCGGCCTGTT	CCTCTACGTA	GCACCTCTCG	ACATGCTCCC	1920
	GGCGATGTTG	AAAGTACGGG	ACCCGCGGCC	CTGGCTCCTC	TTCCTGCTGC	ACAACGTGGG	1980
	CCTGCTGGGC	GGCTGGACCG	TCCTGCTGCT	GCTGTCCCTG	TACGAGGATG	ACATCACCTT	2040
40	CTGATACCTG	GCCCTACCTT	CCCACCTTTG	ACTTAAGATC	CCACACCTCA	CAAACCTACA	2100
	GCCCAAAAC	CAGAAGCCCC	TATAGAGGCC	CCAGTCCCAA	CTCCAGTAAA	GACACTCTTG	2160
	TCCTTGGA	AAAAAAAAAA	AAAAAAAAAA	AA			2192

Seq ID NO: C175 DNA Sequence
Nucleic Acid Accession #: NM_018971
Coding sequence: 1..1128

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	CTGCTGATCG	TGCGGGAGCG	CAGCCTGCAC	CGCGCCCCGT	ACTACCTGCT	GCTCGACCTG	180
	TGCTTGGCCG	ACGGGCTGCG	CGCGCTCGCC	TGCTTCCCGG	CCGTATGCTG	GGCGGCGCGG	240
	CGTGGCGGCG	CCGCGGCGGG	GGCGCCGCGG	GGCGGCTGG	GCTGCAAGCT	GCTCGCCTTC	300
55	CTGGCCGCGC	TCTTCTGCTT	CCACGCCGCC	TTCCTGCTGC	TGGGCGTGGG	CGTCACCCGC	360
	TACCTGGCCA	TGCGGCACCA	CGCTTCTAT	GCAAGAGCGC	TGGCCGCGTG	GCCGTGCGCC	420
	GCCATGCTGG	TGTGCGCCCG	CTGGGCGCTG	GCGCTGGCCG	CGGCCTTCCC	GCCAGTGTCT	480
	GACGGCGGTG	GCGACGACGA	GGACGCGCCG	TGCGCCTTGG	AGCAGCGGCC	CGACGGCGCC	540
	CCCGGCGCGC	TGGGCTTCTT	GCTGCTGCTG	GCCGTGGTGG	TGGGCGCCAC	GCACCTCGTC	600
60	TACCTCCGCC	TGCTCTTCTT	CATCCACGAC	CGCCGCAAGA	TGCGGCCCGC	GCGCCTGGTG	660
	CCCGCCGTCA	GCCACGACTG	GACCTTCCAC	GGCCCGGGCG	CCACCGGCCA	GGCGGCGGCC	720
	AACTGGACGG	CGGGCTTCCG	CCGCGGGCCC	ACGCCGCCCG	CGCTTGTGGG	CATCCGGCCC	780
	GCAGGGCCCG	GCCGCGGCGC	GCGCCGCCTC	CTCGTGCTGG	AAGAATTCAA	GACGAGGAAG	840
	AGGCTGTGCA	AGATGTTCTA	CGCCGTACAG	CTGCTCTTCC	TGCTCCTCTG	GGGGCCCTAC	900
65	GTGCTGGCCA	GCTACCTGCG	GGTCTGCTGG	CGGCCCGGCG	CCGTCCCCCA	GGCCTACCTG	960
	ACGGCCTCCG	TGTGGCTGAC	CTTCGCGCAG	GCGGGCATCA	ACCCGCTCGT	GTGCTTCTCT	1020
	TTCAACAGGG	AGCTGAGGGA	CTGCTTCAGG	GCCCAGTTCC	CCTGCTGCCA	GAGCCCCCGG	1080
	ACCACCCAGG	CGACCCATCC	CTGCGACCTG	AAAGGCATTG	GTTTATGA		1128

Seq ID NO: C176 DNA Sequence
Nucleic Acid Accession #: NM_005631
Coding sequence: 290..2653

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	CGCCAGGGGG	CGGGGCGCGC	GGAGCGTCCG	GGGGGGCCCG	GGCCCGGATT	CTCTGGGCGC	180
	ACAGTCCGCG	TGAGCCGCGT	CCGCGGCCCG	CGAGGTCGTG	CGTGTGGCCG	GGGGGCTCCG	240
80	AGGAGCAGGC	GGGGGCGCCG	GGGCTTTTGC	TGAGTTGGCG	GGGTTGGCCA	TGGCCGCTGC	300
	CGGCCACGCG	CGGGGCGCGG	AGCTCCCGCT	CCTGGGGCTG	CTGCTGCTGC	TGCTGCTGGG	360
	GGACCCGGCG	CGGGGGGCGG	CCTCGAGCGG	GAAACGCGAC	GGGCCCTGGG	CTCGGAGCGC	420
	GGGCGGGAGC	GCGAGGAGGA	GCGCGGCGGT	GACTGGCCCT	CGGCCGCCCG	TGAGCCACTG	480
	CGGCCGGGCT	GCCCCCTGCG	AGCCGCTGCG	CTACAACGTC	TGCCTGGGCT	CGGTGCTGCC	540
	CTACGGGGCC	ACCTCCACAC	TGCTGGCCCG	AGACTCGGAC	TCCAGGAGG	AAGCGCACGG	600

5	CAAGCTCGTG	CTCTGGTCGG	GCCTCCGGAA	TGCCCCCGGC	TGCTGGGCAG	TGATCCAGCC	660
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	TACCCTCTGC	CAGGCCACCC	GAGGCCCTTG	TGCCATCGTG	GAGAGGGAGC	GGGGCTGGCC	780
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	CATCAAGTTT	AACAGTTTCA	GCCAGTGCAG	AGTGCCCTTG	GTTCCGACAG	ACAACCCCAA	900
	GAGCTGGTAC	GAGGACGTGG	AGGGCTGCGG	CATCCAGTGC	CAGAACCCGC	TCTTCACAGA	960
	GGCTGAGCAC	CAGGACATGC	ACAGCTACAT	CGCGGCCTTC	GGGGCCGTCA	CGGGCCTCTG	1020
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10	TGTTATTCTC	TTCTACGTCA	ATGCGTGCTT	CTTTGTGGGC	AGCATTGGCT	GGCTGGCCCA	1140
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	TGCTGAATGC	TTTGAATGAG	GAAATGATCC	CCAAGTGGTG	AATGACACGC	CTAAGGTAC	4860
	AGCTAGTTTG	AGCCAGTTAG	ACTAGTCCCC	CGGTCTCCCG	ATTCCCAACT	GAGTGTATT	4920
	TGCACACTGC	ACTGTTTTCA	AATAACGATT	TTATGAAATG	ACCTCTGTCC	TCCCTCTGAT	4980
80	TTTTCATATT	TTCTTAAAGT	TTCTTTCTGT	TTTTTAATA	AAAAGCTTTT	TCCTCTGGA	5040
	ACAGAAGACA	GCTGCTGGGT	CAGGCCACCC	CTAGGAACCTC	AGTCTGTAC	TCTGGGGTGC	5100
	TGCTGAAATC	CATTAAAAAT	GGGAGTACTG	ATGAAATAAA	ACTACATGGT	CAACAGTAAA	5160
	AAAAAAAAAA	AAAAAA					5176

Seq ID NO: C180 DNA Sequence

Nucleic Acid Accession #: NM_004626
Coding sequence: 124..1188

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5      1      11      21      31      41      51
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TAACCCGCCG CCTCCGCTCT CCCCGGCTGC AGGCGGCGTG CAGGACCAGC GGCGGCCGTG 60
CAGGCGGAGG ACTTCGGCGC GGCTCCTCCT GGGTGTGACC CCGGGCGCGC CCGCCGCGCG 120
ACGATGAGGG CGCGGCCGCA GGTCTGCGAG GCGCTGCTCT TCGCCCTGGC GCTCCAGACC 180
GGCGTGTGCT ATGGCATCAA GTGGCTGGCG CTGTCCAAGA CACCATCGGC CCTGGCACTG 240
10 AACCAGACGC AACACTGCAA GCAGCTGGAG GGTCTGGTGT CTGCACAGGT GCAGCTGTGC 300
CGCAGCAACC TGGAGCTCAT GCACACGGTG GTGCACGCCG CCGCGAGGT CATGAAGGCC 360
TGTGCGCGGG CCTTTGCCGA CATGCGCTGG AACTGCTCCT CCATTGAGCT CGCCCCAAC 420
TATTTGCTTG ACTTGAGAG AGGGACCCGG GAGTCGGCCT TCGTGTATGC GCTGTGGGCC 480
GCGGCCATCA GCCACGCCAT CGCCCGGGCC TGCACCTCCG GCGACCTGCC CGGCTGCTCC 540
15 TGCGGCCCGG TCCAGGTGA GCCACCGGG CCGGGGAACC GCTGGGGAGG ATGTGCGGAC 600
AACTCAGCT ACGGGCTCCT CATGGGGGCC AAGTTTCCG ATGCTCCTAT GAAGGTGAAA 660
AAAACAGGAT CCCAAGCCAA TAAACTGATG CGTCTACACA ACAGTGAAGT GGGGAGACAG 720
GCTCTGCGCG CCTCTCTGGA AATGAAGTGT AAGTGCCATG GGGTGTCTGG CTCCTGCTCC 780
ATCCGCACTT GCTGGAAGGG GCTGCAGGAG CTGCAGGATG TGGCTGCTGA CCTCAAGACC 840
20 CGATACCTGT CGGCCACCAA GGTAGTGCAC GCACCCATGG GCACCCGCAA GCACCTGGTG 900
CCCAAGGACC TGGATATCCG GCCTGTGAAG GACTCGGAAC TCGTCTATCT GCAGAGCTCA 960
CCTGACTTCT GCATGAAGAA TGAGAAGGTG GGCTCCACG GCACACAAGA CAGGCAGTGC 1020
AACAAAGACAT CCAACGGAAG GCACAGCTGC GACCTTATGT GCTGCGGGCG TGGCTACAAC 1080
CCTACACAG ACCCGCTGGT CGAGCGGTGC CACTGTAAGT ACCACTGGTG CTGCTACGTC 1140
25 ACCTGCCGCA GGTGTGAGCG TACCGTGGAG CGCTATGTCT GCAAGTGAGG CCCTGCCCTC 1200
CGCCCAAGCG AGGAGCGAGG ACTCTGCTCA AGGACCTCA GCAACTGGGG CCAGGGGCCCT 1260
GGAGACACTC CATGGAGCTC TGCTTGTGAA TTCCAGATGC CAGGCATGGG AGGCGGCTTG 1320
TGCTTTGCCCT TCACTTGGAA GCCACCAGGA ACAGAAGGTC TGGCCACCTT GGAAGGAGGG 1380
30 CAGGACATCA AAGGAAACCG ACAAGATTAA AATAACTTGG GCAGCCTGAG GCTCTGGAGT 1440
GCCACAGGCG TGGTGTAAAG AGCGGGGCTT GGGATCGGTG AGACTGATAC AGACTTGACC 1500
TTTCAAGGCC ACAGAGACCA GCCTCCGGGA AGGGGTCTCG CGCCTTCTT CAGAATGTTT 1560
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35 GCTACAGAAA TATTTATAAA ACATAGCTTT TTTTGTGGG TGGCACTTCT CAATTCTCTT 1740
TTATATATTT TATATATATA AATATATATG TATATATATA ATGATCTCTA TTTTAAAACT 1800
AGCTTTTAA GCAGCTGATG GAAATAAATG CTGAGTGAGC CCCAGCCCGC CCCTGCAGTT 1860
CCCGGCCCTG TCAAGTGAAC TCGGCAGACC CTGGGGCTGG CAGAGGGAGC TCTCCAGTTT 1920
CCAGGCA 1927

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Seq ID NO: C181 DNA Sequence
Nucleic Acid Accession #: NM_031866
Coding sequence: 6..2090

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TGACGCGCTC TAGCGGCGCT GCGGCCGCCT CCGCCAAGGA GCTGGCATGC CAAGAGATCA 120
CCGTGCGGCT GTGTAAGGGC ATCGGCTACA ACTACACCTA CATGCCCAAT CAGTTCAACC 180
ACGACACGGA AGACGAGGCG GGCTTGGAGG TGCACCAATT CTGGCCGTG GTGGAGATCC 240
50 AGTGCTCGCC CGATCTCAAG TTCTTCTGT GCAGCATGTA CAGCCCATC TGCCTAGAGG 300
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CGCGCTCAT GCGCGAGTGA GGCTTGCCTT GCGCCGACCG CATGCGCTGC GACCGGCTGC 420
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55 CCGCGCCAG CCGCGCCGCG CGCCTGCCGC CCGCGCCGCC CCGCGAGCAG CCGCCTTCGG 540
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GTGGCGCGCG GGAGCGCGCG GCGCCCCAG CTGCGCGCG CCGCGGTGGC GGAAGGCGC 660
GGCGCCCTGG CCGCGCGCG GCTCCCTGCG AGCCCGGGTG CCAGTGCCGC GCGCCTATGG 720
TGAGCGTGTG CAGCGAGCGC CACCCGCTCT ACAACCGCGT CAAGACAGGC CAGATCGCTA 780
ACTGCGGCTG GCCCTGCCAC AACCCCTTTT TCAGCCAGGA CGAGCGCGCC TTCAACCTCT 840
60 TCTGGATCGG CCTGTGGTGC GTGCTCTGCT TCGTGTCCAC CTTGCGCAC GTCTCCACCT 900
TCCTTATCGA CATGGAGCGC TTCAAGTACC CGGAGCGGCC CATTATCTTC CTCTCGGCT 960
GCTACCTCTT CGTGTGCGTG GGCTACCTAG TGCGCTGGT GCGCGGCCAC GAGAAGGTGG 1020
CGTGCAGCTG TGGCGCGCG GCGCGGGGG GCGCTGGGG GCGCGGCGGC GCGCGGCGG 1080
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65 TGGCGCGGCT GGAGCAGCAC GTGCGCTACG AGACCACCG CCGCGCGCTG TGCACCGTGG 1200
TCTTCTTGCT GGTCTACTTC TTGCGCATGG CCAGCTCCAT CTGGTGGGTG ATCTTGTGCG 1260
TCACATGGTT CCTGGCGGCC GGTATGAAGT GGGGCAACGA AGCCATCGCC GGCTACTGCG 1320
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TCAGCTCGGT GGACGGCGAG CCGGTGGCGG GCATCTGCTA CGTGGGCAAC CAGAGCCTGG 1440
70 ACAACCTGCG CGGCTTCTG CTGGCGCGC TGGTCTACTA CCTCTTATC GGCACCATGT 1500
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GCCCCACCAA GACGACAAAG CTGGAGAAGC TGATGATCCG CCTGGGCTG TTCAACCTGTC 1620
TCTACACGCT GCCCGCGCG GTGGTGGTCT CCGCTCTCTT CTACGAGCAG CACAACCGCC 1680
CGCGCTGGGA GGCACGAC AACTGCCCGT GCCTGCGGGA CCTGCAGCCC GACCAGGCAC 1740
75 GCAGGCCCGA CTACGCCGTC TTCATGCTCA AGTACTTCAT GTGCCCTAGT GTGGGCATCA 1800
CCTCGGGCTG GTGGGTCTGG TCCGGCAAGA CGCTGGAGTC CTGGGCTGCC CTGTGCACCC 1860
GCTGTGCTG GGCAGCAAG GCGCGCGCG TGGGCGGGG CCGCGGCGCC ACGGCGCGG 1920
GGGTGTGCGG CCGCGCGGG GCGCGCGCG GCGGGGACC CCGCGCGCG GGGGGGCGG 1980
80 GCGGCGGCGG GGGCTCCCTC TACAGCGAGC TCAGCACTGG CCTGACGTGG CCGTGGGCA 2040
CGGCGAGCTC CGTGTCTTAT CCAAGCAGTA TGCCATTGTC CCAGGTCTGA GCGGAGGGGA 2100
GGGGCGCCCC AGGAGGGGTG GGGAGGGGG CGAGGAGACC CAAGTGACGC GAAGGGACAC 2160
TTGATGGGCT GAGGTTCACA CCCTTCACA GTGTGATTG CTATTAGCAT GATAATGAAC 2220
TCTTAATGCT ATCCATTAGC TGGGACTTAA ATGACTACT TAGAACAAAG TACCTGGCAT 2280
TGAAGCTCC CAGACCCAGC CCCTTTCTCT CCATTGATGT GCGGGGAGCT CCTCCGCCA 2340

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5 CGCGTTAATT TCTGTGGCT GAGGAGGGTG GACTCTGCGG CGTTTCCAGA ACCCGAGATT 2400
 TGGAGCCCTC CCTGGCTGCA CTTGGCTGGG TTTGCAGTCA GATACACAGA TTTCACCTGG 2460
 GAGAACCTCT TTTTCTCCCT CGACTCTTCC TACGTAAACT CCCACCCCTG ACTTACCCCTG 2520
 GAGGAGGGGT GACCGCCACC TGATGGGATT GCACGGTTTG GGTATTCTTA ATGACCAGGC 2580
 AAATGCCTTA AGTAAACAAA CAAGAAATGT CTTAATTATA CACCCACAGT AAATACGGGT 2640
 TTCTTACATT AGAGGATGTA TTTATATAAT TATTTGTTAA ATTGTAAAAA AAAAAAGTGT 2700
 AAAATATGTA TATATCCAAA GATATAGTGT GTACATTTT TTGTAAAAAG TTTAGAGGCT 2760
 TACCCCTGTA AGAACAGATA TAAGTATTCT ATTTTGTCAA TAAATAGACT TTTGATAAAT 2820
 10 GATTTAACCA TTGCCCTCTC CCCCCTCTCT TCTGAGCTGT CACCTTTAAA GTGCTTGCTA 2880
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 TGAACGTAAA TCAAAATTGA GTTTTGTGAC CTTCCTCCAA GACGGTGTIT TTCATGGGAG 3060
 CTCTTTCTG ATCCATGGAT AACAACCTCT ACTTTAGTGG ATGTAAATGG AACTTCTGCA 3120
 15 AGGCAGTAAT TCCCCTTAGG CCTTGTATT TATCTGTCAT GGTATCACTA AAGGTTTCAA 3180
 AACCCTGAAA AAAAA 3195

Seq ID NO: C182 DNA Sequence
 Nucleic Acid Accession #: XM_050625
 Coding sequence: 222..1109

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 25 CGGGTGTCCC GCTTCTCCGC GCCCCAGCCG CCGGCTGCCA GCTTTTCGGG GCCCGAGTCT 120
 GCACCCAGCG AAGAGAGCGG GCCCGGACAC AGCTCGAACT CCGGCGCGCT CGCCCTTCCC 180
 CGGCTCCGCT CCCTCTGCCC CCTCGGGGTC GCGCGCCAC GATGCTGCAG GGCCCTGGCT 240
 CGCTGTCTGT GCTCTTCTCT GCTTCGCACT GCTGCTTGGG CTCGGCGCGC GGGCTCTTCC 300
 TCTTTGGCCA GCCCGACTTC TCCTACAAGC GCAGCAATTG CAAGCCCATC CCGTCCAAAC 360
 30 TGCAGCTGTG CCACGGCATC GAATACCAGA ACATGCGGCT GCCCAACCTG CTGGGCCACG 420
 AGACCATGAA GGAGGTGCTG GAGCAGGCCG GCGCTTGGAT CCCGCTGGTC ATGAAGCAGT 480
 GCCACCCGGA CACCAAGAAG TTCCTGTGCT CGCTCTTCTG CCCCCTCTGC CTCGATGACC 540
 TAGACGAGAC CATCCAGCCA TGCCACTCGC TCTGCGTGCA GGTGAAGGAC CGCTGCGCCC 600
 CGGTATGTG CGCCTCTCGC TTCCCTGGC CCGACATGCT TGAGTGCGAC CGTTTCCCCC 660
 35 AGGACAACGA CCTTTGCATC CCCCTCGCTA GCAGCGACCA CCTCTGCGCA GCCACCGAGG 720
 AAGCTCCAAA GGTATGTGAA GCCTGCAAAA ATAAAAATGA TGATGACAA GACATAATGG 780
 AAACGCTTTG TAAAAATGAT TTTGCACTGA AAATAAAAGT GAAGGAGATA ACCTACATCA 840
 ACCGAGATAC CAAAATCATC CTGGAGACCA AGAGCAAGAC CATTTACAAG CTGAACGGTG 900
 TGTCCGAAAG GGACCTGAAG AAATCGGTGC TGTGGCTCAA AGACAGCTTG CAGTGCACTT 960
 40 GTGAGGAGAT GAACGACATC AACGCGCCCT ATCTGGTCAT GGGACAGAAA CAGGGTGGGG 1020
 AGCTGGTGAT CACCTCGGTG AAGCGGTGGC AGAAGGGGCA GAGAGAGTTC AAGCGCATCT 1080
 CCGCAGACTG CGCAAGCTG CAGTGCTAGT CCGGCATCC TGATGGCTCC GACAGGCGCTG 1140
 CTCCAGAGCA CGGCTGACCA TTTCTGCTCC GGGATCTCAG CTCCTGTTCC CCAAGCACAC 1200
 TCTAGCTGC TCCAGTCTCA GCCTGGGCAG CTTCCTCTG CCTTTTGCAT GTTTGCATCC 1260
 45 CCAGCATTTT CTGAGTTATA AGGCCACAGG AGTGATAGC TGTTTTACC TAAAGGAAAA 1320
 GCCACCCGA ATCTTGTAGA AATATTCAAA CTAATAAAAT CATGAATATT TTTATGAAGT 1380
 TT 1382

Seq ID NO: C183 DNA Sequence
 Nucleic Acid Accession #: NM_001306.1
 Coding sequence: 199..861

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 CGCCAGGCCC AGCGGCCCCG GCCCTCTGTC TCCCGCACCC CGGAGCCACC CGGTGGAGCG 180
 GGCTTTGCGG CGGCAGCCAT GTCCATGGGC CTGGAGATCA CGGGCACCCG GCTGCGCCGTG 240
 CTGGGCTGGC TGGGCACCAT CGTGTGCTGC GCGTTGCCCA TGTGGCGCGT GTCGGCCTTC 300
 60 ATCGGCAGCA ACATCATCAC GTCGAGAAC ATCTGGGAGG GCCTGTGGAT GAATGCGTG 360
 GTGCAGAGCA CCGCCAGAT GCAGTGCAAG GTGTAGCACT CGCTGTGGC ACTGCCACAG 420
 GACCTTCAGG CGGCCCGCGC CCTCATCGTG GTGGCCATCC TGCTGGCCGC CTTGCGGCTG 480
 CTAGTGGCGC TGGTGGGCGC CCAAGTGCACC AACTGCGTGC AGGACGACAC GGCCAAAGCC 540
 AAGATCACCA TCGTGGCAGG CGTGTGTTTC CTCTCTGCGC CCCTGCTCAC CCTCGTCCG 600
 65 GTGTCCTGGT CGGCCAACAC CATTATCCGG GACTTCTACA ACCCCGTGGT GCCCGAGGCG 660
 CAGAAGCGCG AGATGGGCGC GGGCCTGTAC GTGGGCTGGG CCGCCGCGGC GCTGCAGCTG 720
 CTGGGGGGCG CGCTGCTCTG CTGCTCGTGT CCCCACCGC AGAAGAAGTA CACGGCCACC 780
 AAGGTCTGCT ACTCCGCGCC GCGCTCCACC GGCCCGGAG CAGCCTTGGG CACAGGCTAC 840
 GACCGCAAGG ACTACGTCTA AGGGACAGAC GCAGGGAGAC CCCACCACCA CCACCACCAC 900
 70 CAACACCACC ACCACCACCG CGAGCTGGAG CGCGCACCA GCGCATCCAG GTGCAGCCTT 960
 GCCTCGGAGG CCAGCCACCC CCCAGAAGCC AGGAAGCCCC CGCGCTGGAC TGGGGCAGCT 1020
 TCCCCAGCAG CCACGGCTTT GCGGGCGGGG CAGTCGACTT CCGGGCCACG GGACCAACCT 1080
 GCATGGACTG TGAACCTCA CCCTTCTGGA GCACGGGGCC TGGGTGACCG CCAATACTTG 1140
 75 ACCACCCCGT CGAGCCCAT CCGGCGCGTG CCCCATGTC GCGCTGGGCA GGGACCGGCA 1200
 GCCCTGGAAG GGGCATTGTA TATTTTCAA TAAAGCCTC TCGTTTATAG 1250

Seq ID NO: C184 DNA Sequence
 Nucleic Acid Accession #: NM_012449.1
 Coding sequence: 66..1085

80 1 11 21 31 41 51
 CCGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60
 AATTAATGGA AAGCAGAAAA GACATCACAA ACCAAGAAGA ACTTTGGAAA ATGAAGCCTA 120
 GGAGAAATTT AGAAGAAGAC GATTATTTGC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180

5 AAAGACCTGT GCTTTTGCAT TTGCACAAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
 CAGAACTTCA GCACACACAG GAACTCTTTC CACAGTGGCA CTGCCCAATT AAAATAGCTG 300
 CTATTATAGC ATCTCTGACT TTTCTTTACA CTCTTCTGAG GGAAGTAATT CACCCTTTAG 360
 CAACCTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAGTCTTGC 420
 CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG 480
 TCCAACCTCA TAATGGAAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540
 TAACAAGAAA GCAGTTTGGG CTCTCAGTT TCTTTTTCG TGTACTGCAT GCAATTTATA 600
 GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAAACTGG GCATATCAAC 660
 10 AGGTCCAACA AAATAAAGAA GATGCCTGGA TTGAGCATGA TGTTTGGAGA ATGGAGATT 720
 ATGTGTCTCT GGGAAATTGT GGATTGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATT 780
 CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACTA TATTCAGAGC AAGCTAGGAA 840
 TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCCTGGAAT AAGTGGATAG 900
 ATATAAAACA ATTTGTATGG TATACACCTC CAACTTTTAT GATAGCTGTT TTCCTTCCAA 960
 15 TTGTTGTCTT GATATTTAAA AGCATACTAT TCCTGCCATG CTGAGGAAG AAGATACTGA 1020
 AGATTAGACA TGGTTGGGAA GACGTACCA AAATTAACAA AACTGAGATA TGTTCACAGT 1080
 TGTAAGATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140
 TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAA 1195

Seq ID NO: C185 DNA Sequence
 Nucleic Acid Accession #: NM_001775.1
 Coding sequence: 70..972

25 1 11 21 31 41 51
 CTAAAGCTCT CTGCTGCCT AGCCTCCTGC CGGCCTCATC TTCGCCAGC CAACCCCGCC 60
 TGGAGCCCTA TGGCCAACTG CGAGTTTCAG CCGGTGTCCG GGGACAAACC CTGCTGCCGG 120
 CTCTCTAGGA GAGCCCAACT CTGCTTTGGC GTCACTATCC TGGTCTGAT CCTCGTCGTG 180
 GTGCTCGCGG TGGTCTGCCG GAGGTGGCGC CAGACGTGGA GCGGTCCGGG CACCACCAAG 240
 30 CGCTTTCCCG AGACCGTCTT GGCCTGATGC GTCAAGTACA CTGAAATTCA TCCTGAGATG 300
 AGACATGTAG ACTGCCAAAG TGTATGGGAT GCTTTCAAGG GTGCATTTAT TTCAAACAT 360
 CCTTGCACAA TACTGAAGA AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCGTA 420
 CCTTGCACAA AGATTCTTCT TTGGAGCAGA ATAAAAGATC TGGCCCATCA GTTCACACAG 480
 GTCCAGCGGG ACATGTTTCA CCTGGAGGAC ACGCTGCTAG GCTACCTTGC TGATGACCTC 540
 35 ACATGGTGTG GTGAATTCAA CACTTCCAAA ATAACTATC AATCTTGCCC AGACTGGAGA 600
 AAGGACTGCA GCACAAACCC TGTTCAGTA TTCTGGAAAA CCGTTTCCCG CAGGTTTGCA 660
 GAAGCTGCCT GTGATGTGGT CCATGTGATG CTCAATGGAT CCGCAGTAA AATCTTGAC 720
 AAAACAGCA CTTTGGGAG TGTGGAAGTC CATAATTGTC AACCAGAGAA GGTTCAGACA 780
 CTAGAGGCCT GGGTGATACA TGGTGGGAAG GAAGATTCCA GAGACTTATG CCAGGATCCC 840
 40 ACCATAAAG AGCTGGAATC GATTATAAGC AAAAGGAATA TTCAATTTTC CTGCAAGAAT 900
 ATCTACAGAC GTGACAAAGT TCTTCAGTGT GTGAAAAATC CTGAGGATTC ATCTTGACCA 960
 TCTGAGATCT GAGCCAGTCG CTGTGGTGT TTTAGCTCCT TGACTCCTTG TGGTTTATGT 1020
 CATCATACAT GACTCAGCAT ACCTGCTGGT GCAGAGCTGA AGATTTTGA GGGTCTCTCA 1080
 CAATAAGGTC AATGCCAGAG ACGGAAGCCT TTTTCCCAA AGTCTTAAAA TAACCTATAT 1140
 45 CATCAGCATA CTTTATTGT GATCTATCAA TAGTCAAGAA AAATTATGT ATAAGATTAG 1200
 AATGAAATT GTATGTTAAG TTACTTCCTT TAG 1233

Seq ID NO: C186 DNA Sequence
 Nucleic Acid Accession #: XM_120513.2
 Coding sequence: 1..2208

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 55 AGGACCCCAA AGCTCCGTAA ACACCCGCGC ACCACCCGGG CCAAGATCTT CAAGAGGTTT 180
 TTTTCAGAA GATCGGAGAG CAATTCCCGA TTGGTAGAAG AACTTGTCTG AATACACACG 240
 TACTGTAGC AGCCCGCCCC AACGACTAGC CCCTCCTCTG TGCAACCCCG AGAGTTTGGG 300
 GTCATGCAGG GGGCGCCACG AGCTCGTTTC GGAAGCCGGA CCCCGCCCGC AGCCGCGAG 360
 60 GCCTCGAGTC CACATCTGGG CATTTGGCGAG GCAGCTGTTC AATCAGGAGC TCGGGCGGCA 420
 GCCCCCGCGC CGGGGGCTCG CGATGCCAG CCTCAGCGAC AGGCGCGGCG GCGCGCGGCC 480
 ACGGCACAGA CACACACCTC CCCACACGCG CGCACAGGGG CAGACCCGGC GGGCAGGCGG 540
 CGGAGGCACC CTCGAGGCC GCGCGCCGCG GGGGAGGGGA CGTGCTCCGA GGGACCGGCC 600
 CCGAGGCGCC GGTGAGGAGA AGAGATGCAG CCGGCAGAGG AGGGGCGCAG CGTCCCAAA 660
 65 ATCTACAAGC AGCGCAGCCC CTACAGCGTC CTCAAGACGT TCCCAGCAA GAGACCGCGC 720
 CTGGCCAAGC GCTAGGAGCG ACCACCTTG GTGGAGCTGC CGCACGGCCA CTTGAGGACT 780
 CCGGCGCAGC CGCGCGCCGC GTCCCGCGCC GCCTCCTCGT CGTCTTCTGTT CGCCGCTGTC 840
 GTCAGACTCG GGGCTCTTCC GCGTCCGCCA CGCCGTGGAT TTCGGGCGCG GGGAAACCATC 900
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 70 TCCCGGCCAT CCCCTCGTCC CCGTCCGTGG CACGCTGCCG CGCGCGGGG AGGGACCTCA 1020
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 75 TTGGATGCCT TTGCCAGCA GTGCAGTCA GTTCTTAGCC TCTTAAATTG TGGAGGAAAA 1320
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 TACAACGAAA GACAGGAGCA CTGTCACTT GGGAAAGGGG TCCACAGTCA GACCTCAGAC 1440
 AATGTAGACA TAGAGATGCA GTATATGCAA AGGAAACAAC AAACCTTCTGC CTTTGTAGG 1500
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 80 TCGTCAGCCA GTGAATATGG CCATCTGGCC GACGTGGATC CTCTGTCAAC CTCTCCTGTG 1620
 CATACATTAG AAAATATTTC ACTTGATTCC ACAGCTTCCC TGTGTAAATC TAGGCATCTA 1680
 TCCAGAGAGC CCCAGGACAA GAGTGATTTC CCAATCCTT TGCAGCAGGC CTTGGCTGGG 1740
 GGTGCTTCAA GACCAATTTT AGGGGCACAG CAAAGCATCG CTTACAGGGT GAACTCTGAA 1800
 CTTGAGGATG GCATCCGCGC CCCCCTCCTT TTGAGTTGTG AGCCCTTGA AATGGATTG 1860
 ACCTCCTTGG GAAGCAAGCA GCTGTTGAAC AACTATCCTG TCTACATAAC GAGCAACAG 1920

TGGGATGAGG CTGTAAATTC TTCAAAGAAA GATGGGAGAC GGCTCCTTCG ATACCTCATC 1980
 AGATTTGTTT TCACAACCGA TGAGCTTAAG TACTCATGCG GCCTTGGGAA AAGGAAAAGG 2040
 TCAGTGCAGT CAGGAGAGAC AGGTCCCGAA AGACGCCCTC TGATCCAGT TAAAGTAACA 2100
 TGCCTCCGAG GTACTGCATC CTTCGCTCA GTGTACCAT CTGTGATCTC ATTTACCCTG 2160
 ATTGGCTGTG GCTCTCCCGC TACAAGTGTT CAGCCTTCTG TATTTTGA 2208

Seq ID NO: C187 DNA Sequence
 Nucleic Acid Accession #: AB037745.1
 Coding sequence: 26..1744

1 11 21 31 41 51
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 ATGGTGGAA CCGTGTCCCA CAAACATGGA AACGACCGTT CTCAGTGGGA TCAACTTCGA 60
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 CTCAGACAA TACTCATGTA TTCTCACTCT GGTGTGGCCA GGATTTAGAC CTCCGACAGT 180
 GGTGATGGCA GACACAGAGA ATAAAGAGGT GGCCAGAAAT ACATTTGTCT TTGAGACCTT 240
 CTGTTCTGTG AACTGTGAGC TCTACTTCTT GGTGGGTGTG AATTCTAGGA CCAACACTCC 300
 TGTGGAGACG TGGAAAGGTT CCAAGGCGAA ACAGTCTTAT ACCTACATCA TTGAGGAGAA 360
 CACTACCACG AGCTTCACCT GGGCCTTCCA GAGGACCACT TTTTATGAG CAAGCAGGAA 420
 GTACACCAAT GACGTTGGCA AGATCTACTC CATCAATGTC ACCAATGTGA TGAATGGCGT 480
 GGCTCTCTAC TGCCGTCCCT GTGCCCTAGA AGCCTCTGAT GTGGGCTCCT CCTGCACCTC 540
 TTGTCCTGCT GGTACTATTA TTGACCGAGA TTCAGGAACC TGCCACTCCT GCGCCCTTAA 600
 CACAATTTCT AAGGCCACAC AGCCTTATGG TGTCCAGGCC TGTGTGCCCT GTGGTCCAGG 660
 GACCAAGAAC AACAGATCC ACTCTCTGTG CTACAATGAT TGCACCTTCT CACGCAACAC 720
 TCCAAACAGG ACTTTCAACT ACACTTCTCT CGCTTTGGCA AACACCGTCA CTCTTGCTGG 780
 AGGGCCAAAG TTCACTTCCA AAGGGTTGAA ATACTTCCAT CACTTTACCC TCAGTCTCTG 840
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 TGAGGGTGAG TCAGGGTTCT CCAAATCTAT CACAGCCTAC GTCGTCCAGG CAGTCATCAT 960
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 TCGACTTATT GGGGTGACAA CAGATATGAC TCTGGATGGA ATCACTCTCC CAGCTGAAGT 1080
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 GTGAGGTTTG CTTAGGGCGT GGCAGCTTCG GATAAACGCA GGACTCCGCC TGGCAGCCCG 120
 35 ATTTCTCCCG GAACCTCTGC TCAGCCTGGT GAACCAACA GGGCCGAGTT TCACCCAGTC 180
 CCCACTCCAC GGTGCAGGTG CGGCTTATCT CTCAGCCAGC CGAGATGCCA GCCTTCCTGT 240
 CCCGGGCCAG CGCTCTGACA TGCAGAAGGT GACCTGGGC CTGCTTGTGT TCCTGGCAGG 300
 CTTTCTGTCT CTGGACGCCA ATGACCTAGA AGATAAAAC AGTCTTCTT ACTATGACTG 360
 GCACAGCCTC CAGGTGTGGC GGCTCATCTG CGCTGGGGT CTGTGCGCCA TGGGCATCAT 420
 40 CATCGTATG AGTGAAGTGA GGAGCTCGGG GGAGCAGGCG GGGCGGGCT GGGCTCCCC 480
 TCCCTGACC ACTCAGCTCT CCCCAACAGG TGCAAAATGC AAATGCAAGT TTGGCCAGAA 540
 GTCCGGTCAC CATCCAGGGG AGACTCCACC TCTCATCACC CCCGGCTCAG CCCAAAGCTG 600
 ATGAGGACAG ACCAGCTGAA ATTGGGTGGA GGACCGTTCT CTGTCCCCAG GTCTGTCTC 660
 TGCAAGAAA CTTGAACCTC AGGATGGAAT TCTTCTCTCT CTGTGGGAC TCCTTTGCAT 720
 45 GGCAGGCGCT CATCTCACCT CTCGCAAGAG GGTCTCTTGT TTTCAATTTT TTTAATCTAA 780
 AATGATTGTG CCTCTGCCCA AGCAGCCTGG AGACTTCCTA TGTGTGCATT GGGGTGGGGC 840
 TTGGGGCACC ATGAGAAGGT TGGCGTGCCC TGGAGGCTGA CACAGAGGCT GGCAGTGGC 900
 CTGCTTGTG GGAAAGGCC ACAGGCTGT TCCCTTGTGG CTTGGGACAT GGCACAGGCC 960
 CGCCCTCTGC CTCTCAGCC ATGGGACCTC ATATGCAATT TGGGATTAC TAGTAGCCAA 1020
 50 AAGGAATGAA AGAGAGCTCT AACCAGATGG AACACTGGAA CATTCCAGTG GACCCTGGAC 1080
 CATTCCAGGA AAACCTGGAT ATAGGATCGT CCCGCTATGA TGGAAAGTGT CAGACAGTTT 1140
 ATAATAGTAA GCCCTGTGA CCTCTCACT TACCCGAGA CTTCACTTTA TTACAAGATC 1200
 TTTCCAAATA CCAAAATATC CCGTCAAGCC CGTTAAATAA TTCCCTATGC TACCTTAAT 1260
 AACATACAA GACCACATAG TGTGAGAACT TCCAACAAGC CTCAAAGTCC CTTGAGACTC 1320
 55 CCCAATACCT AATAAGGCAT GCGAAATGTT CTCATGAAC ACCCCAACAC ACGCTATAA 1380
 CTCAAAACAC CCAAAATAT CTCTCCAAT GTCCCTGAGAC ATGAACCCAA AAAGAGACCC 1440
 ACAATAAACT CGTGACTTGT CCCCTC 1466

Seq ID NO: C195 DNA Sequence
 Nucleic Acid Accession #: NM_005971.2
 Coding sequence: 176..439

1 11 21 31 41 51
 GTTCTCCACA ACTGCCAGCA ATCCTTCCAC CAGGCAAAAC ACATCATCTA AGGAAAAGAA 60
 GTGAGGTTTG CTTAGGGCGT GGCAGCTTCG GATAAACGCA GGACTCCGCC TGGCAGCCCG 120
 65 ATTTCTCCCG GAACCTCTGC TCAGCCTGGT GAACCAACA GGGCCGAGTT TCACCCAGTC 180
 GAAGGTGACC CTGGGCTGTC TTGTGTTCCT GGCAGGCTTT CTTGTCTTGG ACGCCAATGA 240
 CCTAGAAGAT AAAAACAATA CTTTCTACTA TGACTGGCAC AGCCTCCAGG TTGGCGGGCT 300
 70 CATCTGCGCT GGGGTCTGT GCGCCATGGG CATCATCATC GTCATGAGTG CAAATGCAA 360
 ATGCAAGTTT GGGCAGAAGT CCGGTCAACA TCCAGGGGAG ACTCCACCTC TCATCACCCC 420
 AGGCTCAGCC CAAAGCTGAT GAGGACAGAC CAGCTGAAAT TGGGTGGAGG ACCGTTCTCT 480
 GTCCCCAGGT CTTGCTCTGC CACAGAACT TGAACCTCAG GATGGAATTC TTCTCTCTCT 540
 GCTGGGACTC CTTTGCATGG CAGGGCTCA TCTCACTCT CGCAAGAGGG TCTCTTGTGT 600
 75 CAATTTTTTT TAATCTAAAA TGATTGTGCC TCTGCCCAAG CAGCCTGGAG ACTTCTATG 660
 TGTGCATTGG GGTGGGGCTT GGGGCACCAT GAGAAGGTTG GCGTGCCCTG GAGGCTGACA 720
 CAGAGGCTGG CACTGAGGCT GCTTGTGGG AAAAGCCAC AGGCTGTTC CTTTGTGGCT 780
 TGGGACATGG CACAGGCCCG CCTCTGCTT CCTCAGCCAT GGGACCTCAT ATGCAATTTG 840
 GGATTACTA GTAGCCAAA GGAATGAAAG AGAGCTCTAA CCAGATGGAA CACTGGAACA 900
 80 TTCCAGTGA CACTGGACCA TTCCAGGAAA ACTGGGACAT AGGATCGTCC CGCTATGATG 960
 GAAGTGTTC CACAGTTTAT AATAGTAAGC CCTGTGACC CTCTCACTTA CCCCGAGACC 1020
 TCACCTTATT ACAAGATCTT TCCAATACC CAAATATCCC TGCAAGCCCG TTAATAAATT 1080
 CCCTATGCTA CCTTAAATA CATACAATGA CCACATAGTG TGAGAAGTTC CAACAAGCCT 1140
 CAAAGTCCCT TGAGACTCCC CAATACCTAA TAAGGCATGC GAAATGTTCT CATGAAGTAC 1200
 CCCACAACAC GCCTAAAAC CAAAACACCC AAAAAATATCT CTCCATATG CTGAGACAT 1260

GAACCCAAAA AGAGACCCAC AATAAACTCG TGA CTGTGTCC CCTC

1304

Seq ID NO: C196 DNA Sequence
 Nucleic Acid Accession #: NM_004961.2
 Coding sequence: 55..1575

5

	1	11	21	31	41	51	
10	GCCAGAGCGT	GAGCCGCGAC	CTCCGCGCAG	GTGGTTCGCGC	CGGTCTCCGC	GGAAATGTTG	60
	TCCAAAGTTC	TTCCAGTCCT	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	GGTCGAGGGA	120
	CCTCAGACTG	AATCAAAGAA	TGAAGCCTCT	TCCCGTGATG	TGTGCTATGG	CCCCCAGCCC	180
	CAGCCTCTGG	AAAAATCAGT	CCTCTCTGAG	GAACAAAGT	CAACTGAGAC	TGAGACTGGG	240
	AGCAGAGTTG	GCAAACTGCC	AGAAGCCTCT	CGCATCCTGA	ACACTATCCT	GAGTAATTAT	300
	GACCAACAAAC	TGCGCCCTGG	CATTGGAGAG	AAGCCCACTG	TGGTCACTGT	TGAGATCGCC	360
15	GTCAACAGCC	TTGGTCTCT	CTCTATCCTA	GACATGGAAT	ACACCATTGA	CATCATCTTC	420
	TCCCAGACCT	GGTAGCAGCA	ACGCTCTCTG	TACAACGACA	CCTTTGAGTC	TCTTGTCTCT	480
	AATGGCAATG	TGGTGAGCCA	GCTATGGATC	CCGGACACCT	TTTTTAGGAA	TTCTAAGAGG	540
	ACCCACGAGC	ATGAGATCAC	CATGCCCAAC	CAGATGGTCC	GCATCTACAA	GGATGGCAAG	600
	GTGTTGTACA	CAATTAGGAT	GACCATTGAT	GCCGGATGCT	CACTCCACAT	GCTCAGATTT	660
20	CCAAATGGAAT	CTACCTCTTG	CCCTCTATCT	TTCTCTAGCT	TTTCTATACC	TGAGAATGAG	720
	ATGATCTACA	AGTGGGAAAA	TTTCAAGCTT	GAAATCAATG	AGAAGAACTC	CTGGAAGCTC	780
	TTCCAGTTTG	ATTTTACAGG	AGTGAGCAAC	AAAACTGAAA	TAATCACAAAC	CCCAGTTGGT	840
	GACTTTCATG	TCATACGAT	TTTCTTCAAT	GTGAGCAGGC	GGTTTGGCTA	TGTTGCCCTT	900
	CAAAACATATG	TCCCTTCTTC	CGTGACCACG	ATGCTCTCCT	GGGTTTCTCT	TTGGATCAAG	960
25	ACAGAGTCTG	CTCCAGCCCG	GACCTCTCTA	GGGATCACCT	CTGTTCTGAC	CATGACCACG	1020
	TTGGGCACCT	TTTCTCGTAA	GAATTTCCTG	CGTGTCTCCT	ATATCACAGC	CTTGGATTTC	1080
	TATATCGCCA	TCTGCTTCCT	CTTCTGCTTC	TGCGCTCTGT	TGGAGTTTGC	TGTGCTCAAC	1140
	TTCTGTATCT	ACAACGAGAC	AAAAGCCCAT	GCTTCTCCTA	AACTCCGCCA	TCTCGTATC	1200
	AATAGCCGTG	CCCATGCCCG	TACCCGTGCA	CGTTCCCGAG	CCTGTGCCCG	CCAACATCAG	1260
30	GAGAGCTTTT	TGTGCCAGAT	TGTCAACACT	GAGGGAAGTG	ATGGAGAGGA	GGCGCCGTCT	1320
	TGCTCAGCCC	AGCAGCCCCC	TAGCCAGGTT	AGCCCTGAGG	GTCCCGCCAG	CCTCTGCTCC	1380
	AAGCTGGCCT	GCTGTGAGTG	GTGCAAGCGT	TTTAAGAAAT	ACTTCTGCAT	GGTCCCCGAT	1440
	TGTGAGGGCA	GTACCTGGCA	GCAGGGCCGC	CTCTGCATCC	ATGCTTACCG	CCTGGATAAC	1500
35	TACTCGAGAG	TTGTTTCCCC	AGTGACTTTC	TTCTTCTTCA	ATGTGCTCTA	CTGGCTTGTT	1560
	TGCTTTAACT	TGTAGTACC	AGCTGGTACC	CTGTGGGGCA	ACCTCTCCAG	TTCCCCAGGA	1620
	GGTCCAAGCC	CCTTGCCAAG	GGAGTTGGGG	GAAAGCAGCA	GCAGCAGCAG	GAGCGACTAG	1680
	AGTTTTTCTC	GCCCCATTCC	CCAAACAGAA	GCTTGCAAG	GGTTTGTCTT	TGCTGCCCCT	1740
	CTCCCCCTACC	TGGCCCATTC	ACTGAGTCTT	CTCAGCAGAC	CATTTCAAAT	TATTAATAAA	1800
40	TGGGCCACCT	CCCTCTTCTT	CAAGGAGCAT	CCGTGATGCT	CAGTGTTCAA	AACCAAGCC	1860
	ACTTAGTGAT	CAGCTCCCTA	AAACCATGCC	TAAGTACAGG	CGGATTAGCT	ATCTTCCAAC	1920
	AATGCTGACC	ACCAGACAAT	TACTGCATTT	TTCCAGAAGC	CCACTATTGC	CTTTGTAGTG	1980
	CTTTCCGGCC	AGTTCTGGCC	TCAGCCTCAA	AGTGCACCGA	CTAGTTGCTT	GCCTATACCT	2040
	GGCACCTCAT	TAAGATGCTG	GGCAGCAGTA	TAACAGGAGG	AAGAGATCCC	TCTCCTTTGG	2100
45	TCAGATTATT	ATGTTTCTCAG	TTCTCTCTCC	CTGCTACCCC	TTTCTCTGCA	GATAGATAGA	2160
	CACCTGGCATT	ATCCCTTTAG	GAAGAGGGGG	GGGCAGCAAG	AGAGCCTATT	TGGGACAGCA	2220
	TTCTCTCTC	TCTGCTGCTG	TGACATCTCC	CTCTCCTTGC	TGGCTCCATC	TTTCGTCTGC	2280
	ACTACCAATT	CAATGCCCTT	CATCCAATGG	GTATCTATTT	TTGTGTGTGA	TTATAGTAAC	2340
	TACTCCCTGC	TTTATATGCC	ACCCTCTTCC	TTCTCTTTGA	CCCTGTGAC	TCTTTCTGTA	2400
	ACTTTCCCG	TGACTTCCCC	TAGCCCTGAC	CCAGGCACTA	GGCCTTGGTG	ACTTCTGGG	2460
50	GCCCAAGAAC	TAAGGAAACT	CGGCTTTGCA	ACAGGCATTA	CTCGCCATTG	ATTGGTGCCC	2520
	ACCCAGGGCA	CACGTGCGGA	GTCTATACAC	TTGCTTGACC	CCTGGACCCA	TAAACCAAGT	2580
	CACGTGTTATA	CCCGGGGCGC	TCTAACCATC	ACAATCAATC	AATCAAAATC	CCTTAAATTT	2640
	GTATGGCACT	GGAACTTTGG	CAAAGCACTT	TTGACAAGTT	GTGTCTGATT	GGAGCTTCAT	2700
55	GATAGCCTTG	TGACATCTTT	AGGGCAGGAT	TCTTATCCCC	ATTTTGCAGA	TGAAAACCCCT	2760
	GAGTCACAGA	TTTCTGTGGG	ACTGTGGATC	TCAGTGAAGC	CTATCCAAAG	GGCCACTGTC	2820
	ACCTTCTAGA	CCACATGATA	GGGCTAGACA	GCTCAGTTCA	CCATGATTCT	CTTCTGTCTC	2880
	CTCTGCTGGC	AGCAGAGTGG	CAAGGCCGAG	AATGGCGACC	TCTCTTTAGC	TCAATTTCTG	2940
	GGCCTGAGGT	GCTCAGACTG	CCCCCAAGAT	CAAATCTCTC	CTGGCTGTAG	TAACCCAGTG	3000
60	GAATGAATTT	GGACATGCCC	CAATGCTTCT	ATATGCTAAG	TGAAATCTGT	GTCGTGAATT	3060
	TGTTGGGGGG	TGGATAGGGT	GGGGTCTCCA	TCTACTTTT	GTCAACATCA	TCTGAAATGG	3120
	GGAATATATG	AAATAAATAT	ATCAGCAAAG	CAAAAAGAAA	AAAAAAA		3168

Seq ID NO: C197 DNA Sequence
 Nucleic Acid Accession #: NM_021984.1
 Coding sequence: 572..1753

65

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	TCCAAAGTTC	TTCCAGTCCT	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	AACATGTATA	120
	CAGAGAAGTG	CTCAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAAT	GACCACAGCG	180
	GTGTAAGAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAAG	CCCCCTTTGT	240
	CACCTGCCCTC	CAGCAAGGGC	AGCACTATCC	GGACTTCTAA	CACCATCGGG	TGAGGGGACC	300
75	TCAGACTGAA	TCAAAGAATG	AAGCCTCTTC	CCGTGATGTT	GTCTATGGCC	CCCAGCCCCA	360
	GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGG	420
	CAGAGTTGGC	AAACTGCCCAG	AAGCCTCTCG	CATCCTGAAC	ACTATCCTGA	GTAATTATGA	480
	CCACAAACTG	CGCCCTGGCA	TTGGAGAGAA	GCCCCACTGT	GTCACTGTTC	AGATCTCCGT	540
	CAACAGCCTT	GGTCTCTCT	CTATCTAGA	CATGGAATAC	ACCAATTGAC	TCATCTTCTC	600
	CCAGACCTGG	TACGACGAAC	GCCTCTGTTA	CAACGACACC	TTTGAGTCTC	TTGTTCTGAA	660
80	TGGCAATGTG	GTGAGCCAGC	TATGGATCCC	GGACACCTTT	TTTAGGAATT	CTAAGAGGAC	720
	CCACAGCAT	GAGATCACCA	TGCCCAACCA	GATGGTCCGC	ATCTACAAAG	ATGGCAAGGT	780
	ATTGTACACA	ATTAGGATGA	CCATTGATGC	CGGATGCTCA	CTCCACATGC	TCAGATTTC	840
	AATGGATTCT	CACCTTTGCC	CTCTATCTTT	CTCTAGCTTT	TCCTATCTCT	AGAATGAGAT	900
	GATCTACAAG	TGGGAAAAAT	TCAAGCTTGA	AATCAATGAG	AAGAACTCCT	GGAAGCTCTT	960

	CCAGTTGGAT	TTTACAGGAG	TGAGCAACAA	AACTGAAATA	ATCACAACCC	CAGTTGGTGA	1020
	CTTCATGGTC	ATGACGATTT	TCTTCAATGT	GAGCAGGCGG	TTTGGCTATG	TTGCCTTTCA	1080
	AAACTATGTC	CCTTCTTCCG	TGACCACGAT	GCTCTCCITG	GTTTCTTTT	GGATCAAGAC	1140
5	AGAGTCTGCT	CCAGCCCGGA	CCTCTCTAGG	GATCACCTCT	GTTCTGACCA	TGACCACGTT	1200
	GGGCACCTTT	TCTCGTAAGA	ATTTCCCGCG	TGTCCTCTAT	ATCACAGCCT	TGGATTTCTA	1260
	TATCGCCATC	TGCTTCGTCT	TCTGCTTCTG	CGCTCTGTGT	GAGTTTGCTG	TGCTCAACCT	1320
	CCTGATCTAC	AACCAGACAA	AAGCCCATGC	TCTCTCTAAA	CTCCGCCATC	CTCGTATCAA	1380
	TAGCCGTGCC	CATGCCCGTA	CCCGTGCACG	TTCCCGAGCC	TGTGCCCGCC	AACATCAGGA	1440
10	AGCTTTTGTG	TGCCAGATTG	TCACCACCTGA	GGGAAGTGAT	GGAGAGGAGC	GCCCGTCTTG	1500
	CTCAGCCGAG	CAGCCCCCTA	GCCCCAGGTAG	CCCTGAGGGT	CCCCGCAGCC	TCTGCTCCAA	1560
	GCTGGCCTGC	TGTGAGTGGT	GCAAGCGTTT	TAAGAAGTAC	TCTTGCATGG	TCCCGGATTG	1620
	TGAGGGCAGT	ACCTTGGCAGC	AGGCCCGCCT	CTGCATCCAT	GTCTACCGCC	TGGATAACTA	1680
	CTCGAGAGTT	GTTTTCCGAG	TGACTTTCTT	CTTCTTCAAT	GTGCTCTACT	GGCTTGTGTT	1740
15	CCTTAACTTG	TAGGTACCAG	CTGGTACCCT	GTGGGGCAAC	CTCTCCAGTT	CCCCAGGAGG	1800
	TCCAAGCCCC	TGCCCAAGGG	AGTTGGGGGA	AAGCAGCAGC	AGCAGCAGGA	GCGACTAGAG	1860
	TTTTTCTGTC	CCCATTTCCC	AAACAGAAAG	TGTCAGAGGG	TTTGTCTTTG	CTGCCCTCT	1920
	CCCCTACCTG	GCCCCATTAC	TGAGTTTCTT	CAGCAGACCA	TTTCAAATTA	TTAATAAATG	1980
	GGCCACCTCC	CTCTTCTTCA	AGGAGCATCC	GTGATGCTCA	GTGTTCAAAA	CCACAGCCAC	2040
20	TTAGTGATCA	GCTCCCTAAA	ACCATGCCCTA	AGTACAGGCG	GATTAGCTAT	CTTCCAACAA	2100
	TGCTGACCAC	CAGACAATTA	CTGCAATTTT	CCAGAAGCCC	ACTATTGCCT	TGTCAGTGCT	2160
	TTCGGGCCAG	TTCTGGCCTC	AGCCTCAAAG	TGCACCGACT	AGTTGCTTGC	CTATACCTGG	2220
	CACCTCATTA	AGATGCTGGG	CAGCAGTATA	ACAGGAGGAA	GAGATCCCTC	TCCTTTGGTC	2280
	AGATTATTAT	GTCTCTAGTT	CTCTCTCCCT	GCTACCCCTT	TCTCTGCAGA	TAGATAGACA	2340
25	CTGGCATTAT	CCCTTTAGGA	AGAGGGGGGG	GCAGCAAGAG	AGCCTATTG	GGACAGCATT	2400
	CCTCTCTCTC	TGCTGCTGTG	ACATCTCCCT	CTCCTTGCTG	GCTCCATCTT	TCGTCTGCAC	2460
	TACCAATTTCA	ATGCCCTTCA	TCCAATGGGT	ATCTATTTTT	GTGTGTGATT	ATAGTAACTA	2520
	CTCCCTGCTT	TATATGCCAC	CCTCTTCCCT	CTCTTTGACC	CCTGTGACTC	TTCTGTAAAC	2580
	TTTCCAGTGC	ACTTCCCTCA	GCCCTGACCC	AGGCACTAGG	CCTTGGTGAC	TTCTGGGGCG	2640
30	CAAGAACTA	AGGAACTCG	GCTTTGCAAC	AGGCATTACT	CGCCATGAT	TGGTGCCAC	2700
	CCAGGGGACA	CTGTGCGAGT	TCTATCACTT	GCTTGACCCC	TGGACCCATA	AACCACTCCA	2760
	CTGTTATACC	CGGGGCGTCC	TAACCATCAA	TCAAATTCCT	TTAAATTTGT		2820
	ATGGCACTGG	AACCTTTGGCA	AAGCACTTTT	GACAAGTTGT	GTCTGATTGG	AGCTTCATGA	2880
	TAGCCTTGTG	ACATCTTTAG	GGCAGGATTC	TTATCCCCAT	TTTGCAATG	AAAACCTTGA	2940
35	GTCAAGATT	TCTGTGGGAC	TGTGGATCTC	ACTGGAAGCT	ATCCAAGAGC	CCACTGTAC	3000
	CTTCTAGACC	ACATGATAGG	GCTAGACAGC	TCAAGTTCACC	ATGATTCTCT	TCTGTACCT	3060
	CTGCTGGCAC	ACCAGTGGCA	AGGCCAGAA	TGGCGACCTC	TCTTTAGCTC	AATTTCTGGG	3120
	CCTGAGGTGC	TCAGACTGCC	CCCAAGATCA	AATCTCTCCT	GGCTGTAGTA	ACCCAGTGGG	3180
	ATGAATTTGG	ACATGCCCCA	ATGCTTCTAT	ATGCTAAGTG	AAATCTGTGT	CTGTAATTTG	3240
40	TTGGGGGGTG	GATAGGGTGG	GGTCTCCATC	TACTTTTGTG	CACCATCATC	TGAAATGGGG	3300
	AAATATGTAA	ATAAATATAT	CAGCAAAGC				3320

Seq ID NO: C198 DNA Sequence
Nucleic Acid Accession #: NM_021987.1
Coding sequence: 572..1657

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50	TCCAAAGTTC	TTCCAGTCCT	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	AACATGTATA	120
	CAGAGAAAGTG	CTCAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAAT	GACCACAGCG	180
	GTGTAAAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAAG	CCCCCTTTGT	240
	CACCTGCTCC	CAGCAAAAGC	AGCACTATCC	GGACTTCTAA	CACCATCGGG	TCGAGGGACC	300
	TCAGACTGAA	TCAAAGAAATG	AAGCCTCTTC	CCGTGATGTT	GTCTATGGCC	CCCAGCCCCA	360
55	GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGAG	420
	CAGAGTTGGC	AAACTGCCAG	AAGCCTCTCG	CATCCTGAAC	ACTATCCTGA	GTAATTATGA	480
	CCACAAACTG	CGCCCTGGCA	TTGAGAGAGAA	GCCCACTGTG	GTCACTGTTG	AGATCTCCGT	540
	CAACAGCCTT	GGTCTCTCT	CTATCCTAGA	CATGGAATAC	ACCATTGACA	TCATCTTCTC	600
	CCAGACCTGG	AATTCTAAGA	GGACCCACGA	GCATGAGATC	ACCATGCCCA	ACCAGATGGT	660
60	CCGCATCTAC	AAGGATGGCA	AGGTGTTGTA	CACAATTAGG	ATGACCATTG	ATGCCGGATG	720
	CTCACTCCAC	ATGCTCAGAT	TTCCAATGGA	TTCTCACTCT	TGCCCTCTAT	CTTTCTCTAG	780
	CTTTTCTCTAT	CCTGAGAAATG	AGATGATCTA	CAAGTGGGAA	AATTTCAAGC	TTGAAATCAA	840
	TGAGAAGAAC	TCTTGGAAAGC	TCTTCCAGTT	TGATTTTACA	GGAGTGAGCA	ACAAAACCTGA	900
	AATAATCACA	ACCCCAAGTTG	GTGACTTTCAT	GGTCATGACG	ATTTTCTTCA	ATGTGAGCAG	960
65	GCGGTTTGGC	TATGTTGCCT	TTCAAAACTA	TGTCCCTTCT	TCCGTGACCA	CGATGCTCTC	1020
	CTGGGTTTCC	TTTTGGATTA	AGACAGAGTC	TGCTCCAGCC	CGGACCTCTC	TAGGGATCAC	1080
	CTCTGTTCTG	ACCATGACCA	CGTTGGGCAC	CTTTTCTCGT	AAGAATTTCC	CGCGTGTCTC	1140
	CTATATCACA	GCCTTGGATT	TCTATATCGC	CATCTGCTTC	GTCTTCTGCT	TCTGCGCTCT	1200
	GTTGGAGTTT	GCTGTGCTCA	ACTTCTTGAT	CTACAACCAG	ACAAAAGCCC	ATGCTTCTCC	1260
70	TAAACTCCGC	CATCTCTGTA	TCAATAGCCG	TGCCCATGCC	CGTACCCGTG	CACGTTCCCG	1320
	AGCCTGTGCC	CGCCAACATC	AGGAAGCTTT	TGTGTGCCAG	ATTGTACCA	CTGAGGGAAG	1380
	TGATGGAGAG	GAGCGCCCGT	CTTGCTCAGC	CCAGCAGCCC	CCTAGCCGAG	GTAGCCCTGA	1440
	GGGTCCCCGC	AGCCTCTGCT	CCAAGCTGGC	CTGCTGTGAG	TGGTGCAAGC	GTTTAAAGAA	1500
	GTACTTCTGC	ATGGTCCCGC	ATTGTGAGGG	CAGTACCTGG	CAGCAGGGCC	GCCTCTGCAT	1560
75	CCATGTCTAC	CGCCTGGATA	ACTACTCGAG	AGTTGTTTTC	CCAGTGCATT	TCTTCTTCTT	1620
	CAATGTGCTC	TACTGGCTTG	TTTGCCCTAA	CTTGTAGGTA	CCAGCTGGTA	CCCTGTGGGG	1680
	CAACCTCTCC	AGTTCCCCAG	GAGGTCCAAG	CCCCTTGCCA	AGGGAGTTGG	GGGAAAGCAG	1740
	CAGCAGCAGC	AGGAGCGACT	AGAGTTTTC	CTGCCCATTT	CCCCAAACAG	AAGCTTGACG	1800
	AGGGTTTGTG	TTTGCTGCCC	CTCTCCCTTA	CCTGGCCCAT	TCAGTGAGTT	TTCTCAGCAG	1860
80	ACCATTTCAA	ATTATTAATA	AATGGGCCAC	CTCCCTCTTC	TTCAAGGAGC	ATCCGTGATG	1920
	CTCAGTGTTC	AAAAACACAG	CCACTTAGTG	ATCAGCTCCC	TAAAACCATG	CCTAAGTACA	1980
	GGCGGATTAG	CTATCTTCCA	ACAATGCTGA	CCACCAGACA	ATTACTGCAT	TTTTCCAGAA	2040
	GCCCACTATT	GCCTTTGACG	TGCTTTGCGC	CCAGTTCTGG	CCTCAGCCTC	AAAGTGCACC	2100
	GACTAGTTGC	TTGCCTATAC	CTGGCACCTC	ATTAAGATGC	TGGGCAGCAG	TATAACAGGA	2160
	GGAAGAGATC	CCTCTCCCTT	GGTCAGATTA	TTATGTTCTC	AGTTTCTCTC	CCCTGCTACC	2220

	CCTTTCTCTG	CAGATAGATA	GACACTGGCA	TTATCCCTTT	AGGAAGAGGG	GGGGGCAGCA	2280
	AGAGAGCCTA	TTTGGGACAG	CATTCTCTCT	TCTCTGCTGC	TGTGACATCT	CCCTCTCCTT	2340
	GCTGGCTCCA	TCTTTCTGCT	GCACTACCAA	TTCAATGCCC	TTTCATCAAT	GGGTATCTAT	2400
5	TTTTGTGTGT	GATTGTAGTA	ACTACTCCCT	GC'TTTATATG	CCACCCCTCT	CCTTCTCTTT	2460
	GACCCCTGTG	ACTCTTTCTG	TAAC'TTTCCC	AGTGACTTCC	CCTAGCCCTG	ACCAGGCACT	2520
	AGGCCTTGGT	GACTTCTCTG	GGCCAAGAAA	CTAAGGAAAC	TCGGCTTTGC	AACAGGCATT	2580
	ACTCGCCATT	GATTGGTGCC	CACCCAGGGC	ACACTGTCCG	AGTTCTATCA	CTTGCTTGAC	2640
	CCCTGGACCC	ATAAACCACT	CCACTGTTAT	ACCCGGGGCA	CTCTAACCAT	CACAATCAAT	2700
10	CAATCAAATT	CCCTTAAATT	TGTATGGCAC	TGGAAC'TTG	GCAAAGCACT	TTTGACAAGT	2760
	TGTGCTGTAT	TGGAGCTTCA	TGATAGCCTT	GTGACATCTT	TAGGGCAGGA	TTCTTATCCC	2820
	CATTTTGTCAG	ATGAAAAACC	TGAGTCACAG	ATTTCTGTGG	GACTGTGGAT	CTCACTGGAA	2880
	GCTATCCAAG	AGCCCACTGT	CACCTTCTAG	ACCACATGAT	AGGGCTAGAC	AGCTCAGTTC	2940
	ACCATGATTCT	TCTTCTGTCA	CCTCTGCTGG	CACACCAGTG	GCAAGGCCCA	GAATGGCGAC	3000
	CTCTCTTTAG	CTCAATTTCT	GGGCCTGAGG	TGCTCAGACT	GCCCCCAAGA	TCAAATCTCT	3060
15	CCTGGCTGTA	GTAACCCGAT	GGAAATGAAT	TGGACATGCC	CCAATGCTTC	TATATGCTAA	3120
	GTGAAATCTG	TGTCGTGAAT	TTGTTGGGGG	GTGGATAGGG	TGGGGTCTCC	ATCTACTTTT	3180
	TGTCACCATC	ATCTGAAATG	GGGAAATATG	TAAATAAATA	TATCAGCAAA	GC	3232

20 Seq ID NO: C199 DNA Sequence
Nucleic Acid Accession #: NM_021990.1
Coding sequence: 1309..2490

	1	11	21	31	41	51	
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	TCCAAAGTTC	TTCCAGTCTC	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	AACATGTATA	120
	CAGAGAAAGTG	CTCAAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAATAT	GACCACAGCG	180
	GTGTAAAGAA	AGCCAAATCA	AGGAACCCGAA	TGTGAGCAGG	ACCTCAGAAG	CCCCCTTTGT	240
	CACTGCCTCC	CAGCAAAGGC	AGCACTATCC	GGACTTCTAA	CACCATCGGT	GAGTTTCATA	300
30	CCTTGGCAGA	TGGCCTTTAA	CATTTTGTGT	TAATTCAATT	ATTCTTACTA	ATCTTCTTCT	360
	TTTTCTTGGC	TGTGCTGCAT	GGCTGTGGAG	CTCAGGGTGG	ACTCCTGTTG	GGCAGCCAGT	420
	TCTCTGGATGG	CTGTCTGTGG	GTGGAGGACT	CCTGCCTTTC	CTGTTTAGAC	ACCCACAAGG	480
	GCTGCTCTTT	AGCCTTCTTC	CCTTCATCCC	CTTCCCTGTC	CCCCAGTGCA	ACGAGTATTA	540
35	CACAACCAAC	AAAACCGCAA	AATATTCCCA	CAATTTTCTG	GTCTCTCTCT	GGAGAGGCCG	600
	CTCTGGCTTT	TCCTCTCAGC	CCTGGCCCTC	TGCTGTCTCC	TCACCTCTGG	TTGGTGCTGG	660
	TCAGGCTGAC	TAGAGGCCAA	GGCGACCAAC	ACTAGGCCAA	CGCGGCCAGC	GCTCAGACAT	720
	AAATGCCCTC	TTCA'TTTCAC	GTGTAACATT	CTTTTAAAT	CTAGGTCTTG	GTTTGTGTTGA	780
	TTTTTCTTCTA	AATAAAGAG	TGATCATAAA	AGAGGGACAG	CATAGAAAGT	CCCCAAAGAG	840
40	CAGCAAGGTT	TTAAAGAAAT	TCACAAGCCT	AATCTGTAC	TGTCTTATAA	TTTGCTATTA	900
	CCAGTCACAA	TTTAACTAGG	TTTTGTGTTG	AAAACTTGTT	TGGGTTTGCT	TCTGTCCCAA	960
	GAGGCACTAG	CTGGGGCCCC	TACAGAGTGC	AGGGCAGAGC	TTCA'TTTTTC	GTTTGAATGT	1020
	TCTAGGGTCG	AGGGACCTCA	GACTGAATCA	AAGAATGAAG	CCTCTTCCCG	TGATGTTGTC	1080
	TATGGCCCCC	AGCCCCAGCC	TCTGAAAAAT	CAGCTCCTCT	CTGAGGAAAC	AAAGTCAACT	1140
45	GAGACTGAGA	CTGGGAGCAG	AGTTGGCCAA	CTGCCAGAA	CCTCTCGCAT	CCTGAACACT	1200
	ATCCTGAGTA	ATTATGACCA	CAAACTGCGC	CCTGGCATTG	GAGAGAAGCC	CACTGTGGTC	1260
	ACTGTTGAGA	TCTCCGTCAA	CAGCCTTGGT	CCTCTCTCTA	TCCTAGACAT	GGAAATACAC	1320
	ATTGACATCA	TCTTCTCCCA	GACCTGGTAC	GACGAACGCC	TCTGTTACAA	CGACACCTTT	1380
	GAGTCTCTTG	TCTTGAATGG	CAATGTGGTG	AGCCAGCTAT	GGATCCCGGA	CACCTTTTTT	1440
50	AGGAATTTCTA	AGAGGACCCA	CGAGCATGAG	ATCACCATGC	CCAACCAAGT	GGTCCGCATC	1500
	TACAAGGATG	GCAAGGTGTT	GTACACAATT	AGGATGACCA	TTGATGCCCG	ATGCTCACTC	1560
	CACATGCTCA	GATTTCCAAT	GGATTCTCAC	TCTTGCCTCT	TATCTTTCTC	TAGCTTTTCC	1620
	TATCCTTGAGA	ATGAGATGAT	CTACAAGTGG	GAAAATTTCA	AGCTTGAAT	CAATGAGAAG	1680
	AACTCCTGGA	AGCTCTTCCA	GTTTGATTTT	ACAGGAGTGA	GCAACAAAAC	TGAAATAAAT	1740
55	ACAACCCGAC	TGGTGACTT	CATGGTCATG	ACGATTTTCT	TCAATGTGAG	CAGGCGGTTT	1800
	GGCTATGTTG	CCTTTCAAAA	CTATGTCCCT	TCTTCCGTGA	CCACGATGCT	CTCCTGGGTT	1860
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60	TTTGCTGTGC	TCAACTTCTT	GATCTACAAC	CAGACAAAAG	CCCATGCTTC	TCCTAAACTC	2100
	CGCCATCTCT	GTATCAATAG	CCGTGCCCAT	GCCCCGACCT	GTGCAGTTTC	CCGAGCCTGT	2160
	GCCCGCCCAAC	ATCAGGAAGC	TTTTGTGTGC	CAGATTGTCA	CCACTGAGGG	AAGTGATGGA	2220
	GAGGAGCGCC	CGTCTTGTCT	AGCCCAAGCAG	CCCCCTAGCC	CAGGTAGCCC	TGAGGGTCCC	2280
	CGCAGCCTCT	GCTCCAAGCT	GGCCTGCTGT	GAGTGGTGCA	AGCGTTTAA	GAAGTACTTC	2340
	TGCAATGGTCC	CCGATTGTGA	GGGCAGTACC	TGGCAGCAGG	GCCGCTCTG	CATCCATGTC	2400
65	TACCGCCTGG	ATAAATACTC	GAGAGTTGTT	TTCCCAAGTA	CTTTCTTCTT	CTTCAATGTG	2460
	CTCTACTGGC	TTGTTTGCTT	TAACTTGTAG	GTACCAGCTG	GTACCTCTGT	GGGCAACCTC	2520
	TCCAGTTCCC	CAGGAGGTCC	AAGCCCCTTG	CCAAGGGAGT	TGGGGGAAAG	CAGCAGCAGC	2580
	AGCAGGAGCG	ACTAGAGTTT	TTCTTGCCCC	ATTCCCCAAA	CAGAAGCTTG	CAGAGGGTTT	2640
70	GTCTTTTGTG	CCCCCTCTCC	CTACCTGGCC	CATTCACCTG	GTTTCTCTAG	CAGACCATTT	2700
	CAAAATATTA	ATAAATGGGC	CACCTCCCTC	TTCTTCAAGG	AGCATCCGTG	ATGCTCAGTG	2760
	TTCAAAACCA	CAGCCACTTA	GTGATCAGCT	CCCTAAAACC	ATGCCTAAGT	ACAGGCGGAT	2820
	TAGCTATCTT	CCAACAATGC	TGACCACCAG	ACAATTAAGT	CATTTTCCA	GAAGCCCACT	2880
	ATTGCTCTTG	CAGTGCTTTC	GGCCCACTTC	TGGCCTCAGC	CTCAAGTGC	ACCGACTAGT	2940
75	TGCTTGCCCTA	TACCTGGCAC	CTCATTAAGA	TGCTGGGCAG	CAGTATAACA	GGAGGAAGAG	3000
	ATCCCTCTCC	TTTGGTCAGA	TTATTATGTT	CTCAGTTCTC	TCTCCCTGCT	ACCCCTTTCT	3060
	CTGCAGATAG	ATAGACACTG	GCATTATCCC	TTTAGGAAGA	GGGGGGGGCA	GCAAGAGAGC	3120
	CTATTGGGGA	CAGGATTCCT	CTCTCTGTGC	TGCTGTGACA	TCTCCCTCTC	CTTGCTGGCT	3180
	CCATCTTTTC	TCTGCACATC	CAATTCAATG	CCCTTCATCC	AATGGGTATC	TATTTTGTG	3240
80	TGTGATTATA	GTAACACTCT	CCTGCTTTAT	ATGCCACCCT	CTTCTTCTC	TTTGACCCCT	3300
	GTGACTCTTT	CTGTAAC'TT	CCCAGTGACT	TCCCCTAGCC	CTGACCAGGC	ACTAGGCCCT	3360
	GGTGACTTTT	TGGGGCCCAAG	AAACTAAGGA	AACTCGGCTT	TGCAACAGGC	ATTACTCGCC	3420
	CTTGATTGGT	GCCCAACCAAG	GGCACACTGT	CGGAGTTCTA	TCACTTGCTT	GACCCCTGGA	3480
	CCCAATAAC	AGTCACATGT	TATACCCGGG	GCACCTTAAC	CATCACAATC	AATCAATCAA	3540
	ATTCCTTTAA	ATTGTGATGG	CACCTGGAAT	TTGGCAAGC	ACTTTTGACA	AGTTGTGTCT	3600

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 CAGATGAAAA CCCTGAGTCA CAGATTCTGT TGGGACTGTG GATCTCACTG GAAGCTATCC 3720
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Seq ID NO: C200 DNA Sequence
 Nucleic Acid Accession #: NM_021819.1
 Coding sequence: 39..1619

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 GGGCTGGAAT ACCCTTCTGG AGCCATCATG GAGACGCCAT CCTGGGCTGT GAGGAAGTGC 240
 GGCTGACGCC ATCCATGAGG AACCGAGTGT GCGCCGTGTG GAGCAGGGCC TCTGTCCCCT 300
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 ACCGCATGGC CGTGTGGTAC ACCCGGGGCA GGGGCCATGT AGGCTCTGTG CTTGGGGGGC 420
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 GAGCAGGAT CACCTACTGG GGGCAGAGGC TGGCATGTCT CTTGAACAGT GGCCTCACTC 660
 CCACTGATCC AGGTGAGTTC TGTGTGGATG TGGGGCCCTT GCTTTTGGTC CCTGGAGGTT 720
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 TGACCTTCAG CCTGAGTGTG CCCAGCCCAG AGGTTCCCCC TCAGCCCTTC CTGGAGATGC 840
 AGCAGCTCCG CCTGGCGAGG CAGCTGGAAG GGTGTGGGCG AAGGCTGGGC TTGGGCACCA 900
 GGGAGGATGT AACTCCAAAA TCAGACTCTG AAGCTCAAAG AGAAGGGGAA AGGCTCTTTG 960
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 GTGGCCACCT CTCCATGTCA CTCAATAAGG ACTCTGCCAA GGTGCGTGCC CTGTCCATG 1200
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 CAGAAGCCCA GGTCTCTTAC CTGCTGTGTG GCATTGAGCA TCATTCTTCA GAGCTGGACC 1320
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 TCTACCTCCT CATTGAGACT GTAGGCTTCT TCGGCTACGT GCATCTCAGG CAGGAGCTGA 1500
 ACAAGAGCCT TCAGAGTGT CTGTCCACAG GCAGCCTTCC TCTGGGTCTT GCACCACACA 1560
 CCCCAGGGC CTGGGGATT CTGAGGAGGC AGCCTCTCCC TGCCAGCATG CCTGCTGAC 1620
 CCACCTCAGA GCCTGCTTTG CATCACTGGG AAGCAGGCAG TGTCTTGGT GGGGCTTGG 1680
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 A 1801

Seq ID NO: C201 DNA Sequence
 Nucleic Acid Accession #: XM_117036.1
 Coding sequence: 25..495

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 GGCCCGTGGG GCGTGTTCCT ACCACACAGG TGCCCGAGGG AGGCAGGGCA GGCCCGGTG 240
 GGACCCAGCC CGAAACGCA GGTGTGCGCC CACGTTTGA GCCGCGCTCG CGTGTGCTG 300
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 TGTACCGCG ACAGCGGCGG CACCGTGGT GGCTCTGTTT CCTGGAAACG TCCAGAACAG 420
 GCAGCCCCCG AGACAGGGAG GGGCCAGCG GTGCCAGGG GAAGTGGGGA TGGGAATGAG 480
 TGGCGATGGG GCTGAGGTTT TTCCTGAAGG ATGAATGCTC TGAACCTGTG AATAGACACA 540
 CGGAACCTGT CACGTTTCAAC GGTGAACCGT GTGGGGAGTG AATCCATCTC AACAGAGCTG 600
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Seq ID NO: C202 DNA Sequence
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 Coding sequence: 1162..1488

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 GTGCGCCCCA ACTGCATCCT CCTCTTTGGC GGGCTGGGGA GCGGCCCCCA GCCGGGACGG 180
 GAGGCGAGCG ACCCCAGGCG CTCGTGACG TGGGAGAGAG TGTGGTGGGA AGTCTTGAGC 240
 GGAGGAGGGG ATCTGCCCCT CTCACCTCCT CTCTTGGATC CGCTCGGTT TCTGTCCCC 300
 CCACACCCG CCTGCCCGCG GGAAGACCGC CCAGTGAGCC AGCCCCACC TTCCAGGCGC 360
 CTTGCCCTGT GGGATCCAAAC CAACTTGTAT CGAGTGGGCG GGGCAACGGC TCCCCATTTT 420
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 GGTCTCTTCC CAACCCAGAC CCACCCAGGC ACATTAGCGA CCAGGCTTGG GCTTCCCGAG 540
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 TGGGCCGAGG GCCGGGTAGG CTAGCACGGG AGGTAAGGGT GGTATGGGAT GGGGCGGGGG 660
 CGGTCTAGGG CAATAGGAGA GCAGAGAATG GGGGAACCTG AGGGTGGGGG GAGGGCACCG 720

GAGCCTTGCC ACCATCCAG GACTTTGGGC AAGTCACCCG CACTCCCTGG GCCTCGGTTT 780
 CCCCATCTGT AAAATGATGG TAATAATACT TCACCTACCT CATAGGGGAG GTTGTGAGGC 840
 CACCAATCACC TGACCTGGGG GTCAAGGCAG GAGGACTCCG AAGGTGCTAC CCGTGAGCAA 900
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 TTTCTTGTGA CCATCTCCCC ATGAAAGTGC TGTACAAATT CCACCCGCC CAGGACCCCC 1140
 GCACCTGCCC TCTGGCACC GATGCCAGGG AAGGGACAGA GGAAACAGC CACAAACAAG 1200
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 CGTGAAAAA T 1511

Seq ID NO: C203 DNA Sequence
 Nucleic Acid Accession #: NM_024780.1
 Coding sequence: 31..1023

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 25 ACCTTCATTG GCCAGGACAT CTACCGGCTC CTTCGTATGG ATTTTGTGTT CTCTTTAGTC 240
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 50 CCCCTGTGAG GTGTTATACA TGACCATCAA AGTCCTACGT CAAGCTAGCT TTGCACTGGC 1680
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Seq ID NO: C204 Protein Sequence
 Protein Accession #: Eos sequence

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Seq ID NO: C205 DNA Sequence
 Nucleic Acid Accession #: NM_002250.1
 Coding sequence: 397..1680

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 GCTGACGACC TGCAAGCCAC AGTGGCTGCC CTGTGCGTGC TGCAGGATGG GGGACCTTGG 360
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 45 CTGGGGGCGT GTGAGCGCCG AAAGCGCTTG CTGGAGCAGG AGAAGTCTCT GGCCGCGTGG 480
 GCACTGGTGC TGGCAGGAAC TGGCATTGGA CTCATGGTGC TGATGTCAGA GATGCTGTGG 540
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 ACCTTCTTAC TCCTCTGCCT CATCGTGGCC TTTCATGCCA AAGAGGTCCA GCTGTTTCATG 660
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 50 GTGCTGGAGC TGGTGTGTG TGGGCTGCAC CCGCGCGGCC TCGGGGGCCC GCGTGCCTG 780
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 55 CTCGGCCTCA CGCTTGGCCT CTGGCTGACC ACCGCTGGG TGCTGTCCGT GGCCGAGAGG 1080
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 CACCGGGCCC TGGAGAAACA GATTGACACG CTGGCGGGGA AGCTGGATGC CTGACTGAG 1620
 65 CTGCTTAGCA CTGCCCTGGG GCCGAGGCAG CTTCAGAAC CCAGCCAGCA GTCCAAGTAG 1680
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 CTGCCACTCC TGACCCAGCC CTGAACAAAG CACCTCAAGT GCAAGGACCA AAGGGGGCCC 1800
 TGGCTTGGAG TGGGTGGGCT TGCTGATGGC TGCTGGAGGG GACGCTGGCT AAAGTGGGTA 1860
 GGCTTGGCC CACCTGAGGC CCCAGGTGGG AACATGGTCA CCCCCACTCT GCATACCTTC 1920
 70 ATCAAAACA CTCTCACTAT GCTGCTATGG ACAGCTTCCA GCTCTCAGTT ACAAGTGCAG 1980
 GCGACTGGAG CTAGGACTCC TGGGTCCCTG GAAAAGAGGG TACTAGGGGC CCGATCCAG 2040
 GATTCTGGGA GGCTTCAAGT ACCGCTGGCC GAGCTGAAGA ACTGGGTATG AGGCTGGGGC 2100
 GGGGCTGGAG GTGGCGCCCC CTGGTGGGAC AACAAAGAGG ACACCATTTT TCAGAGCTG 2160
 CAGAGAGCAC CTGGTGGGGA GGAAGAAGTG TAACCTACCA GCCTCTGCTC TTATCTTTGT 2220
 75 AATAAATGTT AAAGCCAG 2238

Seq ID NO: C206 DNA Sequence
 Nucleic Acid Accession #: NM_025257.1
 Coding sequence: 1..2139

80 1 11 21 31 41 51
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CCCCGGCAAG TCCTCTACCC CAGGAACCTCT ACTGGGGCCT ACTGTGGCAT GGGGGAGAAC 240
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CCGGAGGACC CATGGACTGT GGGAAAAAAC GAGTTCTCAC AGACTGTTGG GGAAGTCTTC 420
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TGCTTTCCAT GGACCAACAT TACTCCACCG GCGCTCCCAG GGATCACCAA TGACACCACC 600
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CTGATCTCTG GAGTGTCTGG CGTGCTGGCA TATGGCATCT ACTACTGCTG GGAGGAGTAC 840
CGAGTGTCTG GGGACAAGGG CGCCTCCATC TCCCAGCTGG GTTTCACCAC CAACCTCAGT 900
GCCTACCAGA GCGTGCAGGA GACCTGGCTG GCCGCCCTGA TCGTGTGGC GGTGCTTGAA 960
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ACCTTTGTCC TCCTCTCTAT CTGCAATTGCC TACTGGGCCA TGACTGCTCT GTATCCTCTG 1140
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CCCCAGGACA TCCCTACCTT CCCCTTAATC TCTGCCCTCA TCCGCACACT CCGTTACCAC 1500
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TTGGAGTATA TTGACCACAA GCTCAGAGGA GTGCAGAACC CTGTAGCCCG CTGCATCATG 1620
TGCTGTTTCA AGTGTCTGCT CTGTTGTCTG GAAAAATTTA TCAAGTCTCT AAACCGCAAT 1680
GCATACATCA TGATCGCCAT CTACGGGAAG AATTTCGTGT TCTCAGCCAA AATGCGTTC 1740
ATGCTACTCA TGCGAAACAT TGTCAAGGTG GTCTCTCTGG ACAAGTCTAC AGACCTGCTG 1800
CTGTCTTTTG GGAAGCTGCT GGTGGTCTGA GCGTGGGGG TCCTGTCTCT CTTTTTTTTC 1860
TCCGTCGCA TCCGGGGGCT GGGTAAAGAC TTTAAGAGCC CCCACCTCAA CTATTACTGG 1920
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TTGCGCATGT GTGTGGACAC GCTCTTCTCT TGCTTCTCTG AAGACCTGGA GCGGAACAAC 2040
GGCTCCCTGG ACCGCGCTTA CTACATGTCC AAGAGCCTTC TAAAGATTCT GGGCAAGAAG 2100
AACGAGGCGC CCCCAGGACA CAAGAAGAGG AAGAAGTGAC AGCTCCGGCC CTGATCCAGG 2160
ACTGCACCCC ACCCCACCG TCCAGCCATC CAACCTCACT TCGCCTTACA GGTCTCCATT 2220
TTGTGGTAAA AAAAGGTTT AGGCCAGGCG CCGTGGCTCA CGCCTGTAAT CCAACACTTT 2280
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GTGAAAC 2347
  
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Seq ID NO: C207 DNA Sequence
 Nucleic Acid Accession #: NM_016180.1
 Coding sequence: 26..1618

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CAGCAGACTC ATCATGCACA GCATGGCCAT GTTCGGAAGA GAGTTCTGCT ACGCGGTGGA 180
GGCAGCGTAT GTGACCCAG TCCTGCTCAG CGTAGGCTCT CCCAGCAGCC TGTACAGCAT 240
TGTTGTGGTT CTCAGCCCCA TCCTGGGATT CTGTCTGCAG CCCGTGGTCT GATCGGCCAG 300
CGACCACTGC CGGTCCAGGT GGGGCGCGCG GAGACCCTAC ATCCTCACCC TGGGAGTCAT 360
GATGCTCGTG GGCATGGCTC TGTACCTCAA TGGGGCTACT GTTGTAGCAG CTTTGATTGC 420
TAACCAAGG AGGAAGCTGG TTTGGGCGAT AAGTGTCAAC ATGATAGGTG TCGTCTCTCT 480
TGATTTTGCT GCCGACTTCA TTGATGGGCC CATCAAAGCC TACTTATTTG ATGTCTGCTC 540
CCATCAGGAC AAGGAGAAGG GCCTCCACTA CCATGCCCTC TTCACAGGTT TTGGAGGTGC 600
CCTGGGTTAC CTTTGGGTG CTATAGACTG GGCCCATCTG GAGCTGGGAA GACTGTTGGG 660
TACAGAATTC CAGGTATGCT TCTTCTCTC TGCAATGGTG CTCACCTTGT GTTTTACTGT 720
TCATCTGTG AGTATCTCTG AAGCCCTCAT TACAGAGGTT GCAAAGGGCA TTCCCCCACA 780
GCAAACCCCT CAGGACCCCT CATTTGTCATC AGATGGAATG TACGAGTATG GTTCTATCGA 840
GAAAGTTAAA AATGGTTACG TAAATCCAGA GCTGGCAATG CAGGGAGCAA AAAACAAAAA 900
TCATGCTGAA CAGACTCGCA GGGCAATGAC ATTAAAGTCA CTGCTGAGAG CACTGGTGAA 960
CATGCCCTCT CACTACCGCT ACCTTTGCAT CAGCCACCTC ATTGGATGGA CGGCCTTCCT 1020
GTCCAACATG CTGTTCTTCA CAGATTTTCT GGGCCAGATT GTGTACCGCG GGGATCCCTA 1080
TAGTGCACAC AACTCCACAG AGTTTCTCAT CTACGAAAGA GGAGTCGAGG TTGGATGTTG 1140
GGGCTTCTGC ATCAACTCCG GTTTTCTCTC ACTTTATTCT TACTTTTCTG AAGTTTGGT 1200
ATCCTACATT GGATTAAAGG GTCTTTACTT CACGGGATAT TTGCTGTTG GCCTGGGGAC 1260
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TGTAATGTCC AGCACCTCTG ACCTGTGCC CTTTAACTCT ATTACTGAGT ACCACCGCGA 1380
GGAAGAAAAG GAGAGGCGAG AGGCCCCAGG AGGGGACCCA GACAACAGCG TGAGAGGGAA 1440
GGGCTATGAC TGCGCCACCC TCACATGCAT GGTGCAGCTG GCTCAGATCC TGGTCGGAGG 1500
TGGCTGGGC TTTCTGTGTA ACACAGCCGG GACCGTTGTC GTTGTGGTGA TCACAGCGTC 1560
TGCGGTGGCA CTGATAGGCT GTTGCTTTGT CGCTCTCTT GTTAGATATG TGGATTAGGT 1620
CAATAAAGAG ACAATGACCC TAAAAAATAA 1650
  
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Seq ID NO: C208 DNA Sequence
 Nucleic Acid Accession #: NM_003273.1
 Coding sequence: 255..2024

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CCCACTCAGG CCCCCGGGCC CCGCTGGAAAT TCGGAGGGCC CCTGGGTAAT GGGGACAGAG 180
GATGGGACCT GGGGCAAGAG CTAAGCGAAG GAGAGCTGGA GCGGGTGAAC TAAGAGCGGG 240
GGCGAGATCT GAGGATGGAA GGCTTTGGGG GTGTCCGAGG CAGAGGGACC CCGGGGTTTG 300
  
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CAGCGAAGGG TGTCTGGAGA GGGAGAGCTG AGGAGGGGCC GGTCTGSGGS GCTGCAGAAC 360
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 GACTAAGATG GACGCTCTGGG AAGGGAACTG GGAGGCAGCG GGGTGCTTGG GGGCCGAGGG 480
 CTGAGGACGG GGTGCGGAGG CGCACTCTGG GAATGCCGAG AGGGTCCCGC AGAGACGTCA 540
 GGGCGCCGTG CGGGCCGGCG GGGAGCTGGG GGGCTAGGGG CGGACGCCGA CGTGATGGCC 600
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 GAGGTGCTGT GGAGCCACG GCGCGTCTG CTGTGGCTCG CTGGCTCGG CTGCAGGCG 780
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 GAAGCGAATG GGTCTCGCGA GGGAAAGGAC GCCCGGGGCC TTATCAGAGC CCCCTTGGAC 900
 CCGCAGTGGC CGAGGGGCGA GAATTGAAG ACAAGAGTCG CTGCGCTAT CCTATTAAACG 960
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 GGTGGGGTAT GGTCCGCCAT CCCAACTATC TTGGAGACCT CATCATGCT CTGGCTTGGT 1740
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 GCAGGAGTAC TGCCGCGGTG TGCTTACCG CATCATGCCC TACATCTACT GAAGCGGCTC 1920
 CACCACCCCA GGTGGGGCAT GTGCCACTC ATCCACCAG ACACCCAGGA CCAGGAGCCT 1980
 CGACACACTT GGGACTCAAG GGCTTGACCC CCACCCAGCC CTGAGGATGA ACAACCTCAG 2040
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Seq ID NO: C209 DNA Sequence
 Nucleic Acid Accession #: NM_015720.1
 Coding sequence: 21..1838

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 CTGGCTTGA GCCACTGGAC TCAGAGGAGC CTAGTGAGAC CATGGGCTG GAGCTGGGC 240
 TGGGAGCCCC TGGCTCAGGC TTCCCGAGCG AAGAGAATGA AGAGTCTCGG ATTCTGCAGC 300
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 CTCGCGGGGA CAGGACTCC ACCAGCCAAG AGGCAGAGGC CACAGTGTCT CCAGCTGCAG 840
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 CCGCGCGCTA CCGGCGCGCC CCGCGCGCTG GCCCTCGGCG CGGGCTCCTT CCGGCTTCCC 1980
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 CTCTCTGCGC CCGGGGACTC AATTAACCC GCGCGGAGAC CAGCGGGGCC CAGCGAAAAA 2160
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 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 2269

Seq ID NO: C210 DNA Sequence
 Nucleic Acid Accession #: NM_001197.3
 Coding sequence: 61..543

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 10 GCGCGCTGCT TGCTGTATCT TTTTAACTG TTTTCTCATG ATGCCTTTTT ATATTTAAAC 660
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 AGGGGGAGTG CTGGTCACAC CCTGTGTGA TATGTGATGC CCTCGGCAAA GAATCTACTG 900
 15 GAATAGATTC CGAGGAGCAG GAGTGCTCAA TAAAATGTTG GTTTCAGCA AAAAAAAAAA 960
 AAA 963

Seq ID NO: C211 DNA Sequence
 Nucleic Acid Accession #: AF272357
 Coding sequence: 83..1060

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 35 GGCCGGTGCA GCCGCCCTCT CGTAGCCTC CCTCTGCTGG TGCAGGCTGC AGCGTGAGAT 720
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 CCGGATCTCG CTTGGGGACC AGCGGCTGGC ACAGAGCGCG GAGATGTACC ACTACCAGCA 840
 CCAACGGCAA CAGATGCTGT GCCTGGAGCG GCATAAAGAG CCACCCAAGG AGCTGGACAC 900
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 GCCCTGCGCG GCCCCAGCT CACCGCTGC ACTGCCATGA CCTGGAGGCA GACAGACGCC 1080
 CACCTGCTCC CGACCTCGA GGCCCCCGGG GAGGGGACGG GCCTGGAGCT TCCCACTAAA 1140
 AACATGTTTT GATGCTGTGT GCTTTTGGCT GGGCCTCGGG CTCCAGGCCC TGGGACCCCT 1200
 TGCCAGGGAG ACCCCGAAAC CTTTGTGCCA GGACACCTCC TGGTCCCTCG CACCTCTCCT 1260
 45 GTTCGGTTTA GACCCCAAAC CTGGAGGGGG CATGGAGAAC CGTAGAGCGC AGGAACGGGT 1320
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Seq ID NO: C212 DNA Sequence
 Nucleic Acid Accession #: NM_004445.1
 Coding sequence: 799..3819

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 TCTCGCGGCC GAACGGACCC GGGCCGGTGC AACGGGGTCC CCGGACTGGA GAAGACGCGG 240
 GTGGCACCGT CCGAGCTCCA GGAGCCCGGG GTCCACTGCG AGGCCTCGGG GGGCGCAGAC 300
 60 CTGCAGAGAC TGCGGCCAAC GGAAGAAAT AAAGGGATTA TAGTCCACCC AATTACAGA 360
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 CCCTCTCTTT TGTGTGTGCC TCGAATGGCA GAAAAGGGG TGGCTGTGG AGGAAGGGAG 600
 65 GAGAGTAAAT GAAGAGAAAG AACTGGAATA ACCCTTGCA GAAAAAATA AAAAGGGAAG 660
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 TGGGGCGAT GGTGGACGCC CTGAAGATGT CCCATGGCTA CTGAAGGGGC TGCCAGTTA 780
 GGGAACAGAG TGGCGGCAT GGTGTGTAGC CTATGGGTGC TGCTCTGCT GTCTTCAGTT 840
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 70 ACCTACCCAC CAGGGGGGTG GACGAGGTG AGTGTCTGG ACGACGAGC ACGCTGTACT 960
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 CTTTACTACC GTCAGGCTGA GGAGCCCGAC AGCCCTGACA GCGTTTCTC CTGGCACCTC 1200
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 GCTGGACTGC AACTGAACGT CAAAGAGCGG AGCTTTGGGC CTCTCACCCA ACGCGGCTTC 1380
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 80 GCTGGGGGGG CTTCTCTGTT GGCAGCTGTG GGCACCTGTG TGGCTCATGC AGAGCCAGAG 1560
 GAGGATGGAG TAGGGGGCCA GGCAGGAGGC AGCCCCCA GGTGCACTG CAACGGGGAG 1620
 GGCAAGTGA TGGTAGCTGT CGGGGGCTGC CGTGTCCAGC CTGGATACCA ACCAGCACGA 1680
 GGAGACAAGG CCGGCCAAGC CTGCCACGG GGGCTCTATA AGTCTTCTGC TGGGAATGCT 1740
 CCCTGCTCAC CATGCCCTGC CCGCAGTCA GCTCCCAACC CAGCAGCCCC CGTTTGGCCC 1800
 TGCTGGAGG CCTTCTACCG GGCAGTTCC GACCCACCAG AGCCCCCTG CACTGGTCTC 1860
 CCATCGGCTC CCAAGGAGCT TTGTTTGGAG GTGCAAGGCT CAGCACTCAT GCTACACTGG 1920

	CGCCTGCCTC	GGGAGCTGGG	GGGTCGAGGG	GACCTGCTCT	TCAATGTCGT	GTGCAAGGAG	1980
	TGTGAAGGCC	GCCAGGAACC	TGCCAGCGGT	GGTGGGGGCA	CTTGTCAACG	CTGCAGGGAT	2040
	GAGGTCACCT	TCGACCTCTG	CCAGAGAGGC	CTGACTGAGA	GCCGAGTGT	AGTGGGGGGA	2100
5	CTCCGGGCAC	ACGTACCCCTA	CATCTTAGAG	GTGCAGGCTG	TTAATGGGGT	GTCTGAGCTC	2160
	AGCCCTGACC	CTCCTCAGGC	TGCAGCCATC	AATGTCAGCA	CCAGCCATGA	AGTGCCTCT	2220
	GCTGTCCCTG	TGGTGACCA	GGTGAGCCGG	GCATCCAA	GCATCACGGT	GTCCCTGGCCG	2280
	CAGCCCGACC	AGACCAATGG	GAACATCCTG	GACTATCAGC	TCCGCTACTA	TGACCAGGCA	2340
	GAAGACGAAT	CCCACTCCTT	CACCTGACC	AGCGAGACCA	ACACTGCCAC	CGTGACACAG	2400
10	CTGAGCCCTG	GCCACATCTA	TGGTTTCCAG	GTGCGGGCCC	GGACTGCTGC	CGGCCACGGC	2460
	CCCTACGGGG	GCAAACTCTA	TTTCCAGACA	CTTCTCAAG	GGGAGCTGTC	TTCCCAGCTT	2520
	CCGGAAGAGC	TCTCCTTGGT	GATCGGCTCC	ATCCTGGGGG	CTTTGGCCTT	CCTCCTGCTG	2580
	CGAGCCATCA	CCGTGCTGGC	GGTCTCTTTC	CAGCGGAAGC	GGCGTGGGAC	TGGCTACACG	2640
	GAGCAGCTGC	AGCAATACAG	CAGCCCAGGA	CTCGGGGTGA	AGTATTACAT	CGACCCCTCC	2700
	ACCTACGAGG	ACCCCTGTCA	GGCCATCCGA	GAACCTTGCC	GGGAAGTCGA	TCCTGCTTAT	2760
15	ATCAAGATTG	AGGAGTTCAT	TGGGACAGGC	TCTTTTGGAG	AAGTGCGCCA	GGGCCGCGCTG	2820
	CAGCCACGGG	GACGAGGGGA	GCAGACTGTG	GCCATCCAGG	CCCTGTGGGC	CGGGGGCGCC	2880
	GAAAGCCTGC	AGATGACCTT	CCTGGGCGCG	GCCGCACTGC	TGGGTCACTT	CCAGCACCCC	2940
	AAACATCTCG	GCTCTGGAGG	CGTGGTCAAC	AAGAGCCGAC	CCCTCATGGT	GCTGACGGAG	3000
	TTCATGGAGG	TTGGCCCCCT	GGACAGCTTC	CTCAGGCAGC	GGGAGGGCCA	GTTCAGCAGC	3060
20	CTGCAGCTGG	TGGCCATGCA	GCGGGAGTGC	GCTGCTGCCA	TGCAGTACCT	GTCCAGCTTT	3120
	GCCTTCGTCC	ATCGCTCGCT	GTCTGCCAC	AGCGTGTGTC	TGAATAGCCA	CTTGGTGTGC	3180
	AAGGTGGCCC	GTCTTGCCCA	CAGTCTCCAG	GGCCCAAGTT	GTTTGTCTCG	CTGGGCGAGCC	3240
	CCAGAGGTCA	TTGCACATGG	AAAGCATACA	ACATCCAGTG	ATGTCTGGAG	CTTTGGGATA	3300
25	CTCATGTGGG	AAGTGATGAG	TTATGGAGAA	CGGCCTTACT	GGGACATGAG	TGAGCAGGAG	3360
	GTACTAAATG	CAATAGAGCA	GGAGTTCGGG	CTGCCCCCGC	CTCCAGGCTG	TCCTCTTGGA	3420
	TTACATCTAC	TTATGTGGGA	CACCTTGGCAG	AAGGACCGTG	CCCGGCGGCC	TCATTTTGAC	3480
	CAGCTGTGGG	CTGCATTGGA	CAAGATGATC	CGCAAGCCAG	ATACCCCTGCA	GGCTGGCGGG	3540
	GACCCAGGGG	AAAGGCCCTT	CCAGGCCCTT	CTGACCCCTG	TGGCCCTTGA	CTTCCCTTGT	3600
30	CTGGAATCAC	CCCAGGCGCTG	GCTTTCAGCC	ATTGGACTGG	AGTGCTACCA	GGACAACCTT	3660
	TCCAAGTTTG	GCCTCTGTAC	CTTCAGTGAT	GTGGCTCAGC	TCAGCCCTAGA	AGACCTGCCT	3720
	GCCTCTGGGA	TCACCCCTGGC	TGGCCACCAG	AAGAAGCTGC	TGCACCATAT	CCAGCTCCTT	3780
	CAGCAACACC	TGAGGCACGA	GGGCTCAGTG	GAGGTCTGAG	AATGACGATA	CCCGTGACTC	3840
	AGCCCTGGAC	ACTGCTCCGA	GAAGGGACAT	GTGGGACGTG	AGCCGGGCTC	CAACAGCTTC	3900
35	TGTGAGAGAT	GCCCCACACC	AAACCCAAAC	CTCCCGATGG	CTGCATTCCC	TGGTCTCTCCG	3960
	CCTCTCCACC	AGCCCCCTCC	TCATTAAAGG	GAAAGAAGGG	AATTTGCAAA		4010

Seq ID NO: C213 DNA Sequence
Nucleic Acid Accession #: XM_043340.4
Coding sequence: 195..1067

40	1	11	21	31	41	51	
	GGGCGGCGCC	CAATGGGCTG	CGCGGAGCGT	CACTTCCCGG	CAGCGGGAGG	CGAGTGGCGA	60
45	GTGGCGAGTG	GCGAGTGTCA	GGGGGGCGGC	CGGCGGGGCG	GGGGCGGCGC	GAGGAGGCGT	120
	TGGCAGCGGG	CTCGGACCCA	CGCGGCGCCG	CGGCCCGCCT	GGCCTGCAGC	GCTCCACCCC	180
	CCGGCGGCGG	CACGATGCCC	TTTGACTTCA	GGAGGTTTGA	CATCTACAGG	AAGGTGCCCA	240
	AGGACCTTAC	GACGCCAACG	TACACCGGGG	CCATTATCTC	CATCTGCTGC	TGCCTCTTCA	300
	TCCTCTTCTC	CTTCTCTCTG	GAGCTCACCG	GATTTATAAC	GACAGAAGTT	GTGAACGAGC	360
50	TCTATGTCGA	TGACCCAGAC	AAGGACAGCG	GTGGCAAGAT	CGACGTCAGT	CTGAACATCA	420
	GTTTACCCAA	TCTGCACTGC	GAGTTGGTTG	GGCTTGACAT	TCAGGATGAG	ATGGGCAGGC	480
	ACGAAGTGGG	CCACATCGAC	AACTCCATGA	AGATCCCGCT	GAACAATGGG	GCAGGCTGCC	540
	GCTTGGAGGG	GCAGTTCAGC	ATCAACAAGG	TCCCCGGCAA	CTTCCACGTG	TCCACACACA	600
	GTGCCACAGC	CCAGCCACAG	AACCCAGACA	TGACGCATGT	CATCCACAAG	CTCTCCTTTG	660
55	GGGACACGCT	ACAGGTCACG	AACATCCACG	GAGCTTTCAA	TGCTCTCGGG	GGAGCAGACA	720
	GACTCACCTC	CAACCCCTCG	GCCTCCACAG	ACTACATCCT	GAAGATTGTG	CCCACGGTTT	780
	ATGAGGACAA	GAGTGGCAAG	CAGCGGTACT	CCTACCAGTA	CACGGTGGCC	AACAGGAAT	840
	ACGTGCGCTA	CAGCCACACG	GGCCGCATCA	TCCCTGCAAT	CTGGTTCGCG	TACGACCTCA	900
	GCCCCATCAC	GGTCAAGTAC	ACAGAGAGAC	GGCAGCCGCT	GTACAGATTG	ATCACCACGA	960
60	TCTGTGCCAT	CATTGGCGGG	ACCTTCACCG	TGCGCGGCAT	CCTGGACTCA	TGCATCTTCA	1020
	CAGCCTCTGA	GGCCTGGAAG	AAGATCCAGC	TGGGCAAGAT	GCATTGACGC	CACACCCAGC	1080
	CTAATGGCCG	AGGACCTTGG	GCATCGCCAG	CCTTGCCCTC	AGTGCCCTGT	CTCCTTTGGC	1140
	CCTCAATCTG	GTCCCAATCT	TGGCTGTGTC	CCAAAGGGTG	TGTGGGAAGT	GGGGGGAAG	1200
	TAGAGGATGG	CTCGATGTTT	TGCAGTACC	TCTTTTCCCC	GTGTTTCTTT	TTAGACAAAT	1260
65	TACACTGCCT	GAAAGTGCAG	TTCCCTTTTC	CCTGGGGAGC	CCCAAGAACA	GAGTCAGGCA	1320
	AGGGGTGGGG	AGTCCAGGGG	AACATCCACG	AATGCATATC	GATCAGCTCT	CAGCCAGGCT	1380
	TGCACAATCT	CGCAGCCCCC	ACTAGGTGGA	CACATTAAAT	ATTGTTGTTT	TCCCTTGGGC	1440
	AGCCAACTTG	CCCCAGAGGC	ACCAGACCTG	GGCTTTTACG	TTTGGGACCA	GGCTGCCCAA	1500
	AGGTACTCCT	TTATACACCC	GGCACCTTCC	ACGAAAGATG	GTACTTCCCA	AGCAAGCCCC	1560
70	TATGATTGTT	CACTATAGAT	GGAATGTGTT	GGCATGCACA	TGAGTTGAAA	TTCTTTTATG	1620
	CATTTTTTTG	AAGAAAAAAA	AAAAACAAC	TCTGAGGACA	TAGGGGATGT	CAGTTTCCTA	1680
	TGGAAGAGAC	ACCTCTGACC	CGTTATTCTT	ATAATCAAAA	TCTGAAGGGA	AAAAAATGTT	1740
	TTAGTTCTTT	CCCCACTCGT	TGGGTTCAAC	TAGATTAAAA	GGCTGATTTT	CAG	1793

Seq ID NO: C214 DNA Sequence
Nucleic Acid Accession #: NM_002151.1
Coding sequence: 246..1499

80	1	11	21	31	41	51	
	TCGAGCCCGC	TTTCCAGGGA	CCCTACCTGA	GGGCCCCACG	GTGAGGCAGC	CTGGCCTAGC	60
	AGGCCCCACG	CCACCGCCTC	TGCTCCAGG	CCGCCGCGTG	CTGCGGGGCC	ACCATGCTCC	120
	TGCCACAGCC	TGGAGACTGA	CCGACCCCGG	GCACTACCTC	GAGGCTCCGC	CCCCACCTGC	180
	TGGACCCACG	GGTCCCACCC	TGGCCCAGGA	GGTCAGCCAG	GGAATCATT	ACAAGAGGCA	240
	GTGACATGGC	GCAGAAGGAG	GGTGGCCGGA	CTGTGCCATG	CTGCTCCAGA	CCCAAGGTGG	300

	CAGCTCTCAC	TGCGGGGACC	CTGCTACTTC	TGACAGCCAT	CGGGGCGGCA	TCCTGGGCGCA	360
	TTGTGGCTGT	TCTCCTCAGG	AGTGACCAGG	AGCCGCTGTA	CCCAGTGACG	GTCAGCTCTG	420
	CGGACGCTCG	GCTCATGTGT	TTTGACAAGA	CGGAAGGGAC	GTGGCGGCTG	CTGTGCTCCT	480
5	CGCGCTCCAA	GCCAGGGTGA	GCCCGACTCA	GCTGCGAGGA	GATGGGCTTC	CTCAGGGCAC	540
	TGACCCACTC	CGAGCTGGAC	GTGCGAACGG	CGGGCGCCAA	TGGCAGCTCG	GGCTTCTTCT	600
	GTGTGGACGA	GGGAGGCTGT	CCCCACACCC	AGAGGCTGCT	GGAGGTGATC	TCCGTGTGTG	660
	ATTGCCCCAG	AGGCGTGTTC	TTGGCCGCCA	TCTGCCAAGA	CTGTGGCCGC	AGGAAGCTGC	720
	CCGTGGACCG	CATCGTGGGA	GGCCGGGACA	CCAGCTTGGG	CCGGTGGCCG	TGGCAAGTCA	780
10	GCCTTCGCTA	TGATGGAGCA	CACCTCTGTG	GGGGATCCCT	GCTCTCCGGG	GACTGGGTGC	840
	TGACAGCCGC	CCACTGCTTC	CCGGAGCGGA	ACCGGGTCTT	GTCCCGATGG	CGAGTGTGTT	900
	CCGGTGGCGT	GGCCGAGGCC	TCTCCCCACG	GTCTGCAGCT	GGGGGTGTCG	GCTGTGGTCT	960
	ACCACGGGGG	CTATCTTCCC	TTTCGGGACC	CCAACAGCGA	GGAGAACAGC	AACGATATTG	1020
	CCCTGGTCCA	CCTCTCCAGT	CCCCTGCCCC	TCACAGAATA	CATCCAGCCT	GTGTGCCTCC	1080
	CAGCTGCCGG	CCAGGCCCTG	GTGGATGGCA	AGATCTGTAC	CGTGACGGGC	TGGGGCAACA	1140
15	CGCAGTACTA	TGGCCAAACG	GCCGGGGTAC	TCCAGGAGGC	TGAGTCCCCC	ATAATCAGCA	1200
	ATGATGTCTG	CAATGGCGCT	GACTCTCTAT	GAACCCAGAT	CAAGCCCAAG	ATGTTCTGTG	1260
	CTGGCTACCC	CGAGGGTGGC	ATTGATGCCT	GCCAGGGCGA	CAGCGTGGT	CCCTTTGTGT	1320
	GTGAGGACAG	CATCTCTCGG	ACGCCACGTT	GGCGGCTGTG	TGGCATTGTG	AGTTGGGGCA	1380
20	CTGGCTGTGC	CCTGGCCAG	AAGCCAGGCG	TCTACACCAA	AGTCAGTGAC	TTCCGGGAGT	1440
	GGATCTTCCA	GGCCATAAAG	ACTCACTCCG	AAGCCAGCGG	CATGGTGACC	CAGCTCTGAC	1500
	CGGTGGCTTC	TCGCTGCGCA	GCCTCCAGGG	CCCGAGGTGA	TCCCGGTGGT	GGGATCCACG	1560
	CTGGGCCGAG	GATGGGACGT	TTTCTTCTTT	GGGCCCGGTC	CACAGGTCCA	AGGACACCTT	1620
	CCCTCCAGGG	TCTCTCTTTC	CACAGTGGCG	GGCCCACTCA	GCCCCAGAGC	CACCCACCTT	1680
25	CACCTCTCTG	ACCCCATGTG	AAATATTGTT	CTGCTGTCTG	GGACTCCTGT	CTAGGTGCCC	1740
	CTGATGATGG	GATGCTCTTT	AAATAATAAA	GATGGTTTGT	ATT		1780

Seq ID NO: C215 DNA Sequence
Nucleic Acid Accession #: AB037745.1
Coding sequence: 26..1744

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	ATGGTGGAAC	ACGCTGCCCA	CAAAACATGGA	AACGACCGTT	CTCAGTGGGA	TCAACTTCGA	60
35	GTACAGGGGC	ATGACAGGCT	GGGAGGTGGC	TGGTGATCAC	ATTTACACAG	CTGCTGGAGC	120
	CTCAGACAA	GACTTTCATG	TTCTCACTCT	GGTTGTGCCA	GGATTTAGAC	CTCCGACGTC	180
	GGTGATGGCA	GACACAGAGA	ATAAAGAGGT	GGCCAGAAATC	ACATTTGTCT	TTGAGACCTT	240
	CTGTCTCTGT	AACTGTGAGC	TCTACTTCA	GGTGGGTGTG	AATTTCTAGGA	CCAACACTCC	300
	TGTGGAGACG	TGGAAGAGTT	CCAAAGGCCAA	ACAGTCCCTAT	ACCTACATCA	TTGAGGAGAA	360
40	CACTACCACG	AGCTTTCACCT	GGGCCCTTCCA	GAGGACCACT	TTTCATGAGG	CAAGCAGGAA	420
	GTACACCAAT	GACGTGTGCCA	AGATCTACTC	CATCAATGTC	ACCAATGTTA	TGAATGGCGT	480
	GGCCTCTTAC	TGCCCTCCCT	GTGCCCTAGA	AGCCTCTGAT	GTGGGCTCCT	CCTGCACCTC	540
	TTGTCTCTGT	GGTTACTATA	TTGACCGAGA	TTCAAGAAC	TGCCACTCCT	GCCCCCTTAA	600
	CACAATTCTG	AAAGCCCACC	AGCCTTATGG	TGTCAGGCCC	TGTGTGCCCT	GTGGTCCAGG	660
45	GACCAAGAAC	AACAAGATCC	ACTCTCTGTG	CTACAATGAT	TGCACCTTCT	AACGCAACAC	720
	TCCAACCAAG	ACTTTTCACT	ACAACTTCTC	CGCTTTGGCA	AACACCCGTA	CTCTTGCTGG	780
	AGGGCCAAGC	TTCACTTCCA	AAGGGTTGAA	ATACTTCCAT	CACITTAACC	TCACTCTCTG	840
	TGGAACACAG	GGTAGGAAAA	TGCTGTGTGT	CACCGACAAT	GTCAGTGACC	TCCGGATTCC	900
	TGAGGGTGAG	TCAGGGTTCT	CCAAATCTAT	CACAGCCTAC	GTCCTGCCAG	CAGTCATCAT	960
50	CCCCCAGAG	GTGACAGGCT	ACAAGGCCGG	GGTTTCTCTA	CAGCCTGTCA	GCCTTGCTGA	1020
	TCGACTTATT	GGGGTGACAA	CAGATATGAC	TCTGGATGGA	ATCACTCCC	CAGCTGAACT	1080
	TTTCCACCTG	GAGTCTCTGG	GAATACCGGA	CGTGATCTTC	TTTTATAGGT	CCAATGATGT	1140
	GACCCAGTCC	TGCAGTTCTG	GGAGATCAAC	CACCATCCGC	GTCAGGTGCA	GTCCACAGAA	1200
	AACTGTCCCT	GGAAAGTTTC	TGCTGCCAGG	AACGTGCTCA	GATGGGACCT	GTGATGGCTG	1260
55	CAACTTCCAC	TTCTGTGGG	AGAGCGCGGC	TGCTTGCCCG	CTCTGCTCAG	TGGCTGACTA	1320
	CCATGCTATC	GTGAGCAGCT	GTGTGGCTGG	GATCCAGAAG	ACTACTTACG	TGTGGCGAGA	1380
	ACCCAAGCTA	TGCTCTGGTG	GCATTTCTCT	GCCTGAGCAG	AGAGTCACCA	TCTGCAAAAC	1440
	CATAGATTTC	TGGCTGAAAG	TGGGCATCTC	TGCAGGCACC	TGTACTGCCA	TCTCTCTCAC	1500
	CGTCTTGACC	TGCTACTTTT	GGAAAAAGAA	TCAAAAACCTA	GAGTACAAGT	ACTCCAAGCT	1560
	GGTGATGAAT	GCTACTCTCA	AGGACTGTGA	CCTGCCAGCA	GCTGACAGCT	GCGCCATCAT	1620
60	GGAAGGCGAG	GATGTAGAGG	ACGACCTCAT	CTTTACCAGC	AAGAAGTCAC	TCTTTGGGAA	1680
	GATCAAATCA	TTTACTTCCA	AGCAGCCAGC	TCTGTCAACC	ATCTCTCTTT	CAGAGGACTC	1740
	CTGATGGATT	TGACTCAGTG	CGCTGAAGA	CATCCTCAGG	AGGCCAGAGC	ATGGACCTGT	1800
	GAGAGGCACT	GGCTGCCTCA	CCTGCCTCCT	CACCTTGCTAT	AGCACCTTTG	CAAGCCTGCG	1860
	GCGATTGGGG	TGCCAGCATC	CTGCAACACC	CAGTGTGGA	AATCTCTTCA	TTGTGGCCTT	1920
65	ATCAGATGTT	TGAATTTTCA	ATCTTTTCTT	ATAGAGTACC	CAAAACCTCC	TTTCTGCTTG	1980
	CCTCAAACTT	GCCAAATATA	CCCACTTTT	GTTTGTAAAT	TATGCCCTTG	CTTGTATCTT	2040
	GTTTCCCAAA	ATGGCCCATC	CGCCAGAGCC	ATAGCTTCGT	CTGCTCATAA	TTCTTATAGC	2100
	TTTGGAATGA	AAATATTTCT	ATCTTCTTAA	GTATAGAAAC	TATTTCTCTT	GTCTCTTAAC	2160
	TTAAGGGCAG	AAACAGCTGG	GAGTTTTCCT	CGCATGCCCT	CAGCTCATGA	TCTCTTCAGG	2220
70	AGAGAGGCTG	GGTGAGGAGG	GTGTGGGGGT	TCCCTGGTGG	ATAATCTTCA	TAGCAGCCTG	2280
	GATCCATTTT	CCCTGGATAA	CCAGCTCAAA	GGGAGTGAAA	ATGGTAGTCT	GAGGGCAAGG	2340
	GGAGCAAGGC	CTGGGTAAAG	AAAGCCTTGA	AAAGCATAAA	AAGAGGCCGG	GCGCGGTGGC	2400
	TCACGCTGTT	AATCCAGACA	CTTTGGGAGG	CCGAGGCCGG	CAGATCATGA	GGTCGGGAGA	2460
	TTGAGACCAT	CCTGGCTAAC	ACGGTGAAGC	CCCGTCTCTA	CTGGAATATC	AAAAAATTAG	2520
75	CCGGCGGTGG	TGGCGGGTGC	CTGTGGTCCC	AGCTACTCGG	GAGGCTGAGG	GGGGAGAATA	2580
	GCGTGGGCCT	GGAAGGCGGA	GCTTGCACTG	AGCCGAGATC	GCGCCACTGC	ACTCCATCCA	2640
	GCCTGGGTGA	CAGAGTGAGA	CTCTGCCTCA	AAAAAAGAAA	AAAAAAGAAA	AAGCACAAGG	2700
	AGAGGCAACA	AGGAAATGTTT	TTGTTTTTGA	GACAGGCTCT	CAGTCTGTCA	CCTAGGCTGG	2760
	AGTGACAGTG	CGTAATCACT	GTTCACTGCA	GCCTCAAGCT	CTTGGGCTCA	GGCTATCCTC	2820
80	CCATCTCAGC	CTCTCAAGTA	GCTGGGACTA	CGAGTGTGCA	CCACCAGGCT	CACATAATTT	2880
	TGTGTTTTTT	GTAGACACCG	GGTTTCAACG	TGTTGCCAGG	GCTGGTCTCC	AACTCCTGGG	2940
	CTCAAGTGAT	CTGTCCGCTC	CGGCCCTCCA	AACTGCTGGG	ATTACAGGCA	TAAGCCACTG	3000
	CAGTCAAGCT	TTTATTTGTT	TTTAAACCA	CGTAGCTCAT	TGCCCTTCTT	TAAGTAAATG	3060
	ATAGATATTC	TCACTGAAGC	CAAAGGAATA	AGTTTATCAA	GAAAATGCCC	AAAGCCCTGG	3120

5 TGGATACATC CTCCTATCT TTTTAAAA CCTTCCACTA TCACTCTATG ACACTGAAAA 3180
 GAACCAGGTA AGCCCCAACC CCAGATGTTC CAGCCTTATC CTCTATTGGG TTTACCCACA 3240
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 GTTTGGGCCA TATTATGGAA CAGGGGTCTC TTATTGAAA AGAGCACAAAG GAGGCCAAGA 3360
 TTTTAATGGG GCACTTTAGG GGATACAGCC CACAATGGCA TGGGCCTGAG GTGGCCGTGA 3420
 TGCTGCTTC TAAGCTTAAC GCATCTGCTC AGGCACAGAA TAAACGTCTA GGCTGGCCAA 3480
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 10 GGAAGGCTAG GAGAGTTTAA CAAGATTTTC ACTGGGCCCA GCATGGTGGC TCACACCTGT 3600
 AATCCCAAGG CAGAATGGTG GCTTGAGCTC AGGAGTTCAA GACCAGCCTG GGCAACACAG 3660
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 15 TACCTAGAAT TGGTAAAACC AGAGCAAGAC TTTAAATTAC CTCTCTCTTT CTCTACTGG 3960
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 CCATGATTG TGCCCTGTGC CTTTCTCCAG TGACCATTTG GTGACCAGAT GGTAGATATA 4080
 GAAAGGGGAT GGCATTTGCA AGTGACTAGT CTGCCACAAA ATGCTCATCT GATTAGCCAC 4140
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 20 GGCCATCAAC AGTGTGGTG ACGGCAGGGA GTCCCTTTGG TTTAATAAAT CCAGTTTTTC 4260
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 25 TTGACTTCTT TATTCTGACT CCACTGATTG TAGCCATAAT ACTTTAAGGA GCTACTTTTT 4560
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 GTTAGCTTAC TGGGGTCACC TGTGTCTCCC CTAGCAAGTT AGGCATGTCA TATATTTTTA 4680
 ACAGCTTTAT TGAGATATAA TTCACATATT ATACAATTCA CCTTTAAAAAC ATACGATTCA 4740
 ATGGTTTTC GCAAACTCAC AGAGTTGTCC GCCCACTTGA GAGCAAAACAC ATGTTCAATT 4800
 30 TTCTTTTCTT TTTTTTTTTT GAGACAGAGT CAGCTTTGTC GCCCAGGCTG GAGTGCAGTG 4860
 CCATGATCTT GGCTCACTGC AGCCTCCCA TCCTGGGTTT AAGTGATCCT TCTGCTTCAG 4920
 CCTCCCAAGT AGCTGGGATT ACAGGCATGC GCCACCACGC CTAGCTAATT TTTGTGTTTT 4980
 TAGTAGAGAT GGGGTTTAC CGTGTGGGCC AGGCTGGTCT CAAACTCCTG GACTCAAGTG 5040
 35 ATCCACCCAC CTCGGGCTCC CAAAGTGCTG GGATTGCAGG TGTGAGCCAC CGTGCCTGGC 5100
 CTACGTGTTT AATTTTCTAT GAACAAAGGC TTAGTCTCTT GACCCAGGGC TAAAGTGGTC 5160
 TGTCCAAGCT GTTGTGGTA GAGGGAGTAT GATAAAATGT TTAATCTCA TTTGGTTACC 5220
 TTGAGTCTTG GAACACGAGC TAACTGTGAT GCTATAGTCA TCATCTGTAT TTGGCTGGGA 5280
 ATACAAATGA AGATTGTGGT GTATTCAAGC AGTAGGGTTT TTGCTTTTGT TTTTGTTTTA 5340
 40 TGCCCAACAA AACTTTTTTT TGTCTGACTA CATTAAAGAT AAGACTGACT ATATTATATC 5400
 AACAGAAACT TTGTAATAGA TTTTTCAGC TTTGTGAAAT CGAATTTTTT TTCATCAGGG 5460
 CTGGTTGGAT TTCTTTTTTA CCTGTAAATC CAAGCGTTAA TAGTTTGTGA GAAGATGGGT 5520
 TATTGATGCT CACTTTTTTT TTTTGTAAA ATAAAAACAT ACCTTAC 5567

Seq ID NO: C216 DNA Sequence
 Nucleic Acid Accession #: NM_004864.1
 Coding sequence: 26-952

45 1 11 21 31 41 51
 CGGAACGAGG GCAACCTGCA CAGCCATGCC CGGGCAAGAA CTCAGGACGG TGAATGGCTC 60
 50 TCAGATGCTC CTGGTGTGTC TGGTGCTCTC GTGGCTGCCG CATGGGGGCG CCCTGTCTCT 120
 GGCCGAGGCG AGCCGCGCAA GTTCCCGGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG 180
 ATTCCGAGAG TTGCGGAAAC GCTACGAGGA CCTGCTAACC AGGCTGCGGG CCAACGAGAG 240
 CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCTGCA GTCCGATAC TCACGCCAGA 300
 55 AGTGCAGCTG GGAATCCGGG GCCACCTGCA CCTGCGTATC TCTCGGGCG CCCTTCCCGA 360
 GGGGCTCCCC GAGGCTCTCC GCCTTCACCG GGCTCTGTTC CGGCTGTCCC CGACGCGCTC 420
 AAGGTCTGTG GACGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC 480
 GCCCGCGCTG CACCTGCGAC TGTGCGCGCC GCCGTGCGAG TCGGACCAAC TGCTGGCAGA 540
 60 ATCTTCTGTC GCACGCGCCC AGCTGGAGTT GCACTTGCGG CCGCAAGCCG CCAGGGGGCG 600
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 TCTGCACACG GTCGCGCGCT CGCTGGAAGA CCTGGGCTGG GCCGATTGGG TGCTGTGCGC 720
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 CATGCACGCG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCGGACACCG AGCCAGCGCC 840
 65 CTGCTGCGTG CCGCCAGACT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT 900
 GTCGCTCCAG ACCTATGATG ACTTGTAGC CAAAGACTGC CACTGCTATG GAGCAGTCTT 960
 GGTCTTTCCA CTGTGCACCT GCGCGGGGGA GCGGACCTCA GTTGTCTGTC CCTGTGGAAT 1020
 GGGCTCAAGG TTCTGTAGAG ACCCGATTCC TGCCCAACA GCTGTATTTA TATAAGTCTG 1080
 70 TTATTTATTA TTAATTTATT GGGGTGACCT TCTTGGGAC TCGGGGGCTG GTCTGATGGA 1140
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 AAAA 1204

Seq ID NO: C432 DNA Sequence
 Nucleic Acid Accession #: NM_052858.1
 Coding sequence: 54..1259

75 1 11 21 31 41 51
 GGCACGAGGT GTTGCCTTCA GGTGCTCTCC GGGCGCGGAC ACGGAACCCG GCCATGGAAG 60
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 80 CCCACCCAGA CCAAGGCGCG ACCCACGATC GACCGCGGGA CCGACCCGGG GACCCGCGCA 180
 GGAAGCGAAG CAGCAGCGCG AACCGCGGAA GGGACGGGGA CCGGAGCCCG AAGAGAGACC 240
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 GAGACCCGGA CCGAGGCCCC CGCCGGGACA CACACAGGGA CGCGGGCCCT CGCGCAGGTG 360
 AACACGAGT TTTGGGAAAA CCGGCCAAA GCCGACGCG GGCAGGAGCC CGGGGACTGA 420
 CCTGGGACGC AGCCGCGCCT CCTGGGCCCG CGCCCTGGGA AGCCCGGGAG CCGCCGACGC 480

CGCAGAGGAA GGGAGACCCC GGGCGCCGCA GACCCGAAAG TGAACCCCTT TCGGAGAGAT 540
 ATCTGCCCTC GACCCCAAGG CCTGGACGAG AGGAGGTGGA ATATATACCAG TCAGAGGCGG 600
 AAGGACTCCT GGAATGCCAC AAATGCAAAAT ACTTGTGCAC TGGGAGAGCC TGCTGCCAAA 660
 TGCTGGAGGT TCTCTGTAAC TTGCTGATCC TGGCCTGCAG CTCTGTGTCT TACAGTTCCA 720
 CAGGGGGCTA CACGGGCATC ACCAGCTTGG GGGGCATTTA CTACTATCAG TTCGGAGGGG 780
 CTTACAGTGG CTTTGTAGGT GCTGACGGGG AGAAGGCCCA GCAACTGGAT GTCCAGTTCT 840
 ACCAGCTAAA GCTGCCCATG GTCACCTGTG CAATGGCCTG TAGTGGAGCC CTCACAGCCC 900
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 TGGTGACCGA AGGCTTGTGT GACATGCTCA TCGCGGGGGG GTACATCCCG GCCTTGTACT 1020
 TCTACTTCCA CTACTCTCT GCTGCCTATG GCTCTCCTGT GTGTAAAGAG AGGCAGGCGC 1080
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 CTGGAATCTT TGCTGCCCTG GGCATTGTGG TCTTTGCCCT GGGGGCGGTC CTGGCCATAA 1200
 AGGGCTACCG AAAAGTTAGG AAGCTAAAAG AGAAGCCAG AGAAATGTTT GAATTTTAAG 1260
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 TAAATAACAA AAAAATTAGC CAGGCGTGGT GGCGGGCGCC TGTAATCCCA GCTACTTGGG 1680
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 CGCCACTGCA CTCCAGCCCA GGTGACAGAG CGAGACTCCA TCTCAAAAAA AAAAAAAA 1800

Seq ID NO: C434 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 261..2861

1 11 21 31 41 51
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 AGCTACCACT CGCTTGCCCC AGCGCCCGGG AGCTCGCGGC GCCTGCGCGT CAGCGACCAAG 180
 ACGTCCGGGG CGCTGCGCT CCTGGCCCCG GAGGCGTGAC ACTGTCTCGG CTACAGACCC 240
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 AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GGACTTCCTC TTCAAGGCCA 300
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 CTGGGTGCCC TGACCAGAGC CCTGAGTTGC AACCTTGGAA CCCTGGCCAT GACCAAGACC 420
 ACCATGTGCA TATCGGCCAG GGCAAGACAC TGCTGCTCAC CTCTCTGCC ACGGTCTATT 480
 CCATCCACAT CTCAGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG CCGATTGTTT 540
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 TGCGAAACCG GCACATCCTG ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTGCCCTCT 600
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 ATGGACAGAA AAAGCTCTCC TGGACATTTT TGAACAAGAC CCTTCACCCA GGTGGCATGG 780
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 AGTACCCGAT TCACTTCCAC CTGGCCGCTG ATGTAGACGA AAGGGAGGTT TATGACCCAC 1980
 CCACATACAT CAGGGACCTC TCCATCCATC ATACATTCTC TCGCTGCGTC ACAGTCCATG 2040
 65 | | | | |
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 TCACGGAAGA TGGGCGGAG GAACGCAACA CTTTGAACCA CTGCTTGGC CTCCTTGTCA 2160
 AGTCTGGAAC CCTCTCCCC TCGGACCGTG ACAGCAAGAT GTGCAAGATG ATCAGAGAGG 2220
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 GGATGGCCAA TCCCAACAAC AACCTCATCA ACTGTGCCGC TGCAGGATCT GAGGAAACTG 2340
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 GATTTTGGTT TATTTTTCAC CACGTACCAA CGGGCCCCCT CGTGGGAATG TACTCCCCAG 2400
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 GGGAGCAATG GGCTTTGCTG CTTATGAGCA CAGAGGAATT CAGTCCCAG GCAGCCCTGC 2940
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 5 CCAATTTGGC TGATCTTGGG TGTCTGAACA GCTATTGGGT CCACCCCACT CCCTTTTCAGC 3600
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 10 AGAGGGCCTG CCTGGCTCCC TCCACCCAAC TGCACCCATG AGACTCGGTC CAAGAGTCCA 3840
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 GAACCACTTA GGATGTGATC ACTTTCAGGT GGCCAGGAAT GTTGAATGTC TTTGGCTCAG 4140
 15 TTCAATTTAAA AAAGATATCT ATTTGAAAGT TCTCAGAGTT GTACATATGT TTCACAGTAC 4200
 AGGATCTGTA CATAAAAGTT TCTTTCCTAA ACCATTCAAC AAGAGCCAAT ATCTAGGCAT 4260
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 20 TTTTCTCTTT GCCGAAATAG CTGGTCCTTT TTCGGGAGTT AGATGTATAG AGTGTGTA 4440
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 GAGATGTCTT TTGCATTGCT TGGAAAGGGT GTACCTAGAG CCAAGGAAAT TGGCTCTGGT 4620
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 25 AAAAAAATAA AAAAAAATAA AA 4702

Seq ID NO: C217 Protein Sequence
Protein Accession #: NP_005805.1

1 11 21 31 41 51
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 30 MVGKMPVLW TLCAVRVTVD AISVETPQDV LRASQGKSVT LPCTYHTSTS SREGLIQWDK 60
 LLLTHTERVV IWPFSNKNYI HGELYKNRVS ISNNAEQSDA SITIDQLTMA DNGTYECSVS 120
 LMSDLBGNTK SRVRLVLVLP PSKPECGIEG ETIIIGNNIQL TCQSKEGSEPT PQYSWKRYNI 180
 35 LNQEQLAQP ASGQPVSLKN ISTDTSGYII CTSSNEEGTQ FCNITVAVRP PSMNVALYVG 240
 IAVGVVAALI IIGIIYYCCC CRGKDDNTED KEDARPNREA YEEPEQLRE LSREEREEDD 300
 YRQEQRSTG RESPDHLDQ 319

Seq ID NO: C218 Protein Sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
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 40 MGSRTPEPSP HAVQLRWGPR RRPPLPLLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
 GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVLYCP WGASPTQCTP IEFDSKGSRL 120
 45 LESSLSSESG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYLS 180
 DNFRILEYA PCRSDFSWAA GGQYCGGFS AEFTKTGRVV LGPGSYFWQ GQILSATQEY 240
 IAESYYPEYL INLVQGLQTL RQASSYDDSD YLGYSVAVGE FSGDDTEDFV AGVPKGNLTY 300
 EVVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360
 50 EVGRVYVYLO HPAGIEPTPT LTLTGHDDEFG RFGSSLTPLG DLDDQDGYNDV AIGAPFGGET 420
 QQGVVVFVFP GPQGLGSKPS QVLQPLWAAS HTPDFFGSAL RGRDRLDGNG YPDLVGSFG 480
 VDKAVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
 GFTVELQLDW QKQKGGVRRR LFLASRQATL TQTLILQNGA REDCREMKIY LRNESEFRDK 600
 LSPIHIALNF SLDPQAPVDS HGLRPLAHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
 55 GEQNHVYLG D KVALNITFHA QNVGEGGAYE AELRVTAPE AEYSGLVRHP GNFSSLSCDY 720
 FAVNQSRLLV CDLGNPMKAG ASLWGGRLRFT VPHLRDTKKT IQPDFQILSK NLNNSQSDVV 780
 SFRLSVEAQA QVTILNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
 SQGVLELSCP QALEGGQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLSHH QQKREAPSR 900
 SASSGPQILK CPBAECFRLR CELGPLHQE SQSLQLHFRV WAKTFLQREH QPFSLOCEAV 960
 60 YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020
 YKLGFFKRSI PYGTAMEKAQ LKPPATSDA 1049

Seq ID NO: C219 Protein Sequence
Protein Accession #: NP_002412.1

1 11 21 31 41 51
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 65 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTURIEN 120
 70 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFAQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSGLGSHST DIGALMYP 240
 TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
 FYMRTNPFYP EVELNFISVF WPQLPNGLA AYEFADRDEV RFFKGNKYWA VQGNVLHGY 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWR YDEYKRSMDPG YPKMIAHDFP 420
 75 GIGHKVDADF MKDGGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN 469

Seq ID NO: C220 Protein Sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
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 80 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTURIEN 120
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFAQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSGLGSHST DIGALMYP 240

TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
 FYMRINPFYP EVELNFISVF WFQLPNGLEA AYEFAADRDEV RFFKGNKYWA VQGQNVLHGY 360
 PKDIYSSGFG PRTVKHIDAA LSEENTGKTY FFVANKYWRY DEYKRSMDFG YPKMIAHDFP 420
 GIGHKVDADF MKDGFFYFFH GTRQYKFDPK TKRIITLQKA NSWFNCRKN 469

Seq ID NO: C221 Protein Sequence
 Protein Accession #: NP_055146.1

1 11 21 31 41 51
 MVRKPVVSTI SKGGYLQGNV NGRLPSPGKNG EPFGQEKVQL KRKVTLLRGV SIIIGTIIGA 60
 GIFISPKGVL QMTGSGVMSL TIWTVCGVLS LFGALSYAEL GTTIKSGGGH YTYILEVFGP 120
 LPAFVRVWVE LLIIIRPAATA VISLAFGRYI LEPPFFIQCEI PELAIKLITA VGITVVMVLN 180
 SMSVSWASARI QIFLTFCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY 240
 YGMAYAGWVF YLNFVTEEEVE NPEKTIPLAI CISMAITIGV YVLTNVAYFT TINAEELLS 300
 NAVAVTFSESR LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV 360
 RKHTPLPAVI VLHPLTMIML FSGDLDSLNL FLSFARWLF GLAVAGLIYL RYKCPDMHRP 420
 FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM 480
 SEKITRTLQI ILEVVPEDK L 501

Seq ID NO: C222 Protein Sequence
 Protein Accession #: NP_003237.1

1 11 21 31 41 51
 MGLAWGLGVL FLMHVCGTNR IPESGGDNSV FDIFELTGAA RKGSGRRLVK GPDPSPPAFR 60
 IEDANLIPVP PDDKFDQLVD AVRAEKGFLL LASLRQMKKT RGTLLALERK DHSGQVFSV 120
 SNGKAGTLDL SLTVQKGQHV VSVEEALLAT GQWKSITLFV QEDRAQLYID CEKMEAEELD 180
 VPIQSVFTRD LASIARLRIA KGGVNDNFQO VLQNVRFVFG TTPEDILRNK GCSSTSVLL 240
 TLDNNVNGS SPAIRTNIGY HKTDLQAIC GISCEDELSSM VLELRGLRTI VTTLQDSIRK 300
 VTEENKELAN ELRRPPLCYH NGVQYRNNEE WTVDSCTECH CQNSVTICKK VSCPIMPEN 360
 ATVPDGECCP RCWPSDSADD GWSFWSEWTS CSTSCGNGIQ QGRSCDSLNL NRCEGSSVQT 420
 RTCHIQECDK RFKQDGGWHS WSPWSSCSVT CGDGVITRIR LCNSPSPQMN GKPCGEARE 480
 TKACKDACP INGGWGPWSP WDICSVTCCG GVQKRSRLCN NPAPQFGGKD CVGDVTENQI 540
 CNKQDCPIDG CLSNPCFAGV KCTSYPDGWS KCGACPPGYS GNGIQCTDVD ECKEVPDADF 600
 NHNGEHRCEH TDPGYNCLPC PPRFTGSQPF GQVEHATAN KQVCKPRNPC TDGTHDCNKN 660
 AKCNLYGHYS DPMYRCECKP GYAGNGIICG EDTDLGWPEN ENLVCVANAT YHCKKDNCPN 720
 LPNSGQEDYD KDGIGDACDD DDDNDKIPDD RDNCPPHYNP AQYDYDRDDV GDRCDNCPYN 780
 HNPDAQADTN NGEQDACAAD IDGDGILNER DNCQYVYNVD QRDMDMDGVG DQCDNCPLEH 840
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 WHTGNTPGQV RTLWHDPRHI GWKDTAYRW RLSHRPKTGF IRVVMYEGKK IMADSGPIYD 1140
 KTYAGGRLGL FVFSQEMVFF SDLKYECRDP 1170

Seq ID NO: C223 Protein Sequence
 Protein Accession #: NP_002183.1

1 11 21 31 41 51
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 HILNMLHLKK RPDVQPPVK AALLNAIRKL HVGKVGENG YVEIEDDIGR AEMNELMEQT 120
 SEIITFAESG TARKTLHFEI SKEGSDLSVV ERAEVWLFK VPKANRTRK VTIRLFQQQK 180
 HPQGLDTEGE EAEVGLKGE RSELLLSEKV VDARKSTWHV FVSSSIQRL LDQKGSLLDV 240
 RIACEQCQES GASVLLGK KKEEKEEGEK KKGGEAGAG ADEEKEQSHR PFLMLQARQS 300
 EDHPRHRRRR GLECDGKVINI CCKKQFFVSF KDIGWNDWII APSGYHANYC EGCEPSHIAG 360
 TSGSSLSFHS TVINHYMRG HSPFANLKSC CVPTKLPRMS MLYYDDGQNI IKKDIQNMIV 420
 EECGCS 426

Seq ID NO: C224 Protein Sequence
 Protein Accession #: NP_000086.1

1 11 21 31 41 51
 MVPDTACVLL LTLAALGASG QQSPLGSDL GPQMLRELQE TNAALQDVRD WLRQVREIT 60
 FLKNTVMECD ACGMQQSVRT GLPSVRPLLH CAPGFCFPV ACIQTESGGR CGPCPAGFTG 120
 NGSHCTDVNE CNAHPCFPV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
 INECETGQHN CVPNVCINT RGSFQCGPCQ PGFVGDAQS CQGAQRFCF DGSPSECHHE 240
 ADCVLERDGS RSCVCRVGA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSGQ 300
 EDVDRDGIAD ACDPDADGG VNEKDNCP LVRNPDQRNT EDKWDACDN CRSQKNDQK 360
 DTDQDGRGDA CDDIDIGDRI RNQADNCPRV PNSDQKSDG DGIQDADNC PQKSNPDQAD 420
 VDHFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPS 480
 RDNCRLVPPN GQEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAETVLT DFRFQTVVLD 540
 PEGDAQIDPN WVLNQGREGI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600
 FGQDSSSFY VVMWQMEQT YWQANPFRV AEPGIQLKAV KSSTGPEQL RNALWHTGDT 660
 ESQVRLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG 720
 RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA 757

Seq ID NO: C225 Protein Sequence
 Protein Accession #: NP_612464

1 11 21 31 41 51

MRPQGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKGKQKA QLRQREVVDL YNGMCLQGPA 60
 GVPGRDGSFG ANGIPGTGPI PGRDGFKEGK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
 GKIACTFTFK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECGSL PIEAIIYLDQ 180
 GSPMNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240
 LPK 243

Seq ID NO: C226 Protein Sequence
 Protein Accession #: NP_003216.1

1 11 21 31 41 51
 MATMENKVIC ALVLVSMAL GTLAEAQTET CTVAPRERQN CGFPGVTPSQ CANKGCCFDD 60
 TVRGVPWCYF PNTIDVPPEE ECEF 84

Seq ID NO: C227 Protein Sequence
 Protein Accession #: NP_056234.1

1 11 21 31 41 51
 MPKRAHWGAL SVVLILLWGH PRVALACPHP CACYVPSEVH CTFRSLASVP AGIARHVERI 60
 NLGFNSIQAL SETSFAGLTK LELLMIHGNE IPSIPDGALR DLSSLQVFKF SYNKLRLVITG 120
 QTLQGLSNIM RLHIDHNKIE FIHPQAFNGL TSLRLHLLEG NLLHQLHPST FSTFTFLDYF 180
 RLSTIRHLYL AENMVRTLPA SMLRNMLLE NLYLQGNPWT CDCEMRWFLF WDAKSRGILK 240
 CKKDKAYEGG QLCAMCFSPK KLYKHEIHKL KDMTCLKPSI ESPLRQNRSR SIEEEQBQEE 300
 DGGSQILILEK FQLPQWSISL NMTDEHGMV NLVCDIKKPM DVYKIHNLQT DPPDIDINAT 360
 VALDFECPMT RENYKILWKL IAYSEVPVK LHRELMLSKD PRVSYQYRQD ADEEALYYTG 420
 VRAQILAEP EWMQPSIDIQ LNRQRSTAKK VLLSYTYQYS QTISTKDTQ ARGSRVWMIE 480
 PSAGVQRDQT VLEGGPCQLS CNVKASESPS IFWVLPDGS LKAPMDPDFS KFSILSSGWL 540
 RIKSMEPSDS GLYQCIQAVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGKN PGESVTLPCN 600
 ALALPEAHL WILPNRIIN DLANTSHVM LPNGTSLIPK VQVSDSGYYR CVAVNQGGAD 660
 HFTVGTITVK KSGGLPSKRG RRPAGAKALS VREDIVEDEG GSGMGDEENT SRLLHPKQD 720
 EVFLKTKDDA INGDKKAKKG RRLKLLWKHS EKEPETNVAE GRRVFESRRR INMANKQINP 780
 ERWADILAKV RGNLPLKGT VPPLIKTSP PSLSLEVTPP FPAVSPSPAS PVQTVTSAAE 840
 SSADVPLLE EHVLTGISS ASMGLEHNHN GVILVEPEVT STPLEEVVDD LSEKTEITS 900
 TEGDLKGTA PTLISEPYEP SPLTLTLDTV YEKPTHEETA TEGWSAADVG SSPEPTSSEY 960
 EPPLDAVSLA ESSEMQYFDP DLETKSQPDE DKMKEDTFAH LTPPTIWN DSSTSOLFED 1020
 STIGEPGVPG QSHLQGLTDN IHLVKSSLST QDTLLIKKGM KEMSQTLQGG NMLEGDPHTS 1080
 RSSESEGGES KSITLPDSTL GIMSSMSPVK KPAETTVGTL LDKDTTITVT TPRQKVAPSS 1140
 TMSTHPSRRR PNRRRLRPN KFRHRHKQTP PTTFAPSETF STQPTQAPDI KISSQVSSL 1200
 VPTAWVDNTV NTPKQLEMEK NAEPTSKGTP RRRKHGKRENK HRYTPSTVSS RASGSKPSPS 1260
 PENKHRNIVT PSSETILLPR TVSLKTEGYP DSLDYMTTR KIYSSYFKVQ ETLPTVTKPT 1320
 SDGKEIKDDV ATNVDDHKSD ILVTGESITN AIPTSRSLVS TMGEFKEESS PVGFPPTPTW 1380
 NPSRTAQPR LQTDIPVTS GENLTDPPLL KELEDVDFTS EFLSSLTVST PFHQEEAGSS 1440
 TTLSSIKVEV ASSQAETTL DQDHLETTVA ILLSETRPQN HTPTAARMKE PASSSPSTIL 1500
 MSLGQTTTTK PALSPRISQ ASRDSKENVF LNYVGNPETE ATPVNNEGTO HMSGPNELST 1560
 PSSDRDAFNL STKLELEKQV FGSRSLPRGP DSQRQDGRVH ASHQLTRVPA KPILPTATVR 1620
 LPEMSTQAS RYFVTQSQR HWTNKPEITT YPSGALPENK QFTTPTLST TIPLPLHMSK 1680
 PSIPSKFTDR RTDQFNGYSK VFGNNNIEPA RNPVGKPPSP RIPHYSNGRL PFFTKNTLSF 1740
 POLGVTRRPQ IPTSPAPVSR ERKVIPGSYN RIHSHSTFHL DFGPPAPPLL HTPQTGSPS 1800
 TNLQNIPIVMS STQSSISFIT SSVQSSGSFH QSSSKFFAGG PPASKFWSLG EKPQILTKSP 1860
 QTVSVTAETD TVFPCEATGK PKPFVTWTKV STGALMTPT RIQRFVLEKN GTLVIRKQVQ 1920
 QDRGQYMCTA SNLHGLDRMV VLLSVTVQQP QILASHYQDV TVYLGDTIAM ECLAKGPAP 1980
 QISWIFPDRR VQVTFSPVES RITLHENRTL SIKEASFSDR GYVKCVASNA AGADSLAIRL 2040
 HVAALPPVIH QEKLENISLP PGLSIHIHCT AKAAPLPSVR VVLGDGTQIR PSQFLHGNLF 2100
 VFPNGTLYIR NLAPKDSGRY ECVAAANLVS ARRTVQLNVQ RAAANARITG TSPRRTDVRY 2160
 GGTLKLDCA SGGPWPRILV RLPSKRMIDA LFSFDSRIK FANGTLVVKV VTDKADGYL 2220
 CVARNKVGDD YVVLKVDVVM KPAKIEHKEE NDHKVFYGGD LKVDCAVTLG PNEISWSLP 2280
 DGSLVNSFMQ SDDSGGRTRK YVVFNNGTLY FNEVGMRBEG DYTCAENQV GKDEMRVRVK 2340
 VVTAPATIRN KTYLAVQVPY GDVTVACEA KGEMPKVITW LSPTNKVITP SSEKYQIYQD 2400
 GTLLIQKAQR SDGNYTCLV RNSAGEDRKT VVIHVNVPQP KINGNPNPIT TVREIAAGS 2460
 RKLIDCKAEG IPTPRVLWAF PEGVVLPAFY YGNRITVHGN GSLDIRSLRK SDSQVLVCMA 2520
 RNEGGEARLI VQLTVLEPME KPIFHDPISE KITAMAGHTI SLNCSAAGTP TPSLVVVLN 2580
 GTDLQSGQQL QRFYHKADGM LHIISGLSSVD AGAYRCVARN AAGHTERLVS LKVGLKPEAN 2640
 KQYHNLVSI NGETLKLPT PPGAGQGRFS WTLPGMHLE GPQTLGRVSL LDNGTLTVRE 2700
 ASVFDRTGYV CRMETEYGPS VTSIPVIVIA YPPRITSEPT PVIYTRPGNT VKLNCMAMGI 2760
 PKADITWELP DKSHLKAGVQ ARLYGNRFLH PQGSLTIQHA TQRDAGFYKC MAKNILGSDS 2820
 KTTYIHVF 2828

Seq ID NO: C228 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MPGTKLIRTG APADYRVILK TSQEDELDPV DDISVRVMSS QSVLVSWVDP VLEKQKKVVA 60
 SRQYTVRYRE KGLARWDYK QIANRRVLIE NLIPDVTYEF AVRISQGERD GKWSTSVFQR 120
 TPESAPTAP ENLNVVPVNG KPTVVAASWD ALPETEGKVK VCLLDTLGFS VSSFQPSAKS 180
 FQNTFFHTPR LSNHLEQSPS PILETLLLPW WMVCSLGNAI FSKSGPQTGE AWDLTTPKPSL 240
 SLCQQECSCST QKDFSLCLAYL IDIQTKQVKN DPQLEGSVFG PCFLFYFLT MLDIGGFSFI 300
 MCYEDPVSST LTGNSLKSVA ASKADVQONT EDNGKPEKPE PSSPSPRAPA SSQHPSVPAS 360
 PQGRNAKDL LDKNLKILAN GGAPRKQLR AKKAEELDLQ STEITGEEEL GSREDSPMSP 420
 SDTQDKRRTL RPSRHRHGSV VAPGRTAVRA RMPALPRRG VDKPGFSLAT QPRPGAPPSA 480
 SASPAHHAST QGTSHRPSLP ASLNDNDLVD SDEDERAVGS LHPKGAFAPQ RPALSPSRQS 540
 PSSVLDRDSS VHPGAKPASP ARRTPHSGAA EEDSSASAPP SRLSPHGG SLLPTQPHL 600
 SSPLSKGGKD GEPAPATNSN APSRSTMSSS VSSHLSRTQ VSEGARASDG ESHGDGDRED 660

GGRQAEATAQ TLRARPASGH FHLLRHKPPA ANGRSPSRFS IGRGPRLQPS SSPQSTVPSR 720
 AHPRVPSHSD SHPKLSSGIH GDEDEKPLP ATVVNDHVPS SSRQPISRGW EDLRRSPQRG 780
 ASLHHRKEPI ENPKSTGADT HFQGYSSLA SKAQDVQOST DADTEGHSPK AQPGSTDRHA 840
 5 SPARPPAARS QQHPSVPRRM TPGRAPQQP PPPVATSQHH PGFQSRDAGR SPSQPRLSLT 900
 QAGRPRPTSQ GRSHSSSDPY TASSRGMLPT ALQNQDEDAQ GSYDDDDSTEV EAQDVVRAPAH 960
 AARAKEAAS LPHKQQVESF TGAGAGGDHR SQRGHAAAPA RPSRPGGPQS RARVPSRAAP 1020
 GKSEPPSKRP LSSKQQSVS AEDEEEDAG FFKGGKEDLL SSSVPKWPSS STPRGGKDAD 1080
 GSLAKEEREP AIALAPRGGS LAPVKRPLPP PPGSSPRASH VPSRPPPSA ATVSPVAGTH 1140
 10 PWPRYTTRAP PGHFSTTPML SLRQRMHAR FRNPLSRQPA RPSYRQGYNG RPNVEGKVLP 1200
 GSNKPNQGR IINGQVQDVL VVDLDRGLVL NAEGRYLQDS HGNPLRIKLG GDGRTIVDL 1260
 GTFVVSFDGL PLFGQGRHGT PLANAQDKPI LSLGGKPLVG LEVIKKTTHP PTTTMOPTTT 1320
 TTPLPTTTTP RPTTATTMQP TTTTTPLTTP TPRPTTATTR RTTTRRPTTT VRTTTRTTTT 1380
 TTPKPTTPIP TCPPGTLEHR DDDGNLIMSS NGIPECYAEE DEFSGLEDTT AVPTTEAYVI 1440
 15 YDEDEYEFETS RPTTTEPST TATTPRVIPE EGAISSFPPE EFDLAGRKRF VAPYVTYLNK 1500
 DPSAPCSLTD ALDHFQVDSL DEIIPNDLKK SLPQPHAPR NITVVAVEGC HSFVIVDWDK 1560
 ATPGDLVTGY LVYSASYEDF IRNKFTQAS SVTHLPIENL KNTRYFYFKV QAQNPHGYGP 1620
 ISPSVSFVTE SDNPLLVVRP PGGELSGSHS LSNMIPATRT AMDGNM 1666

Seq ID NO: C229 Protein Sequence
Protein Accession #: NP_003005.1

1 11 21 31 41 51
 MFLSILVALC LNLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ 60
 25 YEELVDVNCV AVLRFFFCAM YAPICTLEFL HDPKPKCKSV CQRARDDCEP LMKMYNHSWP 120
 ESLACDELFP YDRGVCISPE AIVTDLEPVD KWIDITPDMM VQERPLDVC KRLSPDRCK 180
 KVKKPTLATY LSKNYSYVIH AKIKAVQORS CNEVTTVVVD KEIFKSSSPI PRTQVPLITN 240
 SSSQCCHILP HQDVLIMCYE WSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRVTQD 300
 30 KKKTAGRTSR SNPPKPKGKP PAKPKASPKK NIKTRSAQKR TNPKRV 346

Seq ID NO: C230 Protein Sequence
Protein Accession #: NP_005931.1

1 11 21 31 41 51
 MAPAAWLRS AARALLPPML LLLLQPPPLL ARALPPDVHH LHAERRGFPQ WHAALPSSPA 60
 35 PAPATQEAAP PASSLRPPRC GVPDPSDGLS ARNRQKRFLV SGGRWKTDL TYRILRFPWQ 120
 LVQEQVRQTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLFP DPGGILAHA 180
 40 FFPKTHREGD VHFYDDETWT IGDDQGTDL LQVAAHEFGHV LGLQHTTAAK ALMSAFYTFR 240
 YPLSLSPDDC RGQVHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300
 VSTRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIWFFQGA 360
 QYWYDGEKFP VLGPAPLTEL GLVRFVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVDS 420
 45 PVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFD P VKVALEGFP RLVGPDFFGC 480
 AEPANTFL 488

Seq ID NO: C231 Protein Sequence
Protein Accession #: NP_076927

1 11 21 31 41 51
 MGENDPFAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLPLKFFFP IIVIGIIALI 60
 50 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF 120
 TAAWKTMCSS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 55 VTALHHSVYV REGCASGHV TLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQFQGYH 240
 LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AQPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGG DASPVLNHAA 360
 VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF 420
 60 GIGCAEVNKP GYVTRVTSFL DWIHEQMERD LKT 453

Seq ID NO: C232 Protein Sequence
Protein Accession #: NP_003211

1 11 21 31 41 51
 MLWKLTDNIK YEDCEDRHDG TSNGTARLPQ LGTVGQSPYT SAPPLSHTPN ADFQPPYFPP 60
 65 PYQPIYPQSQ DPYSHVNDPY SLNPLHAQPQ PQHPGWPGQR QSQESGLLHT HRGLPHQLSG 120
 LDPRRDYRRH EDLLHGPHAL SSGLGDLSTH SLPHTAIEVP HVEDPGINIP DQTVIKKGPV 180
 70 SLKSNNSNAV SAIPINKDNL FGGVVPNEV FCSVPGRLSL LSSTSXYKVT VAEVQRRLLSP 240
 PECLNASLLG GVLRRRAKSKN GGRSLREKLD KIGLNLPAQR RKAANVTLLT SILVEGEAVHL 300
 ARDFGYVCET EFPKAVAEF LNRQHSDPNE QVTRKNMLLA TKQICKEFTD LLAQDRSPLG 360
 NSRPNPILEP GIQSCSLTFHN LISHGFGSPA VCAAVTALQN YLTEALKAMD KMYLSNNPNS 420
 75 HTDNNAKSSD KEEKHRK 437

Seq ID NO: C233 Protein Sequence
Protein Accession #: NP_002979.1

1 11 21 31 41 51
 80 MKGLAAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKFIVDYSET SPQCCKPGVI 60
 LLTKRGRQIC ADPNKKWVQK YISDLKLNA 89

Seq ID NO: C234 Protein Sequence
Protein Accession #: NP_004054.1

	1	11	21	31	41	51	
5	MILQAHLSL	CLLMLYLATG	YGQEGKFSGP	LKPMFTFSIYE	GQEPSQIIFQ	FKANPPAVTF	60
	ELTGETDNIF	VIEREGLLYY	NRALDRETRS	THNLQVAALD	ANGIIVEGPV	PITIEVKDIN	120
	DNRPTFLQSK	YEGSVRQNSR	PGKPFLYVNA	TDLDDPATPN	GQLYYQIVIQ	LPMINNVMYF	180
	QINNKTGAIS	LTREGSQELN	PAKNPSYNLV	ISVKDMGGQS	ENSFSDTTSV	DIIVTENIWK	240
	APKPVEMVEN	STDPHPKIKT	QVRWNPGBAQ	YSLVDKEKLP	RFFFSIDQEG	DIYVTQPLDR	300
10	EKDAYVFYA	VAKDEYKPL	SYPLEIHVKV	KDINDNPPTC	PSPVTVFVQ	ENERLGNSIG	360
	TLTAHARDDEE	NTANSFLNYR	IVEQTPKLFM	DGLFLIQTYA	GMLQLAKQSL	KKQDTFOYNL	420
	TIEVSDKDFK	TLCFVQINVI	DINDQIPIFE	KSDYGNLTLA	EDTNIGSTIL	TIQATDADEP	480
	FTGSSKILYH	IIKGDSEGR	GVDTDPHTNT	GYVIIKKPLD	FETAAVSNIV	FKAENPEPLV	540
	FGVKYNASSF	AKFTLIVTDV	NEAPQFSQHV	FQAKVSEDVA	IGTKVGNVTA	KDPEGLDISY	600
15	SLRGDTRGWL	KIDHVTEGIF	SVAPLDREAG	SPYRVQVAT	EVGGSSLSV	SEFHLILMDV	660
	NDNPRLAKD	YTGLFFCHPL	SAPGSLIFEA	TDDQHLFRG	PHFTFSLGSG	SLQNDWEVSK	720
	INGTHARLST	RHTEFEEREY	VVLIRINDGG	RPPLEGIVSL	PVTFCSCVEG	SCFRPAGHOT	780
	GIPTVGMAVG	ILLTTLVLIG	IILAVVFIRI	KKDKGKDNVE	SAQASEVKPL	RS	832

Seq ID NO: C235 Protein Sequence
Protein Accession #: NP_004434.1

	1	11	21	31	41	51	
25	MARARPPPPP	SPPPGLLEPLL	PPLLLPLLLL	LPAGCRALEE	TLMDTKWVTS	ELAWTSHPES	60
	GWEEVSGYDE	AMNPIRTYQV	CNVRESSQNN	WLRTGFIWRR	DVQRVYVELK	FTVRDCNSIP	120
	NIPGSCKETF	NLFYIEADSD	VASASSPFWM	ENPYVKVDTI	APDESFSRLD	AGRVNTKVRS	180
	FGPLSKAGFY	LAFOQDQACM	SLISVRAFYK	KCASTTAGFA	LFPETLTGAE	PTSLVIAPGT	240
	CIPNAVEVS	FLKLYCNGDG	EMWVPVGACT	CATGHEPAAK	ESQCRPCPPG	SYKAKQGECP	300
30	CLPCPPNSRT	TSPAASICTC	HNNFYRADSD	SADSACTTVP	SPPRGVISNV	NETSLILEWS	360
	EPRLDGRDD	LLYNVICCKK	HGAGGASACS	RCDDNVEFVP	RQLGLTERRV	HISHLAHTR	420
	YTFEVQAVNG	VSGSKPLPFR	YAAVNITNQ	AAPSEVPTLR	LHSSSGSSLT	LSWAPPERPN	480
	GVILDYEMKY	FEKSEGIAS	VTSQMNSVQL	DGLRPDARYV	VQVRARTVAG	YGQYSRPAEF	540
	ETTSESGGA	QQLQEQLEPL	VGSATAGLVF	VVAVVVIAIV	CLRKQRHGSD	SEYTEKLQQY	600
35	IAPGMKVYID	PFTYEDPNEA	VREFAKEIDV	SCVKIEEVIG	AGEFGEVCRG	RLKQPGRRREV	660
	FVAIKTLKVG	YTERQRDFL	SEASIMGQFD	HPNIIRLEGV	VTKSRPVMIL	TEFMENCALD	720
	SFLRLNDGQF	TVIQLVGLMR	GIAAGMKYLS	EMNYVHRDLA	ARNILVNSNL	VCKVSDFGLS	780
	RFLEDDPSDP	TYTSSLGKIK	PIRWTAPAEI	AYRKFTSASD	VWSYGIWMVE	VMSYGERPYW	840
	DMSNQDVINA	VEQDYRLPPP	MDCPTALHQL	MLDCWVRDRN	LRPKFSQIVN	TLDKLIRNAA	900
40	SLKVIASQS	GMSQPLLDRT	VPDYTTFTTV	GDWLDIAKMG	RYKESFVSAG	FASFDLVAQM	960
	TAEDLLRIGV	TLAGHQKKIL	SSIQDMRLQM	NQTLFPVQV			998

Seq ID NO: C236 Protein Sequence
Protein Accession #: NP_001795.1

	1	11	21	31	41	51	
45	MYVGYVLDDK	SPVYPGPAPR	ASLGLGPANY	GPPAPPPAPP	QYPDFSSSYH	VEPAPAPPTA	60
	WGAPFPAPKD	DWAAAYGPGP	AAPASPASL	AFGPPPDFSF	VPAPFGPGFG	LLAQPLGGFG	120
50	TPSSPGAQRP	TPYEMRRSV	AAGGGGSGSK	TRTKDKYRVV	YTDHQRLELE	KEFHYSRYIT	180
	IRRKSELAAN	LGLTERQVKI	WFQNRRAKER	KVNKKKQQQQ	QPPQPPMAHD	ITATPAGPSL	240
	GGLCPSTSL	LATSSPMPVK	EEFLP				265

Seq ID NO: C237 Protein Sequence
Protein Accession #: NP_068813.1

	1	11	21	31	41	51	
60	MGSDRARKGG	GPKDFGAGL	KYNSRHEKVN	GLEEGVEFLP	VNNVIKKVEKH	GPGRWVVLAA	60
	VLIGLLLVLL	GIGFLVWHLQ	YRDVRVQKVF	NGYMRITNEN	FVDAYENSNS	TEFVSLASKV	120
	KDALKLLYS	VPFLGYPNHE	SAVTAASEGS	VIAAYWSEFS	IPQHLVEEAE	RVMAEERVVM	180
	LPFRARSLKS	FVVTSVVAF	TDSKTVQRTQ	DNSCSFGLHA	RGVELMRFTT	PGFPDSPYPA	240
	HARCQWALRG	DADSVLSLTF	RSFDLASCDE	RGSDLVTVYN	TLSPMEPHAL	VQLCGTYPPS	300
65	YNLTFHSSQN	VLLITLITNT	ERRHPGFEEAT	FFQLPRMSSC	GGRLRKAQGT	FNSPYYPGHY	360
	PPNIDCTWNI	EVENNQHVKV	RFKFFYLLEP	GVPAGTCPKD	YVEINGEKYC	GERSQFVVT	420
	NSNKITVRFH	SDQSYTDTGF	LAELYLSYDSS	DPCPGQFTCR	TGRCIRKBLR	CDGWADCTDH	480
	SDELNCSCDA	GHQFTCKNKF	CKPLFWVCD	VNDCGDNDS	QGCSCPAQTF	RCSNGKCLSK	540
	SQCCNGKDDC	GDGSDASCP	KVNVTCTKH	TYRCLNGLCL	SKGNPECDGK	EDCSGDSDEK	600
70	DCDCGLRSFT	RQARVVGGTD	ADEGEWFWQV	SLHALGQGHI	CGASLISPWN	LVSAAHCYID	660
	DRGFRYSIPT	QWTAFLGLHD	QSQRSAAGVQ	ERRLKRIISH	PFNDFTFDY	DIALLELEKP	720
	AEYSSMVRPI	CLPDASHVFP	AGKAIWVTGW	GHTQYGGTGA	LILQKGEIRV	INQTTCCENLL	780
	PQITPRMMC	VGLSLSGVDS	CQDSDSGPLS	SVEADGRIFQ	AGVVSNGDGC	AQRNKPQVYT	840
	RLPLFRDWIK	ENTGV					855

Seq ID NO: C238 Protein Sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
80	MPPFLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAQFSSSTPH	LEFPLDSFST	QOEVKARIKR	120
	MVFKGGRTE	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
	FAVGVRFRPW	EELHALASEP	RGQHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCEHRTLEMV	REPAGNAPCW	RGSRTTAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCGPGCD	300
	SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVLLFLDLS	SAGTTLDGFL	360

RAKV FVKRFV RAVLS EDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
 LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVG 480
 EAVRAELEEI TGSPKHMVMY SDPQDLFNQI PELQGLKCSR QRPQCRTQAL DLVFM LDTSA 540
 SVGPENFAQM QSFVRSALQ FEVNP DVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLG VGVS A GTALLHIYDK VMTVQRGARP GVPKAVVVL T GGRGAEDAAV PAQKL RNNGI 660
 SVLVVGVPV LSEGLRRLAG PRDSL I HVAA YADLRVHQDV LIEWLCGEAK RPNVNLCKPSP 720
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR FLRRP 755

Seq ID NO: C239 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MPFFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
 SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
 MVFKGGR TET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180
 FAVGVRFPRW EELHALASEP RGQHVL LAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHC PFYSWK RVFLTHPATC YRTTCPGPCD 300
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
 RAKV FVKRFV RAVLS EDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
 LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVG 480
 EAVRAELEEI TGSPKHMVMY SDPQDLFNQI PELQGLKCSR QRPQCRTQAL DLVFM LDTSA 540
 SVGPENFAQM QSFVRSALQ FEVNP DVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLG VGVS A GTALLHIYDK VMTVQRGARP GVPKAVVVL T GGRGAEDAAV PAQKL RNNGI 660
 SVLVVGVPV LSEGLRRLAG PRDSL I HVAA YADLRVHQDV LIEWLCGEAK RPNVNLCKPSP 720
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAPGP 807

Seq ID NO: C240 Protein Sequence
 Protein Accession #: XP_097386.1

1 11 21 31 41 51
 | | | | |
 MPKSEPLGCL SPASRAPGSA AATGAWLPAA SGGPGPLGPP CTCPPRSLGR GRAGSRAGSS 60
 PSGCVCVSGI LRVVSVGDPA SRRWVDLDSN SEDLSLLLT MIVGTGGVGG GWARGWVPAQ 120
 EKEVAEGSGH AGRGNRRRLQ RVVGARSWIL GRKPCLQRLL PASGGPVQPQ PCPSPATACR 180
 WGFKFGVAFW GAAQHPLPCR LGGGRVPSA TRTLDGF 217

Seq ID NO: C241 Protein Sequence
 Protein Accession #: CAC03433

1 11 21 31 41 51
 | | | | |
 MLSTDTFTA SWELVVRVDH PNEEQQKQDV LRVSGDLHVG GVMLKLVEQI NISQDWS DFA 60
 LWWEQKH CWL LKTHWTL DKG VQADAKLLF TPQHKMLRLR LPNLKMVRLR VSFSAVV FKA 120
 VSDICKILNI RRSEELSLK PSGDYFKKK KDKKNKEPI IEDILNLESS PTASGSSVSP 180
 GLYSKTMTP I YDPINGTPAS STMTWFS DSP LTEQNCSILA FSQPPQSPEA LADMYQPRSL 240
 VDKAKLNAG LDSSRSIMEQ GIQEDQLLL RFKYYSFFDL NPKYDAVRIN QLYEQARWAI 300
 LLEIDCTEE EMLIFAALQY HISKLSLAE TQDFAGESEV DEIEAALSNL EVTLEGGKAD 360
 SLLEDITDIP KLANLKLFR PKLLPKAFK QYWFIFK DTS IAYFKNKELE QGEPLEKLNL 420
 RGCEVVPD VN VAGRKFGIKL LIPVADGMNE MYLRCDHENQ YAQWMAACML ASKGKTMADS 480
 SYQPEVLN IL SFLRMKNRNS ASQVASSLEN MDMNPECFVS PRC AKHKSK QLAARILEAH 540
 QNV AQMPLVE AKLRFIQAW SLPEFGLTY LVRFKGSKKD DILGVSYNRL IKIDAATGIP 600
 VTTWRFTNIK QWNVNWETRQ VVIEFDQNVF TAFTCL SADC KIVHEYIGGY IFLSTRSKDQ 660
 NETLDEDLFH KLTGGQD 677

Seq ID NO: C242 DNA Sequence
 Nucleic Acid Accession #: NM_005170
 Coding sequence: 337..918

1 11 21 31 41 51
 | | | | |
 GGGCGTGAGA AAGGCGACGG CGGCGGCGCG GAGGAGGGTT ATCTATACAT TAAAAACCA 60
 GCCGCCTGCG CCGCGCCTGC GGAGACCTGG GAGAGTCCGG CCGCACGCGC GGGACACGAG 120
 CGTCCACGCG TCCCTGGCGC GTACGCGCTG CCACCACTAG GCCTCCTATC CCCGGGCTCC 180
 AGACGACCTA GGACGCTGCG CCTGGGGAGT TGCCTGGCGG CGCCGTGCTTA GAAGCCCCCT 240
 TGGGGGCGCA CAGTTTTCCT CGTCGCTTCC GGTTCCTCTG CCTGCACCTT CCTGCGGCGC 300
 GCCGGGACCT GGAGCGGGCG GGTGGATGCA GGC CGATGG ACCGCGGCAC ACTGCCAGG 360
 TCCGCGCCCC CTGCGCCCCC CGTCCCTGTC GGCTGCGCTG CCCGCGGAG ACCCGCTCC 420
 CCGGAACCTGT TGCCTGTCAG CCGGCGGCGG CGACCGGCCA CCGCAGAGAC CGGAGGCGGC 480
 GCAGCGGCGG TAGCGCGGGG CAATGAGCGC GAGCGCAACC GCGTGAAGCT GGTGAACCTG 540
 GGCTTCCAGG CGCTGCGGCA GCACGTGCGG CACGGCGGCG CCAGCAAGAA GCTGAGCAAG 600
 GTGGAGACGC TGCCTCAGC CGTGGAGTAC ATCCGCGCGC TGCAGCGCCT GCTGGCCGAG 660
 CACGACGCGC TGC CAACGC GCTGGCGGGA GGGCTGAGGC CGCAGGCCGT GCGGCCGTCT 720
 GCGCCCCGCG GCGCGCCAGG GACCACCCCG GTCGCGCGCT CGCCCTCCCG CGCTTCTTCG 780
 TCCCGGGGCC GCGGGGGCAG CTCGGAGCCC GGCTCCCGC GTTCCGCTA CTCGTCGAG 840
 GACAGCGGCT GCGAAGCGC GCTGAGTCTT GCGGAGCGCG AGCTACTCGA CTTCTCCAGC 900
 TGGTTAGGGG GCTACTGAGC GCCCTCGACC TA 932

Seq ID NO: C243 Protein Sequence
 Protein Accession #: NP_060233.1

1 11 21 31 41 51

	MSGGHQLQLA	ALWPWLLMAT	LQAGFGRITGL	VLAAAVESER	SAEQKAVIRV	IPLKMDPTGK	60
	LNLTLLEGVFA	GVAEITPAEG	KLMQSHPLYL	CNASDDDNLE	PGFISIVKLE	SPRRARPRCL	120
5	SLASKARMAG	ERGASAVLFD	ITEDRAAAEQ	LQQPLGLTWP	VVLIWGNDAE	KLMEFVYKNQ	180
	KAHVRIELKE	PPAWPDYDVW	ILMTVVGTIF	VILLASVLRI	RCRPRHSRPD	PLQORTAWAI	240
	SQLATRRYQA	SCRQARGEWP	DSGSSCSCAP	VCAICLEEPS	EQQELRVISC	LHEFHRCNVD	300
	PWLHQHRTCP	LCVFNITEGD	SFSQSLGPSR	SYQEPGRRLH	LIRQHPGHAH	YHLPAAYLLG	360
	PSRSAVARPP	RPQPFPLSQE	PGMGPRHHRF	PRAAHPRAPG	EQQRLAGAOH	PYAQGWGMSH	420
10	LQSTSQHAAA	CPVPLRRARP	PDSSGSGESY	CTERSGYLAD	GPASDSSSGP	CHGSSSDSVV	480
	NCTDISLQGV	HGSSSTFCSS	LSSDFDPLVY	CSPKGDPQRV	DMQPSVTSRP	RLSDSVVPTG	540
	ETQVSSHVHY	HRHRHHHYKK	RFQWHGRKPG	PETGVQPQSR	PIPTQOPQPE	PSPDQQVVTG	600
	SNSAAPSGRLL	SNPQCPRALP	EPAPGPVDAS	SICPSTSSLF	NLQKSSLSAR	HPQRKRGGP	660
	SEPTPGSRPQ	DATVHPACQI	FPHYTPSVAY	PWSPEAHPLI	CGPPGLDKRL	LPETPGPCYS	720
15	NSQPVLWCLT	PRQPLEPHPP	GEGPSEWSSD	TAEGRPCYP	HCQVLSAQPG	SEEELEELCE	780
	QAV						783

Seq ID NO: C244 DNA Sequence
Nucleic Acid Accession #: NM_004289
Coding sequence: 493..1695

	1	11	21	31	41	51	
	GCCGCCGCCCT	CGTCCACCGG	AGGAGCCGGC	GCCAGCGTGG	ACGGCGGCAG	CCAGGCTGTG	60
25	CAGGGGGGCG	GCGGGGACCC	CCGAGCGGCT	CGGAGTGCC	CCTTGGACGC	CGGGGAAGAG	120
	GAGAAGGCAC	CCGCGGAACC	GACGGCTCAG	GTGCCGACG	CTGGCGGATG	TGCGAGCGAG	180
	GAGAATGGGG	TACTAAGAGA	AAAGCACGAA	GCTGTGGATC	ATAGTTCCCA	GCATGAGGAA	240
	AATGAAGAAA	GGGTGTGAGC	CCAGAAGGAG	AACTCACTTC	AGCAGAATGA	TGATGATGAA	300
	AACAAAATAG	CAGAGAAACC	TGACTGGGAG	GCAGAAAAGA	CCACTGAATC	TAGAAATGAG	360
30	AGACATCTGA	ATGGGACAGA	TACTTCTTTC	TCTCTGGAAG	ACTTATTCCA	GTTGCTTTCA	420
	TCACAGCCTG	AAAATTCAC	GGAGGGGATC	TCATTGGGAG	ATATTCTCT	TCCAGGCAGT	480
	ATCAGTGATG	GCATGAATTC	TTCAGCACAT	TATCATGTAA	ACTTCAGCCA	GGCTATAAGT	540
	CAGGATGTGA	ATCTTCATGA	GGCCATCTTG	CTTTGTCCCA	ACAATACATT	TAGAAGAGAT	600
	CCAACAGCAA	GGACTTCACA	GTCACAGAA	CCATTTCTGC	AGTTAAATTC	TCATACCACC	660
35	AATCCTGAGC	AAACCCCTTC	TGGAACATA	TTGACAGGAT	TTCTTTCACC	GGTTGACAAT	720
	CATATGAGGA	ATCTAACCA	CCAAGACCTA	CTGTATGACC	TTGACATAAA	TATATTGTAT	780
	GAGATAAACT	TAATGTCTAT	GGCCACAGAA	GACAACTTTC	ATCCAATCGA	TGTTTCTCAG	840
	CTTTTGTGAT	AACCAGATTC	TGATTCTGGC	CTTTCTTTAG	ATTCAGATCA	CAATAATACC	900
	TCTGTCTACA	AGTCTAATTC	CTCTCACTCT	GTGTGTGATG	AAGGTGCTAT	AGGTTATTGC	960
40	ACTGACCATG	AATCTAGTTC	CCATCATGAC	TTAGAAGGTG	CTGTAGGTGG	CTACTACCCA	1020
	GAACCCAGTA	AGCTTTGTCA	CTTGGATCAA	AGTGATTCTG	ATTTCCATGG	AGATCTTACA	1080
	TTTCAACACG	TATTTTCATA	CCACACTTAC	CACCTACAGC	CACTGCACCC	AGAATCTACT	1140
	TTCGAACCTT	TTCGCTGGCC	TGGGAAGTCA	CAGAAGATAA	GGAGTAGATA	CCTTGAAGAC	1200
	ACAGATAGAA	ACTTGAGCCG	TGATGAACAG	CGTGCTAAAG	CTTTGCATAT	CCCTTTTTCT	1260
45	GTAGATGAAA	TTGTCCGGCAT	GCCTGTTGAT	TCTTTCAATA	GCATGTTAAG	TAGATATTAT	1320
	CTGACAGACC	TACAAGTCTC	ACTTATCCGT	GACATCAGAC	GAAGAGGGAA	AAATAAAGTT	1380
	GCTGCGCAGA	ACTGTCGTAA	ACGCAAAATG	GACATAATTT	TGAATTTAGA	AGATGATGTA	1440
	TGTAACCTTGC	AAGCAAAAGAA	GGAAACTCTT	AAGAGAGAGC	AAGCACAAATG	TAACAAAGCT	1500
	ATTAACATAA	TGAACAGAGAA	ACTGCATGAC	CTTTATCATG	ATATTTTATG	TAGATTAAGA	1560
50	GATGACCAAG	GTAGGCCAAT	CAATCCCAAC	CACATGCTCT	TCCAGTGATC	CCATGATGGA	1620
	AGTATCTTGA	TAGTACCCAA	AGAAGCTGGT	GCCTCAGGCC	ACAAAAGGAA	AACCCAAAAG	1680
	GGAAAGAGAA	AGTGAGAGAA	AACTGAAGAT	GGACTCTATT	ATGTGAAGTA	GTAATGTTCA	1740
	GAAACTGATT	ATTTGGATCA	GAAACCATTC	AAACTGCTTC	AAGAATTGTA	TCTTTAAGTA	1800
	CTGCTACTTG	ATAACTCAG	TTAAGCTGT	TTTGAAGCTT	ACATGGACAA	ATGTTTAGGA	1860
55	CTTCAAGATC	ACACTTGTGG	GCAATCTGGG	GGAGCCACAA	CTTTTCATGA	AGTGCAATTGT	1920
	ATACAAAATT	CATAGTTATG	TCCAAAGAA	AGGTTAACAT	GAAAACCCAG	TAAGACTTTC	1980
	CATCTTGGCA	GCCATCCTTT	TTAAGAGTAA	GTTGGTTACT	TCAAAAAGAG	CAAAACACTGG	2040
	GGATCAAAAT	ATTTTAAGAG	GTATTTCAGT	TTTAAATGCA	AAATAGCCTT	ATTTTCATT	2100
60	AGTTTGTGTTAG	CACTATAGTG	AGCTTTTCAA	ACACTATTTT	AATCTTTATA	TTTAACCTTAT	2160
	AAATTTTGCT	TTCT					2174

Seq ID NO: C245 Protein Sequence
Protein Accession #: NP_004433

	1	11	21	31	41	51	
65	MALRRRLGAAL	LLLPLLAAVE	ETLMDSTTAT	AELGWMVHPP	SGWEEVSGYD	ENMNTIRTQ	60
	VCNVFESSQN	NWLRTKFIRR	RGAHRIHVEM	KFSVRDCSSI	PSVPGSCKET	FNLYYYEADF	120
	DSATKTFPNW	MENPWVKVD	IAADESFSQV	DLGGRVMKIN	TEVRSFGPV	RSQFYLAQD	180
70	YGGCMGLIAV	RVFYRKCPRI	IQNGAIFQET	LSGAESTSLV	AARGSCIANA	EEVDVPIKLY	240
	CNGDGEWLVP	IGRCMKKAGF	EAVENGTVCR	GCPSGTFKAN	QGDEACTHCP	INSRTTSEGA	300
	TNCVCRNGY	RADLDPLDMP	CTTIPSPAPQA	VSSSVNETSL	MLEWTPPRDS	GGREDLVYNI	360
	ICKSCGSGRG	ACTRCGDNVQ	YAPRQLGLTE	PRIYISDLLA	HTQYTFEIQ	VNGVTDQSPF	420
	SPQFASVNIT	TNQAAPSAVS	IMHOVSRTVD	SITLSWSQPD	QPNQVILDYE	LQYYEKELSE	480
75	YNATAIKSPT	NTVTVQQLKA	GAIVVFQVRA	RTVAGYGRYS	GKMYFQIMTE	AEYQTSIQEK	540
	LPLLIGSSAA	GLVFLIAVVV	IAIVCNRRRG	FERADSEYTD	KLQHYTSGHM	TPGMKIYIDP	600
	FTYEDPNEAV	REPAKEIDIS	CVKIEQVIGA	GEFGEVCSGH	LKLPKREIF	VAIKTLKSGY	660
	TEQQRDFLS	EASIMQGFQD	PNVHLEGGV	TKSTPVMII	EFMENGSLDS	FLRQNDGQFT	720
	VIQLVGLMRL	IAAGMKYALD	MNVVHRDLAA	RNIVNSNLV	CKVSDGLSLR	FLEDDTSDPT	780
80	YTSALGGKIP	IRWTAPBAIQ	YRKFTSADV	WSYGIWMWEV	MSYGERPYWD	MINQDVINAI	840
	EQDYRLPPPM	DCPSALHQLM	LDCWQKDRNH	RPKFGQIVNT	LDKMIRNPNS	LKAMAPLSSG	900
	INLPLLDRTI	PDYTSFNTVD	EWLEAIKMGQ	YKESFANAGF	TSFDVVSQMM	MEDILRVGLT	960
	LAGHQKKILN	SIQVMRAQMN	QIQSVEV				987

Seq ID NO: C246 Protein Sequence

Protein Accession #: NP_114148.1

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1      11      21      31      41      51
|      |      |      |      |      |
5 MDARRVPQKD LRVKKNLKKF RYVKLISMET SSSSDSDSCDS FASDNFANTR LQSVREGCRT 60
  RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSSENSVT DSNSDSEDES GMNFLEKRAL 120
  NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL 180
  TRSRSRILGS LDALPMEEEE EEDKYMLVRK RKTVDGYMNE DDLPRSSRRS SSVTLPHIIR 240
  PVEITEGGV GERLQQFSKR RYITVHWALL VINAVRRLLI PKQTAETQTA GAFAESSVAP 300
10 AFETVMVKRS GMLCWIRTGI ARLVEESATA VSAGSEMDGV RLGSLCI 347

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Seq ID NO: C247 Protein Sequence
Protein Accession #: NP_036577.1

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1      11      21      31      41      51
|      |      |      |      |      |
15 MENPSPAAL GKALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAFPKQY 60
  PLFRPPAQWS SLGAAHSSD YSMWRKNQYV SNGLRDFAEER GEAWALMKEI EAAGEALQSV 120
  HAVFSAPAVP SGTGQTSDEL EVQRHSLVS FVVRIVPSPD WFGVVDSDL CDGDRWREQA 180
20 ALDLYPYDAG TDSGFTFSSP NFATIPQDTV TEITSSSPSH PANSFYYPRL KALPPIARVT 240
  LVRLRQSPRA FIPAPVLPK RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRGLGTS 300
  RTRYVRVQPA NNGSPCFELE EEAECVPDNC V 331

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Seq ID NO: C248 Protein Sequence
Protein Accession #: NP_063947.1

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1      11      21      31      41      51
|      |      |      |      |      |
30 MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIV VLIKVILDKY 60
  YFLCGQPLHF IPRKQLCDGE LDCPLGEDDEE HCVKSFPEGP AVAVRLSKDR STLQVLD SAT 120
  GNWFSACFDN FTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
  GPCLSGSLVS LHCLACGKSL KTRPVVGEE ASVDSWPQV SIQYDKQHV GGSILDPHWV 240
  LTAACHFRKH TDVFNWKVRA GSKLGSFSP LAVAKIIIE FNPMPKND IALMKLQFPL 300
  TFSGTVRPIC LPFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
35 AYQGEVTEKM MCAQIPEGGV DTCQGDGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT 420
  KVSAYLNIWY NVWKAE 437

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Seq ID NO: C249 Protein Sequence
Protein Accession #: NP_003036.1

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1      11      21      31      41      51
|      |      |      |      |      |
40 MGCKVLLNIG QQMLRRKVVD CSREETRLSR CLNTFDLVAL GVGSTLGAGV YVLGAVARE 60
  NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELWA FITGWNILS 120
45 YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPGVL AENPDIFAVI IILILTGLLT 180
  LGVKESAMVN KIFTCINLV LGFIMVSGFV KGSVKNWQLT EEDFGNTSGR LCLNNDTKEG 240
  KPGVGGFMFP GFSGVLSGAA TCFYAFVGF D CIATTGEEVK NPQKAI PVGI VASLLICFIA 300
  YFGVSAALTL MNPYCLDNN SPLPDAFKHV GWEGAKYAVA VGSCLALSAS LLGSMFPMR 360
  VIYMAEDGL LFKFLANVND RTKTPIIATL ASGAVAAVMA FLFDLKDLVD LMSIGTLAY 420
50 SLVAACVLVL RYQPEQPNLV YQMASTDEL DPADQNELAS TNDSQLGLFLP EAEMFSLKTI 480
  LSPKNMEPSK ISGLVNIIST SLIAVLIITF CIVTVLGREA LTKGALWAVF LLAGSALLCA 540
  VVTGVIWRQP ESKTKLSFKV PFLPVLPLS IFVNVYLMQ LDQGTWVRFA VWMIGFIY 600
  FGYGLWHSEE ASLDADQART PDGNLDQCK 629

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Seq ID NO: C250 Protein Sequence
Protein Accession #: NP_002767.1

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1      11      21      31      41      51
|      |      |      |      |      |
60 MRAPHLHLSA ASGARALAKL LPLLMAQLWA AEAALLPQND TRLDPEAYGA PCARGSQPWQ 60
  VSLFNLGLSF CAGVLVDQSW VLTAAHCGNK PLWARVGDDH LLLQLQEQLR RTRTSVVHPK 120
  YHQGGSPILP RRTDEHDLML LKLARPVVPG PRVRALQLPY RCAQPGDQCQ VAGWGTTAAR 180
  RVKYNKGLTC SSITILSPKE CEVFYPGVVT NNMICAGLDR GQDPCQSDSG GPLVCDTELQ 240
65 GILSWGVYPC GSAQHFAVYT QICKYMSWIN KVIRSN 276

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Seq ID NO: C251 Protein Sequence
Protein Accession #: XP_095088.3

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1      11      21      31      41      51
|      |      |      |      |      |
70 MTRAAAEAPG RVSPASPARS TAGLPRAFLQ SLRTLDDILD DWQRGCVHLR EIQLSWVEAR 60
  ELPSGVLEGL SQRRGQPGA AVRSRRGGAV PRGARAVPER CAGTETRRGR RCSGLQRLGG 120
  GFRGCPADPC ARGEHRRHTI TSGVDCGLLK QMKELEQKE VLLQGLEMM QGRDWYQQQL 180
75 QQVQERQCR LQSRASADFG AVGSRPRLGR LLPKVQEVAR WLGEELAEAC AGRALPTSSS 240
  GPPCSALTST SSPGWQQII LMLKEQNRLL TQEVTEKSER ITQLEQKSAL IKQLFEARAL 300
  SQDGGGLSPA GHIEPLTRF RLPVLTWAGA LLSPHSPQLL LPLSADSGGP LHELPTWFP 360
  AVLLWVSPG KRTAHARLHF HQRPAEGAWQ LGCGAEAAPE TCGTLPHFES HKTTCEDDSL 420
  GGPCPQEGDR SWSHLGAADF VAPAVAKVTP NREDAAGSRH GDICPLCPKG LLTFRDIAIE 480
80 FSLAEWQCLD HAQNLRYRD MLENYRNLF S LGMTVSKPDL IACLEQNKEP QNIKRNEMAA 540
  KHPVTCSHFN QDLQPEQSIK DSLQKVIPT YGKCGHENLQ LKCKCKRVDE CEVHKGGYND 600
  LNQLSNTQN KIQPTHCKV VFSKFSNSNR HNARYTGKHH LKCKKYGKSF CMFSLNQHQ 660
  IIHTKEKSYK CEECGKSFNH SSSGTTTHKRI LTGEKPYRCE ECGKAFRWPS NLTRHKRIHT 720
  GEKPYACEEC GQAFRRSSTL TNHKRIHTGE RPYKCECGK AFSVSSALII HKRIHTGEKP 780
  YTCEECGKAF NCSSTLTKTHK IIHTGEKPYT CEECGRTFNC SSTVKAHKRI HTGEKPYKCE 840

```

ECDKAFKWHK SLAKHKIHT GEKPYKCSDS KALAKSSEVQ KVSXSGDGENG IRVHKKKETQ 900
 GWLVRNKNEN RTGLFQIRAA VRPNRDPSPWG QOEGSLTDPI QRKEEPLQON HYDHQNALED 960
 QRNTGVGGLL TFRDVVIEFS LEEWQCLDHA QONLYRDMVL ENYRNLVSLG IAVSKPDLIT 1020
 CLEQNKPEWN IKRNEVMVTKH PDLPELGIK DSLQKVIPRR YGKSGHDNLQ VKTCKSMGEC 1080
 EVQKGGCNEV NQCLSTTQNK IFQTHKCVKV FGKFSNSNRH KTRHTGKKHF KCKKYGKSFC 1140
 MVSQHLQHQI IHTRENSVQC EECGKPFNCS STLSKHKRIH TGEKPYRCEE CGKAFWSSST 1200
 LTKHRRIHGT EKPYTECECG QAFSRSTLA NHKRIHTGEK PYTCEECGKA FSLSSSLTYH 1260
 KRIHTGEKPY TCEECGKAFN CSSTLKKHKI IHTGEKPYKC KECGKAFAPS STLNTHKRIH 1320
 TGEPEYKCEE CDKAFKWSST LANHKSMTGT EKPYPKE 1357

Seq ID NO: C252 Protein Sequence
Protein Accession #: NP_114433.1

1 11 21 31 41 51
 MASRSMRLLL LLCLAKTGV LGDIIMRPSG APGWFYHKSQ CYGYFRKLRN WSDAELECSQ 60
 YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG 120
 KSMGGNKHCA EMSNNNFLT WSSNECNKRQ HFLCKYRP 158

Seq ID NO: C253 Protein Sequence
Protein Accession #: XP_051860.2

1 11 21 31 41 51
 MDGVNLSTEV VYKKGQDYRF ACYDRGRACR SYRVRFLCGK PVRPKLTVTI DTNVNSTILN 60
 LEDNVQSWKP GDTFLVIASDT YSMYQAEFEQ VLPSCRSCAPN QVKVAGKPMY LHIGEEIDGV 120
 DMRAEVGLLS RNIIIVGEME DKCYPYRNHI CNFFDFDTFG GHIKFALGFK AAHLEGTELK 180
 HMGQQLVGQY PIHFHLAGDV DERGGYDPPT YIRDLISHTT FSRCVTVHGS NGLLIKDVVG 240
 YNSLGHCFPT EDGPEERTFT DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300
 DCNAVSTFWM ANPNNNLINC AAAGSEETGF WFIFHHVPTG PSVGMYSFGY SEHIPGLKGY 360
 NNRAHSNYRA GMIIDNGVKT TEASAKDKRP FLSTISARYS PHQDADPLKP REPAIRIRHFI 420
 AYKNQDHGAW LRGGDVWLDS CRFADNGIGL TLASGGTFPY DGGSKQETKN SLFVGESGNV 480
 GTEMMDNRIW GPGLDHSRGR TLPIGQNFPPI RGIQLYDGPY NIQNCITFRK VALEGRHTSA 540
 LAFRLNNAWQ SCPHNNVTGI AFEDVPITSR VFFGEPGPWF NQLDMDGDKT SVFHDVDGVS 600
 SEYPGSYLTK NDNLVLRHPD CINVPDWRGA ICSGCAQMY IQAYKTSNLR MKIINKDFPS 660
 HPLYLEGALT RSTHYQQYQP VVTQLKGVTI HWDQTAPAEI AIWLNENKNG DWIRVGLCYP 720
 RGTTFSLSD VHNRLKQTS KTGTVFVRTLQ MDKVEQSYPG RSHYYWDEDS GLLFLKLKQA 780
 NEREKFAFCS MKGCERIKIK ALIPKNAGVS DCTATAYPKF TERAVIDVPM PKKLFGSQLK 840
 TKDHFLEVKM ESSKQHFHFL WNDFAIEVD GKKYPSSEEDG IQVVVIDGNQ GRVVSHTSFR 900
 NSILQGIWQW LFNVVATIPD NSIVLMAKSG RYVSRGPWTR VLEKLGADRG LKLKEQMAFV 960
 GFKGSFRPIW VTLDTEHKA KIFQVVPPIV VKKKKL 996

Seq ID NO: C254 Protein Sequence
Protein Accession #: NP_055188.1

1 11 21 31 41 51
 MTALSSSENS PQYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRRKNT QCNFMEYFCI 60
 SLAFVDLLL VNISIIYFR DFVLLSIRFT KYHICLFTQI ISFTYGLFHY PVFLTACIDY 120
 CLNFSKTKL SFKQKLFYF FTVILIWISV LAYVLGDPPI YQSLKAQNAV SRHCPFFYVSI 180
 QSYWLSFFMV MILFVAFITC WEEVTTLVQA IRTSYMMNET ILYFPFSSHS SYTVRSKKIF 240
 LSKLIVCLFS TWLFPVLQVQ IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN 300
 LKDIGLPLDP FVNWKCCFIP LTIPLNEQIE KPISIMIC 338

Seq ID NO: C255 Protein Sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
 MALVLGSLLL LGLCGNSFSG GQPSSTDAPK AWNYELPATN YETQDSHKG PIGILFELVH 60
 IFLYVVQPRD FPEDTLRKFL QKAYESKIDY DKIVYEEAGI ILCCVLGLLF IILMPLVGYP 120
 FCMCRCKNC GGMHQQRKE NGFFLRKCA ISLLVICIII SIGIFYGFVA NHQVRTRIKR 180
 SRKLADSNFK DLRTLLNETP EKIYILAQY NTKDKAFTD LNSINSVLGG GILDRLRPNI 240
 IPVLDIEKSM ATAIEKTEA LENMNSTLKS LHQQSTQLSS SLTSVKTSLR SSNDPLCLV 300
 HPSSETCNSI RLRLSQLNSN PELRQLPFDV AELDNVNNVL RTDLGLVQVQ GYQSLNDIPD 360
 RVQRQTITV AGIKRVLNSI GSDIDNVTR LPIQDILSAF SVYVNNTESY IHRNLPTELE 420
 YDSYWWLGGI VICSLTLIV IFYYLGLLCG VCGYDRHATP TTRGCVSNTG GVFLMVGVGL 480
 SFELFCWILMI IIVLTFVFGA NVEKLICEPY TSKELFRVLD TPYLLNEDWE YYLSGKLFNK 540
 SKMKLTPEQV YSDCKNRRGT YGTLHLQNSF NISEHLNINE HTGSISSELE SLKVNLIIFL 600
 LGAAGRNKLQ DFAACGIDRM NYDSYLAQTG KSPAGVNNLS FAYDLEAKAN SLPPGNLRNS 660
 LKRDQTIKT IHQQRVLPPIE QSLSTLYQSV KILQRTGNGL LERVTRILAS LDFAQNFTIN 720
 NTSSVIBET KKYGRITIGY FEHYLQWIEF SISEKVASCK PVATALDTAV DVFLCSYIID 780
 PLNLFWFQIG KATVFLPAL IFAVKLAKYY RMDSEDEVYD DVETIPMKNM ENGNNGYHKD 840
 HVYGIHNPVM TSPSQH 856

Seq ID NO: C256 Protein Sequence
Protein Accession #: NP_149038.1

1 11 21 31 41 51
 MKAIHLTLT ALLSVNTATN QGNSADAVTT TETATSGPTV AAADTTETNF PETASTTANT 60
 PSFPTATSPA PPIIHTHSSS TIPTAPPPII STHSSSTIPI PTAADSESTT NVNSLATSDI 120
 ITASSPNDGL ITMVPSETQS NNEMSPPTED NQSSGPPTGT ALLETSTLNS TGPSNPQDQD 180
 PCADNSLCVK LHNTSFCLCL EGYYYNSSTC KKGKVFPGKI SVTVSETFDP EEKHSMAVQD 240

LHSEITSLFK DVFGTSVYQGV TVILTVSTSL SPRSEMRADD KFVNVTIVTI LAETSDNEK 300
 TVTEKINKAI RSSSSNFLNY DLTLRCDYYG CNQTADDCLN GLACDCKSDL QRPNPQSPFC 360
 VASSLKCPDA CNAQHKQCLI KKSOGAPECA CVPGYQEDAN GNCQKCAFQY SGLDCKDKFQ 420
 LILTVGTIA GIVILSMIIA LIVTARSNNK TKHIEENLI DEDFQNLKLR STGFTNLGAE 480
 GSVFPKVRIT ASRDSQMNP YSRHSSMPRP DY 512

Seq ID NO: C257 Protein Sequence
 Protein Accession #: NP_001423.1

1 11 21 31 41 51
 | | | | |
 MTAGRRMEML CAGRPVALL CLGFHLLQAV LSTTVIPSCI PGESSDNCTA LVQTEDNPRV 60
 AQVSITKCSS DMNGYCLHGQ CIYLVDMSQN YCRCEVGYTG VRCEHFFLTV HQPLSKEYVA 120
 LTVILILFL ITVVGSTYYF CRWYRNKRSK EPKKEYERV TSGDPELPQV 169

Seq ID NO: C258 Protein Sequence
 Protein Accession #: AAC63902.1

1 11 21 31 41 51
 | | | | |
 MDRSKENCIS GPFVKATAPVG GPKRVLVTTQ IPCQNPLPVN SGQAQRVLCP SNSSQVRVLPQ 60
 AQKLVSSHKP VQNKQKQQLQ ATSVPHFVSR PLNNTQKSKQ PLPSAPENNP EEELASKQKN 120
 EESKKRQWAL EDFEIGRPGLG KGKFGNVYLA REKQSKFILA LKVLFAQLE KAGVEHQLRR 180
 EVEIQSHLRH PNILRLYGYF HDATRVYLIL EYAPLGTVYR ELQKLSKFDE QRTATYITEL 240
 ANALSYCHSK RVIHRDIKPE NLLLSGAGEL KIADFGWSVH APSSRRTTLC GTLDYLPPEM 300
 IEGRMHDEKV DLWSLGVLCY EFLVGKPPFE ANTYQETVYR ISRVEFTFPD FVTEGARDLI 360
 SRLKHNPSQ RPMLREVLEH PWITANSSKP SNCQNKESAS KQS 403

Seq ID NO: C259 Protein Sequence
 Protein Accession #: NP_037504.1

1 11 21 31 41 51
 | | | | |
 MSRTAYTVGA LLLLLGTLLP AAEKGKKGSQ GAIPPPDKAQ HNDSEQTQSP QQPGSRNRGR 60
 QQGRGTAMPB BEVLESSQEA LHVTERKYLK RDWCCKTQPLK QTIHEEGCNS RTIINRFCY 120
 QCNSFYIPRH IRKEEGSFQS CSFCKPKKFT TMMVTLCNPE LQPPTKKKRV TRVKQCRCIS 180
 IDLD 184

Seq ID NO: C260 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MKVGVWLWIS FFTFTDGHGG FLGKNDGIKT KKELVNKKK HLGPEVEEYQL LLQVTRYRDSK 60
 EKRDLENFLEK LLKPPLLWHS GLIRIIRAKA TDCNSLNGV LQCTCEDSYT WFPSPCLDPQ 120
 NCYLHTAGAL PSCECHLNNL SQSVNFCERT KIWGTFKINE RFTNDLLNSS SAIYSKYANG 180
 IEIQLKKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALHK 240
 LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 300
 LSLLEELNKN FSMIVGNATE AAVSSFVQNL SVIIRQNPST TVGNLASVVS ILSNSSLSL 360
 ASHFRVSNST MEDVISIADN ILSASVTNW TVLLREEKYA SSRLLETLEN ISTLVPTTAL 420
 PLNFSRKFID WKGIPVNKSQ LKRGYSYQIK MCPQNTSIPI RGRVLIGSDQ FQRSLPETII 480
 SMASLTGNI LPVSKNGNAQ VNGPVISTVI QNYSINEVFL FFSKIESNLS QPHCVFWDPS 540
 HLQWNDAGCH LVNETQDIVT CQCTHLTSFS ILMSPFVPST IFPVVKNITY VGLGISIGSL 600
 ILCLIIEALF WQIKKSQTS HTTRICMVNI ALSLLIADVW FIVGATVDT VNP SGVCTAA 660
 VFTTHFFYLS LFFWMMLMGI LLAYRIILVF HHMAQLMMA VGFCCLGYGCP LIISVITIAV 720
 TQPSNTYKRR DVCWLNWSNG SKPLLAFFVPE ALAIVAVNFV VVLLVLTKLW RPTVGERLSR 780
 DDKATIIIRVG KSLILITPLL GLTWGFGIGT IVDSQNLAWH VIFALLNAFQ GFFILCFGIL 840
 LDSKLRQLLF NKLSALSSWK QTEKQNSSDL SAKPKFSKPF NPLQNKGYHA FSHGTGSSDN 900
 IMLTQFVSNE 910

Seq ID NO: C261 Protein Sequence
 Protein Accession #: NP_000575.1

1 11 21 31 41 51
 | | | | |
 MTSKLAVALL AAFLISAALC EGAVLPRSAK ELRCQCIKTY SKPFHPKFIK ELRVIESGPH 60
 CANTEIIVKL SDGRELCLDP KENWVQRVVE KFLKRAENS 99

Seq ID NO: C262 Protein Sequence
 Protein Accession #: NP_005594.1

1 11 21 31 41 51
 | | | | |
 MSTERDSETT FEEDSQPNDE VVPYSDDETE DELDDQGS AV EPEQNRVNRE AEENREPFK 60
 ECTWQVKAND RKYHEQPHFM NTKFLCIKES KYANNAIKTY KYNAFTFIP NLFEQFKRAA 120
 NLYFLALLIL QAVPQISTLA WYTTLVPLLV VLGVTAIKDL VDDVARHKMD KEINNRTCEV 180
 IKDGRFKVAK WKEIQVGDI RLKKNDFVPA DILLSSSEP NSLCYVETAE LDGETNLKFK 240
 MSLEITDQYL QREDTLATFD GFIECEEPNN RLDKFTGTLE WRNTSFPLDA DKILLRGCVI 300
 RNTDFCHGLV IFAGADTKIM KNSGKTRFKR TKIDYLMNYM VYTIFFVLIL LSLAGLAIGHA 360
 YWEAQVGNSS WYLYDGEDDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLGQSHFIN 420
 WDLQMYAEK DTPAKARTTT LNEQLGQIHY IFSDKTGTLT QNIMTFKCC INGQIYGDHR 480
 DASQHNHNKI EQVDFSWNTY ADGKLAFYDH YLIEIQSGK EPEVRQFFFL LAVCHTVMVD 540
 RTDGLNLYQA ASPEDEGLVN AARNFGFAFL ARTQNTITIS ELGTERTYNV LAILDFNSDR 600
 KRMSIIVRTP EGNIKLYCKG ADTVIYERLH RMNPTKQETQ DALDIFANET LRTLCCLCYKE 660

IEEKEFTEWN KKFMAASVAS TNRDEALDKV YEEIEKDIL L GATAIEDKL QDGVPEITISK 720
 LAKADIKIIV L7GDKKETAE NIGFACELLT EDTTICYGED INSLHARME NQRNRGGVYA 780
 KFAPPVQESF FPPGGNRLI ITGSWNLIL LEKTKRKNKI LKLKFPRTTE ERMRMQSKR 840
 RLEAKKEQRQ KNFVDLACEC SAVICCRVTP KQKAMVVDLV KRYKKAITLA IGDGANDVNM 900
 IKTAHIGVGI SQEQEQMAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMCKF LRIFYFYKNA 960
 FTLVHFWSYF FNGYSAQTAY EDWFITLYNV LYTSPLVLLM GLLDQDVSDK LSLRFPGLYI 1020
 VGQRDLLFNY KRFFVSLHLG VLTSMILFFI PLGAYLQTVG QDGEAPSDYQ SFAVTIASAL 1080
 VITVNFQIGL DTSYWTFFNA FSIFGSIALY FGIMFDFHSA GIHVLFPFAF QFTGTASNAL 1140
 RQPYIWLTHI LTVAVCLLPV VAIRFLSMTI WPSESDKIQK HRKRLKAEQ WQRROQVFR 1200
 GVSTRRSAYA FSHQRGYADL ISSGRSIRKK RSPLDAIVAD GTAEYRRTGD S 1251

Seq ID NO: C263 Protein Sequence
 Protein Accession #: XM_044533

1 11 21 31 41 51
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 MLRTAMGLRS WLAAPWALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60
 RFPAEHSIN Y TALLSRDGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQCC 120
 SFKGDQFQD CQNYIKILLP LSGSHLFTCG TAAFSMPCTY INMENFTLAR DEKGNVLLD 180
 GKGRCPFDPN FKSTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAF 240
 VASAYIPESL GSLQGGDDKI YFFPSETGQE FEFENTIVS RIARICKGDE GGERVLQQRW 300
 TSLKAQQLC SRPDDGFPPN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV 360
 FTMKDVQRVF SGLYKEVNRE TQQWYTVTHP VPTFRPGACI TNSARERKIN SSLQLPDRVL 420
 NFLKDHFLMF GQVRSRMLLL QPQARYQVVA VHRVPLGHHT YDVLFLGTGD GRLHKAVSVG 480
 PRVHIEELQ IFSSGQPVND LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
 PYCAWSGSSC KHVSLYQFQL ATRPWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCQVQ 600
 FQNTVNTLA CPLLSNLATV LWRNGAPVN ASASCHVLPT GDLLLVGTQQ LGFEFCWSLE 660
 EGQQLVAS Y CPEVVEDGVA DQDEGGSVP VIISTRVSA PAGGKASWGA DRSYWKFLV 720
 MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780
 PLDHRYGQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV 837

Seq ID NO: C264 Protein Sequence
 Protein Accession #: NP_008950.1

1 11 21 31 41 51
 | | | | |
 MASQNRDPA TSVAAARKGA EPSGGAARGP VGKRLQQLM TLMMSGDKGI SAPPESDNLF 60
 KWVGTHHGA GTVYEDLRYK LSLEFPSSGY YNAPTVMKLT PCYHPNVDTQ GNICLDILKE 120
 KWSALYDVRT ILLSIQSLG EPNIDSPLNT HAAELWKNPT AFKKYLQETY SKQVTSQEP 179

Seq ID NO: C265 Protein Sequence
 Protein Accession #: NP_055399.1

1 11 21 31 41 51
 | | | | |
 MGRGWGFLFG LLGAVWLLSS GHGEEQPPET AAQRCCFCQVS GYLDDCTCDV ETIDRFNNYR 60
 LFPRQLKLE SDYFRYKVN LKRPCFWND ISQCGRRDCA VKPCQSDEVP DGIKSASYKY 120
 SEENANLIEE CEQAERLGA DESLSEETQK AVLQWTKHDD SSDNFCEADD IQSPEAEYVD 180
 LLLNPERVTG YKGPDAWKI NVIYENCCK PQTIKRPLNP LASGQGTSEE NTFYSWLEGL 240
 CVEKRAFYRL ISGLHASINV HLSARYLLQE TWLEKKWGHN ITEFQQRFDG ILTEGEGPRR 300
 LKNLYFLYLI ELRLSKVLVP FFERPDFQLF TGNKIQDEEN KMLLEILHE IKSFLPHFDE 360
 NSFFAGDKKE AHKLKEDFRL HFRNISRIMD CVGCFKCLRW GKLTQGLGT ALKILFSEKL 420
 IANMPESGFS YEFHLTRQEI VSLFNAFGRI STSVKELENF RNLLQNIH 468

Seq ID NO: C266 Protein Sequence
 Protein Accession #: NP_002879.1

1 11 21 31 41 51
 | | | | |
 MQPRRQRLPA PWSGPRGRP TAPLLALLL LAPVAAPAGS GGPDDPGQPQ DAGVPRRLQ 60
 QKARAALHFF NFRSGSPSAL RVLAEVQEGR AWINPKGCK VHVVFSTERY NPESLLQEGE 120
 GRLGKCSARV FFKNQKPRPT INVTCTRLIE KKKRQEDYL LYKQMKQLN PLEIVSIPDN 180
 HGHIDPSLRL IWDLAFLGSS YVMWEMTTQV SHYYLAQLTS VRQWVRKT 228

Seq ID NO: C267 Protein Sequence
 Protein Accession #: NP_005400.1

1 11 21 31 41 51
 | | | | |
 MSVKGMAIAL AVILCATVVQ GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF 94

Seq ID NO: C268 Protein Sequence
 Protein Accession #: FGENSEH predicted

1 11 21 31 41 51
 | | | | |
 MLRQVLRRGL QSFCHRLGL VSRHPVFFLT VPAVLITITF LSALNRFQPE GDLERLVAPS 60
 HSLAKIERSL ASSLFPLDQS KSQLYSDLHT PGRYGRVILL SPTGDNILLQ AEGILQTHRA 120
 VLEMKVNHKG YNYTFSHLCV LRNQDKKCVL DDIISVLEDL RQAAVSNKTT ARVQVRYPN 180
 KLVCSFCML LPIKEAALHF LP 202

Seq ID NO: C269 Protein Sequence
 Protein Accession #: NP_002429.1

	1	11	21	31	41	51	
5	MRLPLLVLFA	SVIPGAVLLL	DTROFLIYNE	DHKRCVDAVS	PSAVQTAACN	QDAESQKFRW	60
	VSESQIMSV	FKLCLGVPSK	TDWVAITLYA	CDSKSEFQKW	ECKNDTLLGI	KGEDLFFNYG	120
	NRQEKIMLY	KGSGLWSRWK	IYGTDDNLCS	RGYEAMYTL	GNANGATCAF	PFKFENKWWA	180
	DCTSAGRS	WLWCGTTT	DTDKLFGYCP	LKFEGSESLW	NKDPLTSVSY	QINSKSALTW	240
	HQARKSCQQ	NAELLSITEI	HEQTYLTGLT	SSLTSGLWIG	LNSLSFNSGW	QWSDRSPFRY	300
10	LNWLPGSPSA	EPGKSCVSLN	PGKNAKWENL	ECVQKGLYIC	KKGNTTLLNSF	VIPSESDVPT	360
	HCPSQWHPYA	GHCYKIHRE	KKIQRDALT	CRKEGGDLTS	IHTIEELDFI	ISQLGYEPND	420
	ELWIGLNDIK	IQMYFEWSDG	TPVTFTKWLR	GEPHENNRQ	EDCVVMKGKD	GYWADRGEW	480
	PLGYICKMKS	RSQGFPEIVE	EKGRKGWKK	HHFYCYMIGH	TLSTFAEANK	TCNNENAYLT	540
	TIEDRYEQAF	LTSFVGLRPE	KYFWTGLSDI	QTKGTFQWTI	EEEVRFTHWN	SDMPGRKPGC	600
15	VAMRTGIAGG	LWDVLKCDCK	AKFVCKHWAE	GVTHPPKPTT	TPEPKCPEDW	GASSRTSLCF	660
	KLYAKGKHEK	KTFWESRDFC	RALGGDLASI	NNKEEQOTIW	RLITASGSYH	KLFWLGLTYG	720
	SPSEGFTWSD	GSPVSYENWA	YGEPNNYQNV	EYCGELKGDP	TMSWNDINCE	HLNNWICQIQ	780
	KGQTPKPEPT	PAPQDNPPVT	EDGWVIYKDY	QYYFSKEKET	MDNARAFCKR	NFGDLVSIQS	840
	ESSEKFLWKY	VNRNDQAQSA	FIGLLISLDK	KFAWMDGSKV	DYVSWATGEP	NFANEDENCV	900
	TMYSNSGFWN	DINGCYPNAF	ICQRHNSIN	ATTVMPTMPS	VPSGCKEGWN	FYSNKCCKIF	960
20	GMEEERKNW	QEARAKCIGF	GGNLVSIQNE	KEQAFITYHM	KDSTFSAWTG	LNDVNSEHTF	1020
	LWTDGRGVHY	TNWGKGYPGG	RRSSLSYEDA	DCVVIIGGAS	NEAGKWMDDT	CDSKRGYICQ	1080
	TRSDPSLTNP	PATIQTDGFE	KYKSSSYSLM	RQKFQWHEAE	TYCKLHNSLI	ASILDPSYNA	1140
	FAWLQMETSN	ERVVIALNSN	LTDNQYTWD	KWRVRYTNWA	ADEPKLKSAC	VYLDLDGYWK	1200
25	TAHCNESFYF	LCKRSDEIPA	TEPPQLPGRC	PESDHTAWIP	FHGHCCYIES	SYTRNWQOAS	1260
	LECLRMGSSL	VSIESAAESS	FLSYRVEPLK	SKTNFWIGLF	RNVEGTWLWI	NNSPVSVFNW	1320
	NTGDPGGERN	DCVALHASSG	FWSNIHCSSY	KGYICKRPKI	IDAKPTHELL	TTKADTRKMD	1380
	PSKPSSNVAG	VVITVILLIL	TGAGLAAIFY	YKKRRVHLPO	EGAFENTLYF	NSQSSPGTSD	1440
	MKDLVGNIEQ	NEHSVI					1456

Seq ID NO: C270 Protein Sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
35	MVLLHWCLLW	LLFPLSSRTQ	KLPTREDELF	QMQIRDKAFF	HDSSVIPDGA	EISSYLFRDT	60
	PKRYFFVVEE	DNTPLSVTVT	PCDAPLEWKL	SLQELPEDRS	GEGSGDLEPL	EQQKQIINE	120
	EGTELFSYKG	NDVEYFISSS	SPSGLYQLDL	LSTEKDTDFK	VYATTTPESD	QPYPELPYDP	180
	RVDVTSLGRT	TVTTLAWKPS	TASLLKQPIQ	YCVVINKEHN	FKSLCAVEAK	LSADDAFMMA	240
40	PKPLGLDFSP	DFAHGFPPSD	NSGKERSFQA	KPSPKLGRHV	YSRPKVDIQK	ICIGNKNIFT	300
	VSDLKPDQYQ	YFDVVEVNN	SNMSTAYVGT	FARTKBEAKQ	KTVELKDGKI	TDVVFVKRGA	360
	KFLRFAPVSS	HQKVTFIFIH	CLDAVQIQVR	RDGKLLLSQN	VEGIIQQQLR	GKPKAKYLVR	420
	LKGNKKGASM	LKILATTRPT	KQSFPSLPED	TRIKAFDKLR	TCSSATVAVL	GTQERNKFCI	480
	YKKEVDDNYN	EDQKKREQNQ	CLGPDIRKKS	EKVLCKYFHS	QNLQKAVTTE	TIKGLQPGKS	540
45	YLLDVYVIGH	GGHSVKYQSK	VVKTRKFC				568

Seq ID NO: C271 Protein Sequence
Protein Accession #: AAH34229.1

	1	11	21	31	41	51	
50	MEKVQLEFEN	QEMEKKLQEF	RSTRNKEKED	RESSEYYWKS	GKVGKLVNQS	YMSQNKGNV	60
	VKFSAGKVKL	KLLKEQIQEP	VKPTVNYKMA	NSSECEKPKI	NGKVCQCEN	KAALLVCLEC	120
	GEDYCSGCPA	NVHQKALKL	HRTTLLQARS	QILFNVLDA	HQFIKDVND	EPKEENNSTK	180
55	ETSKIQHKKP	SVLLQRSSSE	VEITTMKRAQ	RTKPKRSLLC	EGSFDEEASA	QSPQEVLSQW	240
	RTGNHDDNKK	QNLHAAVKDS	LEECEVQTNL	KIWREPLNIE	LKEDILSYME	KLWLKHHRR	300
	PQEQLFKCQ	IRSHIHMKPL	VMHSVLKMK	MKIVMVRPK	YNTQLFYCQ		349

Seq ID NO: C272 Protein Sequence
Protein Accession #: NP_078963.1

	1	11	21	31	41	51	
60	MEKLWLKKHR	RTPQEQLFKM	LSDTFPPHPE	TTGDAQCSQN	ENDEDSDGEE	TKVQHTALL	60
	PVETLNIERP	EPSLKIVELD	DTYEEFEFEA	ENIVPYKVKL	ADADSQRSCA	FHDCQKNSFP	120
65	YENGIIHQHHV	FDKGRDFLN	LCLRNSSTYY	KDNKGETSN	TDFDNIVDPD	VYSSDIEKIE	180
	ESTSPERNLK	EKNIGLESNQ	KSDDCSVSLE	SKDTLLGRDL	EKAPIEEKLS	QDIKESLELS	240
	NLYKRPSPFE	SKTTKSSLLL	QEIACRSKPI	TKQYQGLERF	FIFDTNERLN	LLPSHRLECN	300
	NSSTRITLAE	DREWIPDHS	SEYADNAIVL	GVLQGAQSPS	SSRKQKMGQ	KSQRPSTANF	360
70	PLSNSVKESS	SCLSSSHPRS	RSAAAQSSSR	AASEISEIEY	IDITDQNELS	LDTTTQHTL	420
	DNLEKELQVL	RLADTSEKL	YSLTSEFFPD	FSSQSLNISQ	ISTDFLKTSH	VRGPCGVEEL	480
	SCSGRDTIKQ	SLLSLESST	DEEEEDFLNK	QHVITLPWSK	ST		522

Seq ID NO: C273 Protein Sequence
Protein Accession #: NP_005399.1

	1	11	21	31	41	51	
75	MKVSAYLLCL	LLMTAAFPNQ	GLAQPDALNV	PSTCCFTFSS	KKISLQRLKS	YVITTSRCPQ	60
80	KAVIFRTKLG	KEICADPEK	WVQNYMKHLG	RKAHTLKT			98

Seq ID NO: C274 Protein Sequence
Protein Accession #: BAC05158.1

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MFLLTGGVSL	KSAEKNPDPT	WLQDKSWEEI	CRASEFPAPR	GLRQHFCEHI	YEWREIYDSK	60
EPHNAKFAP	MDKNLNLQK	IIILRCRLPD	KITPAITNVV	TDKLGKGFVE	PPFFDLTKSY	120
LDSNCTIPLI	FVLSPGADPM	ASLLKFANDK	SMSGNKFQAI	SLGQGGQPIA	AKMIKAAIEE	180
GTWVCLQNC	LAVSWMPMLE	KICEDFTSET	CNSSPRLWLT	SYPSKFFPVT	ILQNGVKMTN	240
EPPTGLRLNL	LQSYLTDPVS	DPEFFKGCGR	KELLFINEYD	TIPFEAISYL	TGECNYGGRV	300
TDDWDRRLLL	TMLADFNLY	IVENPHYKFS	PSGNYFAPPK	GTEDYIEFI	KKLPFTQHPE	360
IFGLHENVDI	SKDLQQTCTL	FESLLLTQGG	SKQTGASGST	DQILLEITKD	ILNKLPSDFD	420
IEMALRKYPV	RYEESMNTVL	VQEMERFNLL	IITIRNTLRD	LEKAIKGVV	MDSALEALSS	480
SLLVGKVPEI	WAKRSYPSLK	PLGSYITDFL	ARLNFLQDWY	NSGKPCVFWL	SGFFFTQAFI	540
TGAMQNYARK	YTTPIDLLGY	EFEVIPSSTS	DTSPEDGVYI	HGLYLDGARW	DRESGLLAEQ	600
YPKLLFDLMP	IWIWIKPTQKS	RIIKSDAYVC	PLYKTSERKG	TLSTTGHSTN	FVIAMLLKTD	660
QPTRHWIKRG	VALLCQLDD					679

Seq ID NO: C275 Protein Sequence
Protein Accession #: AAA60212.1

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MAESHLQLWL	LLLLLPTLCGP	GTAAWTSSSL	ACAQGPFWC	QSLQALQCR	ALGHCLQEVW	60
GHVGADDLQ	ECEDIVHILN	KMAKEAIFQD	TMRKFLEQEC	NVLPLKLLMP	QCQVLLDDYF	120
PLVIDYFQNG	TDNNGTCHML	GLCKSRQPEP	EQEPGMSDPL	PKPLRDPLPD	PLLDKLVLPV	180
LPGALQARPG	PHTQDLSEQQ	FPIPLPYCWL	CRALIKRIQA	MIPKALAVA	VAQVCRVVP	240
VAGGICQCLA	ERYSVILLDT	LLGRMLPQLV	CRVLVLRCSMD	DSAGPRSETG	EWLPRDSECH	300
LCMSVTQAG	NSSEQAIPQA	MLQACVGSWL	DREKCKQFVE	QHTPQLLTLV	PRGWDATTC	360
QALGVCGTMS	SPLQCIHSPD	L				381

Seq ID NO: C276 Protein Sequence
Protein Accession #: NP_631911.1

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MLGCGIPALG	LLLLLQGSAD	GNGIQGFYFP	WSCEGDIWDR	ESCGGQAAD	SPNLCLRLRC	60
CYRNGVCYHQ	RPDENVRKH	MWALVWTCG	LLLLSCSICL	FWWAKRRDVL	HMPGFLAGPC	120
DMKSVSLLS	KHRGTKKTSP	TGSVPVALSK	ESRDVEGGTE	GEGTEEGEET	EGEEEEED	177

Seq ID NO: C277 Protein Sequence
Protein Accession #: NP_473364.1

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MKLVTIFLLV	TISLCSYSAT	AFLINKVPLP	VDKLAPLPLD	NILPFMDPLK	LLLKTLGISV	60
EHLVEGLRKC	VNELGPEASE	AVKKLLEALS	HLV			93

Seq ID NO: C278 Protein Sequence
Protein Accession #: FGENESH predicted

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MPLSYAYKNA	ETLAGRHTSS	WMSRGAYQRR	NTRAAGRPEE	CTDRNWHAGR	TRGIWLGQLE	60
ERCSDFGVGS	FFWVVRGLAG	SGAKLQTFPT	AQEGAPTQVR	QAEALLKCRQ	SGRPGRGGA	120
SERARDASML	SPLSAAMRNY	PTSTIPPRR	SYSPTEIAHK	SYSCSLPDMK	ISMAESGPSL	180
DSLDTLEDGE	SGSPFLVTHL	YFLGVVTTGM	EQLDFETGPN	IFDLQIYVKD	EVGVTDLQVL	240
TVQVTDVNEP	PQFQGNLAED	HLRADQPHFN	AHSHTYVRVV	ATALARHRLR	SSIGSPFLGT	300
FCVVVMQYF	LISPPKSEFM	SANGTLFSTT	ELDFEAGHRS	PHLIVEVRDS	GGLKASTELQ	360
VNIVNLNDEV	PRFTSPTRVY	TVLEELSPGT	IVANITAEDP	DDEGFPSHLL	YSITTVSKYF	420
MINQLTGTIQ	VAQRIDRDAG	ELRQNPTISL	EVLVKDRPYG	GQENRIQITF	IVEDVNDNPA	480
TCQKFTFRSS	LHPALCSKTL	TWMDTVLDCF	HAADKDIPVT	GRFTKERGLI	GLTVPHGWGS	540
LTIMAEKKEE	QVTSYMDGSR	QRDRACVGKL	LLIKPSDLMR	LSHYHENSNG	KTCPHDSISS	600
YQVPTTCRN	SRIQATNNED	TSSVTVTVNI	LEENDEKPIC	TPNSYFLALP	VDLKVGTNIQ	660
NFKLTCTDLD	SSPRSFYRSI	GPGNVNNHFT	FSPNAGSNVT	RLLLTSRFDY	AGGFDKIWDY	720
KLIVVVTDDN	LMSDRKKAEA	LVETGTVTLS	IKVIPHPPTI	ITTTTPRPVT	YQVLRKNVYS	780
PSAWYVPFVI	TLGSILLGL	LVYLVLLAK	AIHRHCPCKT	GKNKEPLTKK	GETKTAERDV	840
VVETIQMNTI	FDGEAIDPEP	EQASLELYAL	LPSCCDPSPV	TLRKVQVCGE	SEETQCSCGH	900
ITLPGKIPVD	DRKQETGLQ	GDFEVWTLCP	AVKVVVGSQP	AERCIRLALS	LKKYSSD	957

Seq ID NO: C279 Protein Sequence
Protein Accession #: XP_168571.1

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MINQLTGTIQ	VAQRIDRDAG	ELRQNPTISL	EVLVKDRPYG	GQENRIQITF	IVEDVNDNPA	60
TCQKFTFSIM	VPERTAKGTL	LLDLNKFCFD	DDSEAFNNRF	NFTMPSGVGS	GSRLQDDPAG	120
SGKIVLIGDL	DYENPSNLAA	GNKYTVIIQV	QDVAPPYYKN	NVYVYILTSP	ENEFPLIFDR	180
PSYVFDVSR	RPAQGHLSGP	BEKRLLSICM	VRVCHHFLGL	HIASGSPRPV	GRPIQGSHPQ	240
TLPLQDWEQ	GTSDKERRNE	DCRERRRGNN	YPDEHYL			277

Seq ID NO: C280 Protein Sequence
Protein Accession #: NP_005257.2

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41
51

MGDWSFLGNF	LEEVHKHSTV	VGVVWLTVLV	IFRMLVLGTA	AESSWGDEQA	DFRCDTIQPG	60
CQNVCYDQAF	PISHIRYVWL	QIIFVSTPSL	VYMGHAMHTV	RMQEKRLKLE	AERAKEVRGS	120

GSYEYPVAEK AELSCEWEEGN GRIALQGTLL NTYVCSILIR TTMEVGFIVG QYFIYGIFLT 180
 TLHVCRRSPC PHPVNCYVSR PTEKNVFFIVF MLAVAALSLL LSLAELYHLG WKKIRQRFVK 240
 PRQHMMAKQQL SGPSVGIVQS CTPPPDFNQC LENGPGGKFF NPFSSNNMASQ QNTDNLVTEQ 300
 VRGQEQTPEE GFIIQVRYGQK PEVPNGVSPG HRLPHGYHSD KRRLSKASSK ARSDDLSV 358

Seq ID NO: C281 Protein Sequence
 Protein Accession #: NP_055274.2

1 11 21 31 41 51
 | | | | |
 MYLSICCCFL LWAPALT LKN LNYSVP EEG AGTVIGNIGR DARLQPGLEP AERGGGGRSK 60
 SGSYRVLENS APHLLD V DAD SGLLYTKQRI DRESLCRHNA KCQLSLEVFA NDKEICMIKV 120
 EIQDINDNAP SFSSDQIEMD ISENAAPGTR FPLTSAHDPD AGENGLRTYL LTRDDHGLFG 180
 LDVKSRGDDGT KFPELVIQKA LDREQQNHHT LVLTLADGGE PPRSATVQIN VKVIDSNDNS 240
 PVFEAPSVLV ELPENAPLGT VVIDLNATDA DEGPNGEVLY SFSSYVPDRV RELFSIDPKT 300
 GLIRVKGNLD YEENGML EID VQARDLGPNP IPAHCKVTVK LIDRNDNAPS IGFVSVRQGA 360
 LSEAAPPGTV IALVRVTD RD SGKNGQLQCR VLGGGGTGGG GGLGGPGGSV PFKLEENYDN 420
 FYTVVTDRLP DRETQDEYNY TIVARDGGSF PLNSTKSAI KILDENDNPP RFTKGLYVLQ 480
 VHENNIPGEY LGSVLAQDPD LGQNGTVSYS ILPSHIGDVS IYTVSVNPT NGAIYALRSF 540
 NFEQTKAFEF KVLAKDSGAP AHLESNATVR VTVLDVNDNA PVIVLPTLQN DTAELOVPRN 600
 AGLGYLVSTV RALDSDFGES GRLTYEIVDG NDDHLFEIDP SSGEIRTLHP FWEDVTPVVE 660
 LVVKTVDHKG PTLSSAVAKLI IRSVSGSLPE GVP RVNGEQH HWDMSLPLIV TLSTISIILL 720
 AAMITIAVKC KRENKEIRTY NCRIAEYSHP QLGGGKGKKK KINKNDIMLV QSEVEERNAM 780
 NVMNVSSPS LATSPMYFDY QTRLPLSSPR SEVMYLKPAS NNLTVPQGHG GCHTSFTGQG 840
 TNASETPATR MSIIQTDNFP AEPNYMGSRQ QFVQSISVAP RLRTQKEPA 889

Seq ID NO: C282 Protein Sequence
 Protein Accession #: NP_005592.1

1 11 21 31 41 51
 | | | | |
 MELCRSLALL GGSGLGLMFC L IALSTDFWFE AVGP THSAHS GLWPTGHGDI ISGYIHVTQT 60
 FSIAMVLWAL VSVSFLVLSC FPSLFPPGHG PLVSTTAFAA AAISMVVAMA VYTSEWRDQP 120
 PHPQIQTFFS WSPYLGWVSA ILLCTGALS LGAHCGGPRP GYETL 165

Seq ID NO: C283 Protein Sequence
 Protein Accession #: NP_006424.2

1 11 21 31 41 51
 | | | | |
 MATWALLLLA AMLLGNPGLV FSRLSPEYYD LARAHLRDEE KSCPCLAQEG PQGDLLTKTQ 60
 ELGRDYRTCL TIVQKLKMMV DKPTQRSVSN AATRVCR TGR SRWRDVC RNF MRRYQSRVTQ 120
 GLVAGETAQQ ICDLRLCIP STGFL 145

Seq ID NO: C284 Protein Sequence
 Protein Accession #: NP_005594.1

1 11 21 31 41 51
 | | | | |
 MKVSAALAV ILIATALCAP ASAPYSSDT TPCCFAYIAR PLPRAHIKEY FYTSGKCSNP 60
 AVVFVTRKNR QVCANPEKKW VREYINSLEM S 91

Seq ID NO: C285 Protein Sequence
 Protein Accession #: NP_071437.1

1 11 21 31 41 51
 | | | | |
 MAPGRAVAGL LLLAAAGLGG VAEGPGLAFS EDVLSVFGAN LSLSAAQLQH LLEQMGAASR 60
 VGVPEPGQLH FNQCLTAE EI FSLHGFSNAT QITSSKFSVI CPAVLQQLNF HPCEDRPKHK 120
 TRPSHSEVWG YGFLSVTIIN LASLLGLILT PLIKKSYPFK ILTFFVGLAI GTLFSNAIFQ 180
 LIPEAFGFDP KVDSYVEKAV AVFGGFYLLF FFERMLKMLL KTYGQNGH TH FGNDNFGPQE 240
 KTHQPKALPA INGVT CYANP AVTEANGHIH FDNVSVVSLQ DGKKEPSSCT CLKGPKLSEI 300
 GTIAWMITLC DALHNFIDGL AIGASCTLSL LQGLSTSI AI LCEEFPHEL G DFVILLNAGM 360
 STRQALLNF LSAACSCYVGL AFGILVGNNF APNIIFALAG GMFLYISLAD MFPEMNDMLR 420
 EKVTGRKTDF TFFMIQNAGM LTGFTAILLI TLYAGEIELE 460

Seq ID NO: C286 Protein Sequence
 Protein Accession #: NP_004175.1

1 11 21 31 41 51
 | | | | |
 MPNSEPASLL ELFN SIATQG ELVRS LKAGN ASKDEIDSAV KMLVSLKMSY KAAAGEDYKA 60
 DCPPGNPAPT SNHGPDAT EA EEDFVD PWT V QTSSAKGIDY DKLIVRFSGS KIDKELINRI 120
 ERATGQRP HH FLRRGIFFSH RDMNQVL DAY ENK KPFYLYT GRGPSSEAMH VGH LIPFIFT 180
 KWLQDVFNVP LVIQMTDD EK YLWKDLTLDQ AYGD AVENAK DIIACGF DIN KTFIFSDLDY 240
 MGMSSGFYKN VVKIQKHVTF NQVKGIFGFT DSDCIGKISF PAIQAAPSPS NSFPQIFRDR 300
 TDIQCLIPCA IDQDPYFRMT RDVAPRIGYP KPALLHSTFF PALQGAQTKM SASDPNSSIF 360
 LTDTAQIKT KVNKHA FSGG RDTIEEHRQF GGNCDVDVSF MYLTFLEDD DKLEQIRKDY 420
 TSGAMLTGEL KKALIEVLQP LIAEHQARRK EVIDEIVKEF MTPRKL SFDF Q 471

Seq ID NO: C287 Protein Sequence

Protein Accession #: NP_004929.1

	1	11	21	31	41	51	
5	MTVFRQENVD	DYYDTGEEELG	SGQFAVVKKC	REKSTGLQYA	AKFIKKRRTK	SSRRGVSR	60
	IEREVSILKE	IQHPNVITLH	EVYENKTDVI	LILELVAGGE	LFDFLAEKES	LTEEEATEFL	120
	KQILNGVYYL	HSLQIAHFDL	KPENIMLLDR	NVPKPRIKII	DFGLAHKIDF	GNEFKNIFGT	180
	PEFVAPEIVN	YEPLGLEADM	WSIGVITYIL	LSGASPLFGD	TKQETLANVS	AVNYEFEDFY	240
10	FSNTSALAKD	FIRRLVKDP	KKRTIQDLS	QHPWIKPKDT	QQALSRKASA	VNMEKFKKFA	300
	ARKKWKQSVR	LISLCQRLSR	SFLSRSNMSV	ARSDDTLDEE	DSFVMAKIIH	AINDDNVPGL	360
	QHLLGSLSNY	DVNQPNKHGT	PPLLIAAGCG	NIQILQLLIK	RGSRIDVQDK	GGSSNAVYWA	420
	RHGHVDTLKF	LSENKCLPDV	KDKSGEMALH	VAARYGHADV	AQVTCASAAQ	IPISRTKEEE	480
	TPLHCAAWHG	YYSVAKALCE	AGCNVNIKNR	EGETPLLTAS	ARGYHDIVCE	LAEHGADLNA	540
15	CDKDGHIHAL	LAVRRQMEV	IKTLLSQGCF	VDYQDRHGNT	PLHVACKDGN	MPIVVALCEA	600
	NCNLDISNKY	GRTPLHLAAN	NGILDVVRYL	CLMGASVEAL	TTDGKTAEDL	ARSEQHEHVA	660
	GLLARLRKDT	HRGLFIQQLR	FTQNLQPRIK	LKLFHSGSGS	KTTLVESLKC	GLLRSFFRRR	720
	RPRLSSTNSS	RFPSPSLASK	PTVSVSINN	YPGCENSVSR	SRSMMFEPGL	TKGMLEVFVA	780
	PTHHPHCSAD	DQSTKAIDIQ	NAYLNGVDF	SVWEFSGNPV	YFCYDYFAA	NDPTSIVHVV	840
20	FSLEEPYEQ	LNPVIFWLSF	LKSLVPVEEP	IAFGGKLKNP	LQVVLVATHA	DIMNVPRPAG	900
	GEFGYDKDTS	LLKEIRNRFG	NDLHISNKL	VLDAGASGSK	DMKVLNRHLQ	EIRSQIVSVC	960
	PPMTHLCEKI	ISTLPSWRKL	NGPNQLMSLQ	QFVYDVQDQL	NPLASEEDLR	RIAQQHLSTG	1020
	EINIMQSETV	QDVLILLDRW	LCTNVLGKLL	SVETPRALHH	YRGRTYVEDI	QRLVPDSDFE	1080
	ELLQILDAMD	ICARDLSSGT	MVDVPAIKT	DNLHRSWADE	EDEVMMVYGGV	RIVPVEHLTP	1140
25	FPCGFIHVKQ	VNLRCRWIQQ	STEGDADIRL	WVNGCKLANR	GAELLVLLVN	HGQGIQVQVR	1200
	GLETEKIKCC	LLDSVSCSTI	ENVMATTLPG	LLTVKHLYSP	QQLREHHEPV	MIYQPRDFFR	1260
	AQTLKETSLT	NTMGYKESF	SSIMCFGCHD	VYSQASLGMD	THASDLNLLT	RRKLSRLDDP	1320
	PDPLGKDWCL	LAMNLGLPDL	VAKYNTNNGA	PKDFLPSPLH	ALLREWTYP	ESTVTGLMSK	1380
	LRELGRDDAA	DLKLKASSVF	KINLDGNGQE	AYASSCNSGT	SYNSISSVVS	R	1431

Seq ID NO: C288 Protein Sequence

Protein Accession #: NP_002072.1

	1	11	21	31	41	51	
35	MELRARGWWL	LCAAAALVAC	ARGDPASKSR	SCGEVRQIYG	AKGFSLSDVP	QAEISGEHLR	60
	ICPGYGTCTC	SEMENLANR	SHAELETALR	DSSRVLQAML	ATQLRSFDDH	FQHLNDSER	120
	TLQATFPFAP	GELYTQNAAR	FRDLYSELRL	YRGANLHLE	ETLAEFWARL	LERLFKQLHP	180
	QLLLPDDYLD	CLGKQAEALR	PFGEAPREL	LRATRAFVAA	RSFVQGLGVA	SDVVRKVAQV	240
40	PLGPECSRRAV	MKLVCYCAHCL	GVPGARPCPD	YCRNVLGKCL	ANQADILDAEW	RNLDSMVL	300
	TDKFWGTSGV	ESVIGSVHTW	LAEAINALQD	NRDTLTAKVI	QCGGNPKVNP	QGPPEEKRR	360
	RGKLAPREPR	PSGTLLEKLV	EAKAQLRDVQ	DFWISLPGTL	CSEKMALSTA	SDDRCWNGMA	420
	RGRYLPVVMG	DGLANQINNP	EVEVDITKPD	MTIRQQIMQL	KIMTNRLRSA	YNGNDVDFQD	480
	ASDDGSGSGS						490

Seq ID NO: C289 Protein Sequence

Protein Accession #: AAH30205.1

	1	11	21	31	41	51	
50	MIILYLFLL	LWEDTQGWGF	KDGIFHNSIW	LERAAGVYHR	EARGSKYKLT	YAEAKAVCEF	60
	EGGHLATYKQ	LEAARKIGFH	VCAAGWMAGK	RVGYPIVKG	PNCGFGKGTI	IDYGIRLNRS	120
	ERWDAYCYNP	HAKECGGVFT	DPKQIFKSPG	FPNEYEDNQI	CYWHIRLKYG	QRIHLSFLDF	180
	DLEDDPGCLA	DYVEIYDSYD	DVHGFGVGRYC	GDELPPDIIS	TGNVMTLKFL	SDASVTAGGF	240
55	QIKYVAMPDV	SKSSQGGKNTS	TTSTGNKNFL	AGRFSHL			277

Seq ID NO: C290 Protein Sequence

Protein Accession #: NP_001973.1

	1	11	21	31	41	51	
60	MRANDALQVL	GLLFSLARGS	EVGNSQAVCP	GTLNGLSVTG	DAENQYQTLY	KLYERCEVVM	60
	GNLEIVLTGH	NADLSFLQWI	REVTGYVLVA	MNEFSTLPLP	NLRVVRGTQV	YDGKFAIFVM	120
	LNNTNTSSHA	LRQLRLTQLT	EILSGGVYIE	KNDKLCHMDT	IDWRDIVRDR	DAEIVVKDNG	180
65	RSCPPCHEVC	KGRGCGPGSE	DCQTLTKTIC	APQCNGHCFG	PNPQCCHDE	CAGGCSGPD	240
	TDCAFACRHF	DSGACVPRCP	QPLVYNKLT	QLEPNPHTKY	QYGGVVCVASC	PHNFVVDQTS	300
	CVRACPPDKM	EVDKNGKLMC	EPCGGCLCPKA	CEGTGSGSRF	QTVDSNIDG	FVNCTKILGN	360
	LDLFLITGLNG	DPWHKIPALD	PEKLNVFRTV	REITGYLNIQ	SWPPHMHNFS	VFSNLTITIG	420
	RSLYNRGFSL	LIMKNLNVTS	LGFRSLKEIS	AGRIYISANR	QLCYHHSNLN	TKVLRGPTTE	480
70	RLDIKHNRPR	RDCVAEGKVC	DPLCSSGGCW	GPFGGQCLSC	RNYSRGVVCV	THCNFLNGEP	540
	REFAHEAECF	SCHPECQPMG	GTATCNGSGS	DTCAQCAHFR	DGPHCVSSCP	HGVLGAKGPI	600
	YKYPDVQNEC	RPCHENCTQG	KCGPELQDCL	GQTLVLIGKT	HLTMALTVIA	GLVVFIMMLG	660
	GTFLYWRGRR	IQNKRAMRRY	LERGESIEPL	DPSEKANKVL	ARIKETEELR	KLKVLGSGVF	720
	GTVHKGVWIP	EGESIKIPVC	IKVIEDKSGR	QSFQAVTDHM	LAIGSLDHAH	IVRLLGLCPG	780
75	SSLQLVTQYL	PLGSLLDHVR	QHRGALGPQL	LLNWGVQIAK	GMYYLEEHGM	VHRNLAARNV	840
	LLKSFSQVQV	ADFGVADLLP	PDDKQLLYSE	AKTPIKWMAL	ESIHFGKYTH	QSDVWSYGV	900
	VWELMTFGAE	PYAGLRLAEV	PDLEKGERL	AQPQICTIDV	YVMVMKWCMI	DENIRPTFKE	960
	LANEFTRMAR	DPFRYLVIKR	ESGPGIAPGP	EPHGLTNKKL	EEVELEPELD	LDLDEAEED	1020
80	NLATTTLGSA	LSLPVGTLMR	PRGSQSLSP	SSGYMPMNQ	NLGSCQESA	VSGSSERCP	1080
	PVSLHPMPRG	CLASESSEGH	VTGSEAELE	KVSMCRSRSR	SRSRPRGRDS	AYHSQRHSL	1140
	TPVTPLSPPG	LEEDVDNNGV	MPDTHLKGTP	SSREGTLSSV	GLSSVLGTTE	EDEDEEYEM	1200
	NRRRRHSPPH	PPRPSLEEL	GYEYMDVGS	LSASLGSTQS	CPLHEVPIMP	TAGTTPDEYD	1260
	EYMNQRDGG	GFGDYAAMG	ACPASEQGYE	EMRAFQGP	QAPHVHYARL	KTLRSLEATD	1320
	SAFDNPDYWH	SRLFFKANAQ	RT				1342

Seq ID NO: C291 Protein Sequence
Protein Accession #: NP_001207.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MAPLCPSPWL PLLIPAPAPG LTVQLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL 60
GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG 120
DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180
ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240
10    VEGHRFPABI HVVHLSTAFV RVDEALGRPG GLAVLAAFL EGPENSAYE QLLSRLEEIA 300
      BEGSTQVFG LDISALLPSD FSRVFQYEGS LTTPPCAQGV IWTVFNQTM LSAKQLHTLS 360
      DTLWGPQDSR LQLNFRATQP LNGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420
      GLLFAVTSVA FLVQMRQRQR RGTGKGVSYSR PAEVAETGA 459

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Seq ID NO: C292 Protein Sequence
Protein Accession #: NP_004198.1

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20      1      11      21      31      41      51
      |      |      |      |      |      |
MGGAVVDEGP TGVKAPDGGW GWAVLFGCFV ITGFSYAFPK AVSVFFKELI QEFGIGYSDT 60
AWISSILLAM LXTGTPLCSV CVNRFGCRPV MLVGGLFASL GMVAASFCSR IIQVYLTTGV 120
ITGLGLALNF QPSLIMLNRY FSKRRPMANG LAAAGSPVFL CALSPLGQLL QDRYGWRGGF 180
LILGGLLLNC ILKSAMCAEA VVTAQPGSGP PRPSRRLDLD SVFRDRGFVL YAVAASVMVL 240
25    GLFVPPVFFV SYAKDLGVDP TKAAPLLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSS 300
      SMFFNGLADL AGSTAGDYGG LVVFCIFFGI SYGMVGALQF EVLMAIVGTH KFSASIGLVL 360
      LMEAVAVLVG PPSGGKLLDA THVYMYVFIL AGAEVLTSSL ILLGNFFCI RKKPKPEQPE 420
      VAAABEEKLH KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETS V 465

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Seq ID NO: C293 Protein Sequence
Protein Accession #: NP_000349.1

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30      1      11      21      31      41      51
      |      |      |      |      |      |
MALFVRLAL ALALALGPAA TLAGPAKSPY QLVQLHSRLR GRQHGPNVCA VQKVIGTNRK 60
YFTNCKQWYQ RKICGKSTVI SYRCCPGYEK VPGEKGCPAA LPLSNLNYETL GVVGSTTTQL 120
YTDRTKLRP EMEGPGSFTI FAPSNEAWAS LPAEVLDSL SVNVIELLNA LRYHVMGRRV 180
LTDELKHGMT LTSMYQNSNI QIHHPNGIV TVNCARLLKA DHHATNGVVH LIDKVISITIT 240
NNIQQIIIEIE DTFETLRAAV AASGLNTMLE GNGQYTLAP TNEAFEKIPS ETNLNRLGDP 300
40    EALRDLNNH ILKSAMCAEA IVAGLSVETL EGTTELVGCS GDMLTINGKA IISNKDILAT 360
      NGVIHYIDEL LIPDSAKTLF ELAASDVST AIDLFRQAGL GNHLSGSERL TLLAPLNSVF 420
      KDGTTPPIDAH TRNLLRNHII KDQLASKYLY HGQTLETGG KKLRFVYVRN SLCIENSCIA 480
      AHDKRGRYGT LFTMDRVLTP PMGTVMVLK GDNRFMSLVA AIQSAGLTET LNREGVYTVF 540
      APTNEAFRAL PPRERSRLG DAKELANILK YHIGDEILVS GGIGALVRLK SLQGDKLEVS 600
45    LKNVSVSNK EPVAEPDIMA TNGVVHVITN VLQPPANRPQ ERGDELADSA LEIFKQASAF 660
      SRASQSRVRL APVYQKLLER MKH 683

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Seq ID NO: C294 Protein Sequence
Protein Accession #: NP_006527.1

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50      1      11      21      31      41      51
      |      |      |      |      |      |
MTQRSIAGPI CNLKFVTLV ALSELPLFG AGVQLQDNGY NGLLIAINPQ VPENQNLISS 60
IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGHA 120
GDDPYTLQYR GCGKEGYIY FTFNELLNDN LTAGYGSRRG VFVHEWAHLR WGVFDEYNND 180
55    KPFFYINGQK IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240
      MFMQSLSSVV EFCNASTHNO EAPNLQNMCM SLRSADWDVIT DSADFHSFPP MNGTELPPPP 300
      TFSLVQAGDK VVCLVLVDSS KMAEADRLQ LQQAAEFYLM QIVEIHTFVG IASFDSKGEI 360
      RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGF EVVEKLNGKA YGSVMILVTS 420
      GDDKLLGNCL PTVLSSSGSTI HSIALGSSAA PNLEELSRIT GGLKFFVPDI SNSNSMIDAF 480
60    SRISSTGDI FQHQHILEST GENVKPHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL 540
      FDPDGRKYIT NNFITNLTFR TASLWIPGTA KPGHWYTYLN NTHHSLQALK VTVTSRASNS 600
      AVPPATVEAF VERDSLHFPF PVMIYANVKQ GFYPIILNATV TATVEPETGD PVTLRLLDDG 660
      AGADVINKNDG IYSRYFFSFA ANGRYSKLVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN 720
      IQMNAPRKSV GRNEEERKNG FSRVSSGGSF SVLGVPAGPH PDVFPCKII DLEAVKVEEE 780
65    LTLSTWAPGE DFDQCATSY EIRMSKSLQN IQDDFNAIL VNTSKRNPQQ AGIREIFTFS 840
      PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
      LILKGLTAM GLIGIICILV VVTHHTLSRK KRADKENGIT KLL 943

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Seq ID NO: C295 Protein Sequence
Protein Accession #: Eos sequence

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75      1      11      21      31      41      51
      |      |      |      |      |      |
MKFLLILLIQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHFF REMPGGPVWR KHYITYRINN 120
YTPDMNREDV DYAIRKAFQV WSNVTPFKFS KINTGMADIL VVFARGAHD FHAFDGKGGI 180
LAHAFPGSGG IGGDAHFEDD EFWTTHSGGT NLFLTAVHEI GHSGLGLGHS DPKAVMFPTY 240
80    KVVDTINTFRL SADDIRGIQS LYGDPEKQNR LPNPDNSEPA LCDPNLSFDA VTTVGKNIFF 300
      FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360
      EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420
      NFQIGIPKID AVFYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC 470

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Seq ID NO: C296 Protein Sequence
Protein Accession #: Eos sequence

Seq ID NO: C297 Protein Sequence
Protein Accession #: NP_008883.1

Seq ID NO: C298 Protein Sequence
Protein Accession #: NP_001784.2

Seq ID NO: C299 Protein Sequence
Protein Accession #: NP_005620.1

Seq ID NO: C300 Protein Sequence
Protein Accession #: NP_006507.1

Seq ID NO: C301 Protein Sequence
Protein Accession #: XP_035292.2

1352

GNIVLALYSYGFAYGGWNYL NRVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
 STEQMLSSSEA VAVDFGNYHL GVMWSIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360
 SILSMIHPQL LTPVPSLVFT CVMITLLYAFS KDIFSVINFF SFFNWLSCVAL AIIGMIWLRH 420
 RKPELERPIK VNLALPVFFI LACFLIAVS FWKTFVECGI GFTIILSGLP VYFPGVWVKW 480
 KPKWLLQGIF STTVLCQKLM QVVPQET 507

Seq ID NO: C302 Protein Sequence
 Protein Accession #: NP_005259.1

1 11 21 31 41 51
 MNWSIFEGLL SGVKNYSTAF GRIWLSLVFI FRVLVYLVT A ERVWSDDHKD FDCNTRQPGC 60
 SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRRHREAHG ENSGRLYLNP 120
 GKKRGLLWWT YVCSLVFKAS VDIAPLYVFH SFYPKYLPP VVKCHADPCP NIVDCFISK 180
 SEKNIFTLFM VATAICILL NLVELIYLV KRCHECLAAR KAQAMCTGHH PHGTSSCKQ 240
 DLLSGDLIF LGSDSHPLL PDRPRDHVK TIL 273

Seq ID NO: C303 Protein Sequence
 Protein Accession #: NP_005121.1

1 11 21 31 41 51
 MKICSLTLLS FLLLAQVLL VEGKKVKNG LHSKVSEQK DTLGNTQIKQ KSRPGNKKGK 60
 VTKDQANCRW AATQEEGIS LKVECTQLDH EFSCVFAGNP TSCLKLKDER VYWKQVARNL 120
 RSQKDICRYS KTAVKTRVCR KDFPESSKL VSSTLFGNTK PRKEKTEMSP REHIKKGKETT 180
 PSSLAVTQTM ATKACEVED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC 234

Seq ID NO: C304 Protein Sequence
 Protein Accession #: AAH22542

1 11 21 31 41 51
 MCSEIILRQE VLKDGFRDL LIKVKFGESI EDLHTCRLLI KQDIPAGLYV DPYELASLRE 60
 RNITEAVMVS ENFDIEAPNY LSKSEVLIY ARRDSQCIDC FQAFLPVHCR YHRPHSEDEGE 120
 ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180
 WNKMKYKSVY KNVILQVPVG LTVHTSLVCS VTLITILCS KKKKK 225

Seq ID NO: C305 Protein Sequence
 Protein Accession #: NP_004985.1

1 11 21 31 41 51
 MSLWQPLVLV LVLGCCFAA PRQRQSTLVL FPGDLRTNLT DRQLAEEYLY RYGYTRVAEM 60
 RGEKSLGPA LLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLGRFQTF EGDLLKWHHN 120
 ITYWTQNYSE DLPRVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP 180
 FDGKDGLLAH AFPPGPGIQQ DAHFDDDELW SLGKGVVVPT RFGNADGAAC HPPFIFEGRS 240
 YSACTDGRS DGLPWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGQSYS 300
 ACTTDGRSDG YRWCAATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST 360
 CTSEGRGDRG LWCATSNFD SDDKMGFCPD QGYSLELVAA HEFGHALGLD HSSVPEALMY 420
 PMYRFTEGPP LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSER 480
 PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIABIGNQ LYLFPKDGKYW 540
 RFSEGRGSRP QGPFLIADKV PALPRKLDV FEEPLSKLF FFSGRQVWVY TGASVLGPRR 600
 LDKLGLGADV AQVTGALRSR GKMMLFSGR RLWRFDVKAQ MVDPRSASEV DRMPFGVPLD 660
 THDVQYREK AYFCQDRFYW RVSSRSELNQ VDQGVGVTYD ILQCPED 707

Seq ID NO: C306 Protein Sequence
 Protein Accession #: NP_000204

1 11 21 31 41 51
 MAGPRPSPWA RLLAALISV SLSGTLANRC KKAPVKSCTE CVRVDKDCAY CTDEMFRDRR 60
 CNTQAELLA GCQRESIVM ESSFQITEET QIDTTLRSQ MSPQGLRVRL RPGEERHFEL 120
 EVFEPLESPV DLYILMDFSN SMSDDLNLK KMGQNLARVL SOLTSDYTIG FGKFDVKVSV 180
 PQTDMRPEKL KEPWNSDDP FSFKNVISLT EDVDEFNKL QGERISGNLD APEGGFDAI 240
 QTAVCTRDIG WRPDSTHLLV FSTESAFHYE ADGANVLAGE MSRNDERCHL DTTGTYTQYR 300
 TQDYPVSPTL VRLAKHNII PIPAVTNYSY SYEKLHTYF PVSSLGVLQE DSSNIVELLE 360
 EAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGVGIYQV QLRALHVDG 420
 THVCQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480
 CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYEGR YEGQFCEYDN 540
 FQCPRTSGFL CNDRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR 600
 CHCHQQSLYT DTICEINYS IHPGLCEDLR SCVQCQAWGT GEKKGRTCEE CNFKVMKMD 660
 LKRAEEVVVR CSFRDEDDDC TYSYTMEDGD APGPNSTVLV HKKCDPPGS FWLIPLLL 720
 LLEPLLALLL LCWKYCACCK ACLALLPCCN RGHMVGFKEH HYMLRENMA SDHLDTPMLR 780
 SGNLKGDRDV RWKVNTNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTR 840
 AQLRQVEEEN LNEVYRQISG VHLQQTQKFR QQPAGKKQD HTIVDTVLMA PRSAKPALLK 900
 LTEKQVEQRA FHDLVKAPGY YTLTADQDAR GMVEFQEGVE LVDVRVPLFI RPEDDDEKQL 960
 LVEAIDVPAG TATLGRRLVN ITIIEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020
 KSQVSVRTQD GTAGQNRDYI PVEGELFQD GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080
 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGDLAGP QNPNAKAAGS 1140
 RKTHFNWLP SGKPMGYRVK YWIQGDSESE AHLSDSKVPS VELTNLYPYC DYEMKVCAYG 1200
 AQGEGPYSSL VSCRTHQVY SEPGRFAFNV VSSTVTQLSW AEPATNGEI TAYEVCYGLV 1260
 NDDNRPIGPM KKVLDNPKN RMLLIENLRE SQPYRYTVKA RAGAGWGPFR EAIINLATQP 1320
 KRPMSPPIIP DIPIDVDAQS EDYDSFLMYS DDVLRSPSGS QRPSVSDDTG CGWKFEPLLG 1380
 EEDLDRRTW RLPELIPRL SASSGRSSDA EAPTAPRTTA ARAGRAAVP RSATPGPPGE 1440

HLVNGRMDFA FPGSTNSLHR MTTTSAAAYG THLSPHVPHR VLSTSSSTLTR DYNLSLRSEH 1500
 SHSTTLPRDY STLTSSVSSHD SRLTAGVPDT PTRLVFSALG PTSLRVSWQE PRCEPLQGY 1560
 SVEYQQLNGG ELHRNINPNP AQTSSVVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES 1620
 QVHPQSPCLP LFGSAFTLST PSAPGFLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCEM 1680
 AQGGGPFATF RVDGDSPESE LTVPGLSNV PYKFKVQART TEGFGPEREG IITIESQDGG 1740
 PFPQLGSRAG LFQHPQLQSEY SSITTTHTSA TEPFLVDGLT LGAQHLEAGG SLTRHVTQEF 1800
 VSRITLTSGT LSTHMDQQFF QT 1822

Seq ID NO: C307 Protein Sequence
 Protein Accession #: NP_076404.1

1 11 21 31 41 51
 MGFNLTAKL PNNELHGQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
 GLAVWIFFHI RNKTSFIFYL KNIVVADLIM TLTFFPRIVH DAGFGPWYFK FILCRYTSVL 120
 FYANMYTSIV FLGLISIDRY LKVVKFFGDS RMYSTFTTKV LSVCVWVIMA VLSLPNIILT 180
 NGQPTEDNIH DCSKLKSPLG VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRRKRKH NQSIRVVAV FETCFLPYHL CRIPFTFSLH DRLLESAQK ILYYCKEITL 300
 FLSACNVCLD PIIFYMCRS FSRRLFKSN ITRSESIRS LQSVRRSEVR IYYDYTDV 358

Seq ID NO: C308 Protein Sequence
 Protein Accession #: NP_065840.1

1 11 21 31 41 51
 MVWCLGLAVL SLVISQGDG RGKPEVSVV GRAEESVVLG CDLLPPAGRP PLHVIEWLRF 60
 GFLLPIFIQF GLYSRIDPD YVGRVRLQKG ASLQIEGLRV EDQGWYECRV FFLDQHIPED 120
 DFANGSWHL TNSPPQPE TTPPAVLEVE LEPVTLRCVA RGSPLPHVTW KLRGKDLGQG 180
 QQQVQVQNT LRIRVERGES SGVYTCQASS TEGSATHATQ LVLVGPVIV VPPKNSTVNA 240
 SQDVSLACHA EAYPANLTS WFQDNINVFH ISRLQPRVQI LVDGSLRLA TQPDAGCYT 300
 CVPSNGLLHP PSASAYLTVL CMPGVIRCPV RANPPLLFVS WTKDGKALQL DKFPQWSQGT 360
 EGSLLIALGN EDALGEYST PYNSLGTAGP SPVTRVLLKA PPAFIERPKE EYFQEVGREL 420
 LIPCSAQGD PPVVSMTKV RGLQQAQVD SNSSLILRPL TKEAHGHWEK SASNAVARVA 480
 TSTNVVVLGT SPHVVTNVSV VALPKGANVS WEPGFDGGYL QRFVSVYTP LAKRPMRHHH 540
 WVSLAVPVA AHLLVFGLPQ HTQYQFSVLA QNKLGSPPFS EIVLSAPEGL PTPAAPGLP 600
 PTEIPPLSP PRGLVAVRT RGVLHWDPP ELVPKRLDGY VLEGRQGSQG WEVLDPVAVG 660
 TETELLVPLG IKDVLVEFRL VAFAGSFVSD PSNTANVST GLEVYPSRTQ LPGLLPQVPL 720
 AGVVGVCFL GVAVLVSLA GCLLNRRRAA RRRRKRLRQD PPLIFSETGK SAAPSALGSG 780
 SPDSVAKLKL QGSPVPSLRQ SLLWGDPAQT PSPHPDPPSS RGPLPLEPIC RGPDRFVVG 840
 PTVAAPQERS GREQAEPRTP AQRLARSFDC SSSSPSGAPQ PLCIEDISPV APPPAAPPSP 900
 LFGPGPLQY LSLPFFREM VDGWPFLEE PSPAAPDDY DTRRCPTSSF LRSPETPPVS 960
 PRESLEPAVV GAGATAEPY TALADWTLRE RLLPGLLPAA PRGSLTSQSS GRGSASFRLP 1020
 PSTAPSAGGS YLSPAPGDT SWAGSPERP RREHVTVSK RRNTSVDENY EWDSEFPDGM 1080
 ELLETLLHGL ASSRLRPEAE TELGKTPPEE GCLLNTAHVT GPEARCAALR EEFLAFRRRR 1140
 DATRARLPAY RQPVHPEQA TLL 1163

Seq ID NO: C309 Protein Sequence
 Protein Accession #:

1 11 21 31 41 51
 MLTKPLQGGP APFGTPTPPP GKKDREAFEA EYRLGPLLGK GFGTVFAGH RLTDRLQVAI 60
 KVIPRNRVLG WSPLSDSVTC PLEVALLWKV GAGGGHPGVI RLLDWFETQE GFMLVLERPL 120
 PAQDLFDYIT EKGPLGEGPS RCFFGQVVA IQHCHSRGVV HRDIKENIL IDLRRCACKL 180
 IDFGSGALLH DEPYTDFDGT RVYSPPewis RHQYHALPAT VWSLGILLYD MFCGDIPIFER 240
 DQEILEAELH FPAHVSPDCC ALIRRCCLAPK PSSRPSLEEI LDLPWMQTPA EDVTPQPTQR 300
 RCPFPGLVIA TISLAWFGLA PNGQKSHMA MSQG 334

Seq ID NO: C310 Protein Sequence
 Protein Accession #: NP_002501.1

1 11 21 31 41 51
 MECLYYFLGF LLLAARLPLD AAKRFHDVLG NERPSAYMRE HNQLNGWSSD ENDWNEKLYP 60
 VWKRGDMRWK NSWKGGRVQA VLTSDSPALV GSNITFAVNL IFPRCQKEDA NGNIVYEKNC 120
 RNEAGLSADP YVYNWTAWSE DSDGENGTOG SHHNVFPDGG PFPHPGWRR WNFIVVFHTL 180
 GQYFQKLGRG SVRVSVNTAN VTLGPQLMEV TVYRRHGRAY VPVIAQVKDV VVTDIQIPV 240
 TMFQKNDNRN SDETFLKDLF IMFVLIHDP SHFLNYSTIN YKWSFGDNTG LRVSTNHTVN 300
 HTYVNLGTFS LNLTVKAAAP GPCPPPPPPP RPSKPTPSLG PAGDNPLELS RIPDENCQIN 360
 RYGHFQATIT IVEGILEVNI IQMTDVLMPV WPPESSLIDE VVTCQGSIPT EVCTIISDPT 420
 CEITQNTVCS PVDVDEMCLL TVRRTFNGSG TYCVNLTLGD DTSALTSTL ISVPDRDPAS 480
 PLRMANSALI SVGCLAIFVT VISLLVYKHH KEYNPNIENSP GNVVRSKGLS VFLNRAKAVF 540
 FPGNQEKDPL LKNQEFKGV 560

Seq ID NO: C311 Protein Sequence
 Protein Accession #: Eos seq

1 11 21 31 41 51
 MRILKRLFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60
 QSPINIDEL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITFWH GKCNMSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KKGKGLRLAS 180
 ILFEVGTEN LDFKALIDGV ESVSFRGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300

	TGKEEIH	EA	CSSE	EN	VQ	DPEN	YTS	LLV	TWER	PR	VVD	TMIE	KFAV	LY	QQLD	GED	QTK	360
	HEFL	TD	GY	QD	LGAI	LN	LLP	NMSY	VL	QIVA	ICTN	GLY	GKY	SDQL	IV	DM	PT	420
	LIGT	EE	IIKE	EEEG	KD	IEEG	AI	VN	PG	RDSA	TN	QIRK	KEPQ	ISTT	TH	YNR	GT	480
5	RSPT	RG	SEFS	GKGD	V	PNTSL	NST	SQ	PV	TKL	ATEK	DIS	LTS	QTV	TEL	PPHT	VEGT	540
	GSKT	VL	RS	SPH	MNLS	GTAE	SL	NTV	S	ITEYEE	ESLL	TS	FKLD	TGA	ED	SSG	SS	600
	ENIS	QGY	I	F	SEN	PET	ITYD	VL	IP	ESAR	NA	SED	ST	SSG	SE	ESL	KD	660
	TAQP	DV	G	SGR	ESFL	Q	TNYTE	IR	V	DESE	KTT	KSFS	AG	PVMS	QGPS	V	TD	720
	TEVT	PH	AFT	P	SSRQ	Q	DLVST	VNV	V	YSQT	TQ	PV	Y	NEAS	NS	HES	R	780
10	LVIV	S	AL	TFI	CLV	V	LGILI	YWR	K	C	FQTAH	F	Y	LED	S	TSP	P	840
	IKHF	PK	H	VAD	LH	SSG	FTEE	FEE	V	Q	SCTVD	LG	I	T	A	D	SS	900
	KLAQ	LA	E	KD	G	KL	T	D	Y	I	N	A	N	A	N	A	N	960
	NL	VE	K	R	R	K	C	D	Q	Y	P	A	D	G	S	E	Y	1020
	GR	V	T	Q	Y	H	Y	T	Q	W	P	D	M	G	V	E	Y	1080
15	SML	Q	Q	I	Q	H	E	G	T	V	N	I	F	G	L	K	H	1140
	YV	N	A	L	I	P	G	P	A	G	K	T	K	E	K	Q	F	1200
	SS	L	S	G	E	G	T	D	Y	I	N	A	S	Y	I	M	G	1260
	A	E	D	E	F	V	W	P	N	K	D	E	F	I	N	C	E	1320
	CP	K	W	N	P	D	S	P	I	S	K	T	F	E	L	I	S	1380
20	SVD	V	Y	Q	V	A	K	M	I	N	L	M	R	P	G	V	F	1440
	A	E	S	L	E	S	L	V										1448

Seq ID NO: C312 Protein Sequence
Protein Accession #: XP_031379

25	1	11	21	31	41	51		
	MRIL	KR	FLAC	IQLL	CV	CRLD	WANG	YYRQQR
	QSPIN	IDE	DL	TQVN	VN	LKKL	KFGQ	GW
30	FKAS	KIT	FWH	GKCN	M	SSDGS	EHS	LEGQKFP
	ILFE	V	GTEEN	LDFK	A	I	D	GV
	TDT	V	D	W	I	V	F	K
	TGKE	E	I	H	E	A	V	
	HEFL	TD	GY	QD	LGAI	LN	LLP	NMSY
35	LIGT	EE	IIKE	EEEG	KD	IEEG	AI	VN
	RSPT	RG	SEFS	GKGD	V	PNTSL	NST	SQ
	GSKT	VL	RS	SPH	MNLS	GTAE	SL	NTV
	ENIS	QGY	I	F	SEN	PET	ITYD	VL
	TAQP	DV	G	SGR	ESFL	Q	TNYTE	IR
40	TEVT	PH	AFT	P	SSRQ	Q	DLVST	VNV
	LNTT	P	A	ASS	S	A	L	H
	ILP	Q	V	T	S	A	T	E
	K	T	L	M	F	S	Q	V
	S	L	F	S	G	P	S	H
45	P	V	S	V	A	E	F	T
	L	N	A	S	L	Q	E	T
	K	P	V	L	S	A	N	S
	A	V	P	S	D	I	L	V
	T	I	S	Y	A	S	E	K
50	E	P	L	N	T	L	I	N
	P	H	R	D	S	V	T	S
	K	C	M	S	C	S	S	Y
	S	P	G	K	S	P	S	A
	E	N	E	T	S	T	D	F
55	H	E	S	R	I	G	L	A
	V	I	S	T	P	T	P	I
	T	A	D	S	S	N	H	P
	Q	G	P	L	K	S	T	A
	V	L	A	Y	T	V	R	N
60	A	K	R	H	A	V	P	V
	Q	Y	V	I	H	D	T	L
	S	A	A	L	K	Q	C	N
	H	E	I	K	D	F	W	R
	N	E	E	K	L	I	I	Q
65	V	H	D	E	H	G	V	T
	S	L	V	S	T	R	Q	E

Seq ID NO: C313 Protein Sequence
Protein Accession #: NP_002842

70	1	11	21	31	41	51		
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	QSPIN	IDE	DL	TQVN	VN	LKKL	KFGQ	GW
75	FKAS	KIT	FWH	GKCN	M	SSDGS	EHS	LEGQKFP
	ILFE	V	GTEEN	LDFK	A	I	D	GV
	TDT	V	D	W	I	V	F	K
	TGKE	E	I	H	E	A	V	
	HEFL	TD	GY	QD	LGAI	LN	LLP	NMSY
80	LIGT	EE	IIKE	EEEG	KD	IEEG	AI	VN
	RSPT	RG	SEFS	GKGD	V	PNTSL	NST	SQ
	GSKT	VL	RS	SPH	MNLS	GTAE	SL	NTV
	ENIS	QGY	I	F	SEN	PET	ITYD	VL
	TAQP	DV	G	SGR	ESFL	Q	TNYTE	IR
	TEVT	PH	AFT	P	SSRQ	Q	DLVST	VNV

PLVIVSALTFL ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840
 PIKHFPHKVA DLHASSGFTE EFETLKEFYQ EVQSCITVDLG ITADSSNHPD NKHKRYINI 900
 VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960
 VEVIVMITNL VEKGRRKCDQ YWPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020
 GSQKGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080
 GTYIVLDSM LQQIQHEGTV NIFGFLKHIR SQRYLVQTE EQYVFIHDTL VEAILSKETE 1140
 VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200
 VERSRVGISS LSGEGTDYIN ASYIMGYYSQ NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
 MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320
 VLEVRHFQCP KWNPNPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTT 1380
 MHQLEKENSVDVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
 AALPDGNIAE SLESVL 1456

Seq ID NO: C314 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60
 QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 MVFKASKITF HWGKCNMSSD GSEHSLGQK FPLEMQIYCF DADRFSSEFE AVKGKGLRA 180
 LSILFEVGT EENLDFKAIID GVESVSRFGK QAALDPFILL NLLFNSTDKY YIYNGSLTSP 240
 PCTDTDWIVF KDTVSISESQ LAVFCEVLTM QSGYVMLMD YLQNNFREQQ YKFSRQVFSS 300
 YTGKEEIHAE VCSSEPENVO ADPENYTSLL VTWERPRVYV DTMIEKFAVL YQQLDGEDQT 360
 KHEFLTIDGY DLGAILNNLL PNMSYVLQIV AICTNGLYK YSDQLIVDMP TDNPELDLFP 420
 ELIGTEEIIK EEEEGKDIEE GAIVNPRGRS ATNQIRKKEP QISTTHYNR IGTKYNEAKT 480
 NRSPTRGSEF SGKGDVNTS LNSTSQPVTK LATEKDISLT SQTVTELPHP TVEGTSASLN 540
 DSGKTVLRSP HMNLSGTAES LNTVSITEYE EESLLTSFKL DTGAEDSSGS SPATSAIPFI 600
 SENISQGIYF SSNPETITY DVLIPESARN ASEDSTSSGS EESLKDPSME GNVWFPSSD 660
 ITAQPDVGS GRESFLQNTY EIRVDESEKT TKSFSAGPVM SQGPSVTDLE MPHYSTFAYF 720
 PTEVTPHAPT PSSRQQLVST TVNVVYSQTT QPVYNEASNS SHESRIGLAE GLESEKKAVI 780
 PLVIVSALTFL ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840
 PIKHFPHKVA DLHASSGFTE EFETLKEFYQ EVQSCITVDLG ITADSSNHPD NKHKRYINI 900
 VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960
 VEVIVMITNL VEKGRRKCDQ YWPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020
 GSQKGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080
 GTYIVLDSM LQQIQHEGTV NIFGFLKHIR SQRYLVQTE EQYVFIHDTL VEAILSKETE 1140
 VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200
 VERSRVGISS LSGEGTDYIN ASYIMGYYSQ NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
 MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320
 VLEVRHFQCP KWNPNPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTT 1380
 MHQLEKENSVDVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
 AALPDGNIAE SLESVL 1456

Seq ID NO: C315 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60
 QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITPHW GKCNMSSDGS EHSLEQKFP LEMQIYCFDA DRFSSEFEAV KGKGLRALS 180
 ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
 TDTVDWIVF KDTVSISESQ LAVFCEVLTM QSGYVMLMDY LQNNFREQQY KFSRQVFSS 300
 TGKEEIHAEV CSSEPENVO ADPENYTSLL TWERPRVYV TMIEKFAVL YQQLDGEDQT 360
 HEFLTIDGYD LGAILNNLLP NMSYVLQIVA ICTNGLYK YSDQLIVDMP TDNPELDLFP 420
 LIGTEEIIKE EEEEGKDIEE GAIVNPRGRS ATNQIRKKEP QISTTHYNR IGTKYNEAKT 480
 RSPTRGSEFS KGDVNPVTSL NSTSQPVTKL ATEKDISLTS SQTVTELPHP TVEGTSASLN 540
 GSKTVLRSPH MNLSGTAESE LNTVSITEYE EESLLTSFKL DTGAEDSSGS SPATSAIPFI 600
 ENISQGIYF SSNPETITY DVLIPESARN SEDSTSSGSE ESLKDPSMEG NNVWFPSSDI 660
 TAQPDVGSGR ESFLQNTYTE IRVDESEKT TKSFSAGPVM SQGPSVTDLE MPHYSTFAYF 720
 TEVTPHAPT SSRQQLVST TVNVVYSQTT QPVYNEASNS SHESRIGLAE GLESEKKAVI 780
 LVIVSALTFL ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840
 IKHFPHKVA DLHASSGFTE EFETLKEFYQ EVQSCITVDLG ITADSSNHPD NKHKRYINI 900
 AYDHSRVKLA QLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960
 EVIVMITNLV EKGRRKCDQ YWPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020
 SQKGRPSGRV VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080
 GTYIVLDSM LQQIQHEGTV NIFGFLKHIR SQRYLVQTE EQYVFIHDTL VEAILSKETE 1140
 LDSDHIHAYV NALLIPGPAG KTKLEKQFQL TSPRLCECRG TISAHCNLPL PGLTDPPTSA 1200
 SRVAGTILLS QSNIQQSDYS AALKQCNR NRTSSIIPVE RSRVGISSLS GEGTDYINAS 1260
 YIMGYYSQNE FIITQHPLH TIKDFWRMIW DHNAQLVVM PDGQNMADFE FVYWPNDKDEP 1320
 INCESFKVTL MAEEHKCLSN EEEKLIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPIST 1380
 FELISVIKEE AANRDGPMIV HDEHGGVTAG TFCALTTLMH QLEKENSVDV YQVAKMINLM 1440
 RGVVFADIEQ YQFLYKVI LSGVTRQENP STSLDSNGAA LPDGNIAESL ESLV 1494

Seq ID NO: C316 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITPHW GKCNMSSDGS EHSLEQKFP LEMQIYCFDA DRFSSEFEAV KGKGLRALS 180
 ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240

TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300
 TGKEEIHAEV CSSEPENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360
 HEFLTGDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPEASNSH 420
 ESRIGLAEGE ESEKKAVIPL VIVSALTFIC LVVLVGLIY WRKCFQTAHF YLEDSTSPRV 480
 ISTPPTPIFP ISDDVGAIPK KHFPKHVADL HASSGFTEEF ETLKEFYQEV QSCITVDLGIT 540
 ADSSNHPDNK HKNRYINIVA YDHSRVKLAQ LAEKDGKLT D YINANYVDGY NRPKAYIAA 600
 GPLKSTAEDF WRMIWEHNV VIVMITNLVE KGRRKCDQYW PADGSEEGN FLVTQKSVQV 660
 LAYYTVRNFN LRNTKIKKGS QKGRPSGRV V TQYHYTQWPD MGVPYSLPV LTFVRKAAYA 720
 KRHAVGPPVV HCSAGVGRTG TYIVLDSMLQ QIQHEGTVNI FGFLKHRSQ RNYLVQTEEQ 780
 YVFIHDTLVE AILSKETEVL DSHIHAYVNA LLIPGPAGKT KLEKQFQLS QSNIQQSDYS 840
 AALKQCNREK NRTSSIIPEV RSRVGISSLS GEGTDYINAS YIMGYQSN FIIITQHPLH 900
 TIKDFWRMIW DHNAQLVVM I PDGQNMMAEDE FVYWPKNDEP INCESFKVTL MAEEHKCLSN 960
 EEKLIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISKT FELISVIKEE AANRDGPMIV 1020
 HDEHGGVTAG TFCALTLMH QLEKENSVDV YQVAKMINLM RGVFADIEQ YQFLYKVILS 1080
 LVSTRQEENP STSLDSNGAA LPDGNIAESL ESL 1113

Seq ID NO: C317 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60
 QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITFWH GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAAV KGKGLRLALS 180
 ILFEVGTEN LDFKAIIDGV ESVSFRFGKA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300
 TGKEEIHAEV CSSEPENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360
 HEFLTGDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE 420
 LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
 RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540
 GSKTVLRSPH MNLSTGAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
 ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSTDI 660
 TAQPDVSGSR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
 TEVTPHAFIP SSRQDVLVST VNVVYSQTTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780
 LVIVSALTFI CLVVLVGLI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840
 IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCITVDLGI TADSSNHPDN KHKNRYINIV 900
 AHDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAED FWRMIWEHNV 960
 EVIVMITNLV EKGRRKCDQY WPAADGSEEGY NFLVTQKSVQ VLAYYTVRNF TLRNTKIKKG 1020
 SQKGRPSGRV TQYHYTQWP DMGVPEYSLP VLTFRVKAAY AKRHAVGPPV VHCAGVGRT 1080
 GTYIVLDSML QIQHEGTVN IFGFLKHRS QRYLVQTEE QYVFIHDTLV EAILSKEDEV 1140
 LDSSHAYVN ALLIPGPAGK TKLEKQFQLS TLSPRLCEG TISAHCNLP LGLTDPPTSA 1200
 SRVARTILLS QSNIQQSDYS AALKQCNREK NRTSSIIPEV RSRVGISSLS GEGTDYINAS 1260
 YIMGYQSN FIIITQHPLH TIKDFWRMIW DHNAQLVVM I PDGQNMMAEDE FVYWPKNDEP 1320
 INCESFKVTL MAEEHKCLSN EEKLIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISKT 1380
 FELISVIKEE AANRDGPMIV HDEHGGVTAG TFCALTLMH QLEKENSVDV YQVAKMINLM 1440
 RGVFADIEQ YQFLYKVILS LVSTRQEENP STSLDSNGAA LPDGNIAESL ESL 1493

Seq ID NO: C318 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60
 QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITFWH GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAAV KGKGLRLALS 180
 ILFEVGTEN LDFKAIIDGV ESVSFRFGKA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300
 TGKEEIHAEV CSSEPENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360
 HEFLTGDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE 420
 LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
 RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540
 GSKTVLRSPH MNLSTGAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
 ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSTDI 660
 TAQPDVSGSR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
 TEVTPHAFIP SSRQDVLVST VNVVYSQTTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780
 LVIVSALTFI CLVVLVGLI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840
 IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCITVDLGI TADSSNHPDN KHKNRYINIV 900
 AHDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAED FWRMIWEHNV 960
 EVIVMITNLV EKGRRKCDQY WPAADGSEEGY NFLVTQKSVQ VLAYYTVRNF TLRNTKIKKG 1020
 SQKGRPSGRV TQYHYTQWP DMGVPEYSLP VLTFRVKAAY AKRHAVGPPV VHCAGVGRT 1080
 GTYIVLDSML QIQHEGTVN IFGFLKHRS QRYLVQTEE QYVFIHDTLV EAILSKEDEV 1140
 LDSSHAYVN ALLIPGPAGK TKLEKQFQLS QSNIQQSDY SAALKQCNRE KNRTSSIIPEV 1200
 ERSRVGISSL SGEGETDYINA SYIMGYQSN EFIITQHPLH HTIKDFWRMI WDHNAQLVVM 1260
 IPDQNMMAED EFVYWPKNDE PINCESFKVT LMAEEHKCLS NEEKLIQDFI LEATQAWRS 1320
 DGRNFLCSDN PYAPTRKRKF RGCLPGSQDD QSDEARSLC 1359

Seq ID NO: C319 Protein Sequence
 Protein Accession #: XP_002914.4

1 11 21 31 41 51
 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRF TRPLECQDAL ETAARAEGLS 60
 LDASMSQLR ILDEHPKPK YHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSLAR 120
 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQBELNEV GPDAASLRRV VWIFCRTRLI 180

LSIVCLMITQ LAGFSGPAPM VKHLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW 240
ALNYRTGVRL RGAILTMAFK KILKLNKIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300
PVVAILGMIY NVIILGPTGF LGSASFILFY PAMMFASRLT AYFRKRCVAA TDERVQKMNE 360
5 VLTYYIKFIK YAWVKAFSPS VQKIREEERR ILEKAGYFQS ITVGVAPIVV VIASVVTFSV 420
HMTLGFDLTA AQAFVTVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEVEHMIK 480
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTHEQA 540
VLAQKQGHLL LDSDERPSPE EEEKGHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVSGG 600
KTSLSAISLG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660
10 CCLRPDLAIL PSSDLTEIGE RGANLSSGQR QRISLARALY SDRSIYILDD PLSALDAHVG 720
NHIFNSAIRK HLKSKTVLFV THQLQYLVDV DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780
FNNLLLGGETP PVEINSKKT SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKQGS 840
VPWSVYGVYI QAAGGPLAFV VIMALFMLNV GSTAFSTWWL SYWIKQSGN TTVTRGNETS 900
VSDSMKDNPH MQYYASIAL SMAMVILKA IRGVVFKGT LRASSRLHDE LFRRLRSPM 960
15 KFFDTTPTGR ILNRFSDMD EVDVRLPFQA EMFIQNVILV FFCVGMIAV FPWFLVAVGP 1020
LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFHLRYQEL 1080
LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
GLFOFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDPQE GEVTFENAEM 1200
RYRENLPVLV KKVSTFIKPK EKIGIVGRTG SGKSSLGMAF FRLVELSGG IKIDGVRISD 1260
20 IGLADLRSLK SIIPQEPVLF SGTVRSLNDP FNQYTEDQIW DALERTHME CIAQLPLKLE 1320
SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIIQE TIREAFADCT 1380
MLTIAHRLHT VLGSDRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG 1437

Seq ID NO: C320 Protein Sequence
Protein Accession #: NP_005679.1

1 11 21 31 41 51
MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFR TRPLECQDAL ETAARAEGLS 60
LDASMHSQRL IDDEEHPKKG YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSLAR 120
30 VAHKGELSM EDVWSLSKHE SSDVNCRRLE RLWQELNEV GPDAASLRV VWIFCRTL 180
LSIVCLMITQ LAGFSGPAPM VKHLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW 240
ALNYRTGVRL RGAILTMAFK KILKLNKIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300
PVVAILGMIY NVIILGPTGF LGSASFILFY PAMMFASRLT AYFRKRCVAA TDERVQKMNE 360
5 VLTYYIKFIK YAWVKAFSPS VQKIREEERR ILEKAGYFQS ITVGVAPIVV VIASVVTFSV 420
HMTLGFDLTA AQAFVTVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEVEHMIK 480
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTHEQA 540
VLAQKQGHLL LDSDERPSPE EEEKGHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVSGG 600
KTSLSAISLG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660
10 CCLRPDLAIL PSSDLTEIGE RGANLSSGQR QRISLARALY SDRSIYILDD PLSALDAHVG 720
NHIFNSAIRK HLKSKTVLFV THQLQYLVDV DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780
FNNLLLGGETP PVEINSKKT SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKQGS 840
VPWSVYGVYI QAAGGPLAFV VIMALFMLNV GSTAFSTWWL SYWIKQSGN TTVTRGNETS 900
VSDSMKDNPH MQYYASIAL SMAMVILKA IRGVVFKGT LRASSRLHDE LFRRLRSPM 960
15 KFFDTTPTGR ILNRFSDMD EVDVRLPFQA EMFIQNVILV FFCVGMIAV FPWFLVAVGP 1020
LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFHLRYQEL 1080
LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
GLFOFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDPQE GEVTFENAEM 1200
RYRENLPVLV KKVSTFIKPK EKIGIVGRTG SGKSSLGMAF FRLVELSGG IKIDGVRISD 1260
20 IGLADLRSLK SIIPQEPVLF SGTVRSLNDP FNQYTEDQIW DALERTHME CIAQLPLKLE 1320
SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIIQE TIREAFADCT 1380
MLTIAHRLHT VLGSDRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG 1437

Seq ID NO: C321 Protein Sequence
Protein Accession #: NP_005553.1

1 11 21 31 41 51
MPALWLGCCF CFSLLPAAR ATSRREVCDG NGKSRQCIFD RELHRTQNG FRCILNCNDNT 60
DGIHCEKCKN GFYRHRERDR CLPCNCSKG SLSARCDNSG RCSCKPGVTG ARCDRLCPGF 120
60 HMLTDAGCTQ DQRLDSDKCD CDPAAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDGDN 180
PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQVDVGWKA VQRNGSPAKL QWSQRHQDVF 240
SSAQRLDPVY FVAPAKFLGN QQVSYGQSL SFDYRVDGRG HPSAHDVILE GAGLRITAPL 300
MPLGKTLPG LTKTYTFRILN EHPNNWSEF LSYPEYRRL RNLTLALIRA TYGEYSTGYI 360
65 DNVTLISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLGPF GTICPCNCQG 420
GGACDPDTGD CYSGDENPDI ECADCPIGFY NDPHDPRSC PCPCNHGFSV SVMPETEEVV 480
CNNCPFGVTG ARCELCAADY GDDPFGEHGP VRPCQPCQN NNVDPSASGN CDRLTGRCCLK 540
CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCPMGS EPVGCSDGT CVCKPGFGGP 600
NCEHGAFSCP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVDPDELE GRMQQAEQAL 660
70 QDILRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLDDLKM TVERVRLGS QYQNRVRDTH 720
RLITQMLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR 780
ETEDYSKQAL SLVRKALHEG VSGSGSPDG AVVQGLVEKL ETKSLAQQL TREATQAEIE 840
ADRSVQHSIR LLDVSRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNLG 900
NWKBEAQQLL EMKSGREKS DQLSRANLA KSRAQALSM GNATFYEVES ILKNLREFDL 960
75 QVDNRKAEAE EAMKRLSYIS QKVSDASDKT QQAERALGSA ADAQRAKNG AGEALEISSE 1020
IQEIGSLNL EAVVTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE 1080
AQKVDTRAKN AGVTLQDTLN TLDGLHLMD QPLSVDEEGL VLEQKLSRA KTQINSQLRP 1140
MMSELEERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ 1193

Seq ID NO: C322 Protein Sequence
Protein Accession #: NP_066924.1

1 11 21 31 41 51
MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGE WMSCVSQSTG 60

QIQCKVFDLS LNLSTLQAT RALMVVGILL GVIAIFVATV GMKCMKCLED DEVQKMRMAV 120
 IGGAIFLLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCCLLGA 180
 LLCSCSRPKT TSYTPRPFPY KPAFSSGKDY V 211

5 Seq ID NO: C323 Protein Sequence
 Protein Accession #: AAM77876

10 1 11 21 31 41 51
 | | | | | |
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSTILSCSV AGDPVPNMYW DVGNLVSKHM 240
 15 NETSHTQGS L RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 WCIPTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

20 Seq ID NO: C324 Protein Sequence
 Protein Accession #: NP_006171.1

25 1 11 21 31 41 51
 | | | | | |
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSTILSCSV AGDPVPNMYW DVGNLVSKHM 240
 30 NETSHTQGS L RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 WCIPTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGPASV ISNDDDSASP 480
 35 LHHISNGSNT PSSSEGGPDA VIIGMTKIPV IENPQYFGIT NSQLKPDFTV QHIKRHNIVL 540
 KRELGEAGFG KVFLAECYNL CPEQDKILVA VKTLKDASN ARKDFHREAE LLTNLQHEHI 600
 VKFYGVCEVEG DPLIMVFEYM KHGDLNKLFLR AHGPDALVMA EGNPPTLTQ SQMLHIAQQI 660
 AAGMVVLASQ HFVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYRVG GHTMLPIRWM 720
 PPESIMYRKF TTESDVWSLG VVLWEIFTYG KQPWYQLSNN EVIECITQGR VLQRPRTCPQ 780
 EVELMLGCW QREPHMRKNI KGIHTLLQNL AKASFPVLDI LG 822

40 Seq ID NO: C325 Protein Sequence
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51
 | | | | | |
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSTILSCSV AGDPVPNMYW DVGNLVSKHM 240
 50 NETSHTQGS L RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 WCIPTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

55 Seq ID NO: C326 Protein Sequence
 Protein Accession #: NP_570843.1

60 1 11 21 31 41 51
 | | | | | |
 MPLKHYLLLL VGCQAWGAGL AYHGCPSSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60
 LNTHTIELNE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPGL 120
 FQGLDSLES L LSSNQQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFF HLVLTKLNL 180
 GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL 240
 FHNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRELWL 300
 YDNHISSEPD NVFSNLRQLQ VLILSRNQIS FISPFAFNGL TELRELSHT NALQDLQDGNV 360
 65 FRMLANLQNI SLQNNRLRLQ PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGLCELRL 420
 YDNFWRCDSD ILPLRNWLLL NQPRLGTDIV PVCFSANVR QGSLIIINVN VAVPSVHVPE 480
 VPSYPETPWY PDTPSPDIT SVSSTTELTS PVEDYDILT IQVTDTRSVW GMTQAQSGLA 540
 IAAIVIGIVA LACSLAACVG CCCCKRSQA VLMQMKAPNE C 581

70 Seq ID NO: C327 Protein Sequence
 Protein Accession #: NP_002649.1

75 1 11 21 31 41 51
 | | | | | |
 MRALLARLLL CVLVVSDSKG SNEHMQVPSN CDCLNGGTCV SNKYFSNIHW CNCPKKFGGQ 60
 HCEIDKSKTC YBGNHGFYRG KASTDTMGRP CLPWSNATVL QQTYHAHRSD ALQLGLGKH 120
 YCRNPNNRRR PWCYVQVGLK PLVQECMVHD CADGKPPSP PEELKFQCGQ KTLRPRFKII 180
 GGEFTTIENQ PWFAAIYRRH RGSVTVYVCG GSLISPCWVI SATHCFIDY KKBEDYIVYL 240
 RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHNNDIALK IRSKEGRCAQ PSRTIQTICL 300
 80 PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLKMTVVKLI SHRECCQPHY YGSEVTTKML 360
 CAADPQWKTD SCQGDGGGGL VCSLQGRMTL TGIWSWGRGC ALKDKPGVYT RVSHFLPWIR 420
 SHTKEENGLA L 431

Seq ID NO: C328 Protein Sequence
 Protein Accession #: XP_087254.1

	1	11	21	31	41	51	
5	MQFRECSING	MKYQEINGRL	VPEGTPPDSS	EGNLSYLSSL	SHLNNLSHLT	TSSSFRTSPE	60
	NETELIKEHD	LFFKAVSLCH	TVQISNVQTD	CTGDGPWQSN	LAPSQLYYA	SSPDEKALVE	120
	AAARIGIVFI	GNSEETMEVK	TLGKLERYKL	LHILEPDSDR	RRMSVIVQAP	SGEKLLFAKG	180
	AESSILPKCI	GGIEKTRIH	VDEFALKGLR	TLCIAVRKFT	SKEYEEDKR	IFEARTALQQ	240
	REEKLAAVFQ	FIEKDILLG	ATAVEDRLQD	KVRETIEALR	MAGIKVWVLT	GDKHETAVSV	300
10	SLSCGHFHRN	MNILELINQK	SDSECAEQLR	QLARRITEDH	VIQHGLVVDG	TSLSLALREH	360
	EKLMEVCRN	CSAVLCCRMA	PLQKAKVIRL	IKISPEKPIT	LAVGDGANDV	SMIQEAHVGI	420
	GIMKKEGRQA	ARNSDYAIAR	FKFLSKLFLV	HGHFYIIRIA	TLVQYFFYKN	VCFITPQFLY	480
	QFYCLFSQQT	LYDSVYLTLV	NICFTSLPIL	IYSLLEQHVD	PHVLQNKPTL	YRDISKNRLL	540
	SIKTFLYWTI	LGFSHAFFIF	FGSYLLIGKD	TSLLGNGQMF	GNWTFGTLVF	TVMVITVTVK	600
	MALETHFTW	INHLVTWGS	IFYFVFSLFY	GGILWPFLGS	QNMVYFVFIQ	LSSGSAWFAI	660
15	ILMVVTCLEL	DIKKKVFDRH	LHPTSTAKAQ	LTETNAGIKC	LDSMCCFPFG	EACASVGRM	720
	LERVIGRCSP	THISRSWSAS	DPFYTNDRSI	LTLSTMSST	C		761

Seq ID NO: C329 Protein Sequence
Protein Accession #: XP_087461.1

	1	11	21	31	41	51	
20	MLPLLAALLA	AACPLPPVRG	GAADAPGLLG	VPSNASVNAS	SAASPSPRGC	WPRRPPGPFS	60
	ARARRRRRRR	RRLCNISVQR	QMLSSLLVRW	GRPRGFQCDL	LLFSTNAHGR	AFFAAAFHRV	120
25	GPPLLIIEHLG	LAAGGAQDQL	RLCVGCGWVR	GRRTGRLRPA	AAPSAATAA	GAPTALPAYP	180
	AAEPPGPHWL	QGEPLHFCCL	DFSLEELQGE	PGWRLNRKPI	ESTLVACFMT	LVIVVSVVAA	240
	LWVPPIIAG	FLPNGMEQRR	TTASTTAATP	AAVPAGTTAA	AAAAAAAAAA	AVTSGVATK	299

Seq ID NO: C330 Protein Sequence
Protein Accession #: XP_051522.2

	1	11	21	31	41	51	
35	MDLHLFDYSE	PGNFSDISWP	CNSSDCIVVD	TVMCPNMPNK	SVLLYTLSEI	YIFIFVIGMI	60
	ANSVVVVVNI	QAKTGYDTH	CYILNLAIAD	LWVLTIPVW	VVSLVQHNQW	PMGELTCKVT	120
	HLIFSINLFG	SIFFLTICMSV	DRYLSITYFT	NTPSSRKKMW	RRVVCILVWL	LAFCVSLPDT	180
	YYLKTVTSAS	NNETYCRSFY	PEHSIKEWLI	GMELVSVVLG	FAVPFSIIAV	FYLLARAIAS	240
	ASSDQEKHSS	RKIIFSYYVV	FLVCWLPYHV	AVLLDIFSIL	HYIPPTCRLE	HALFTALHVT	300
40	QCLSLVHCCV	NPVLYSFINR	NYRYELMKAF	IFKYSAKTGL	TKLIDASRV	ETEYSALQES	360
	TK						362

Seq ID NO: C331 Protein Sequence
Protein Accession #: NP_000341.1

	1	11	21	31	41	51	
45	MGEFVRQIQL	LWKNWTLRKR	QKIRFVVVELV	WPLSLFLVLI	WLRNANPLYS	HHECHFENKA	60
	MPSAGMLPWL	QGIFCNVWNP	CFQSPTPGES	PGIVSNYNNS	ILARVYRDFQ	ELLMNAPESQ	120
50	HLGRIWTELH	ILSQFMDTLR	TPHERIAGRG	IRIRDILKDE	ETLTFLFIKN	IGLSDSVVYL	180
	LINSQVRPEQ	FAHGVPDLAL	KDIACSEALL	ERFIIFSQR	GAKTVRYALC	SLSQGTQLWI	240
	EDTLYANVDF	FKLFRVLPTL	LDSSRSQGINL	RSWGGILSDM	SPRIQEFIHR	PSMQDLLWVT	300
	RPLMQNGGPE	TFTKLMGILS	DLLCGYPEGG	GSRVLSFNWY	EDNNYKAFGL	IDSTRKDPYI	360
	SYDRRTTSFC	NALIQSLESN	PLTKIAWRRA	KPLLGMKILY	TPDSPAARRI	LKNANSTFEE	420
	LEHVRLKLVKA	WEEVGPQIY	FFDNSTQMNM	IRDTLGNPTV	KDFLNRLQGE	EGITAEAILN	480
55	FLYKGPRESQ	ADDMANFDWR	DIFNITDRTL	RLVNQYLECL	VLDKFESYND	ETQLTQRALS	540
	LLEENMFWAG	VVFPDMYPWT	SSLPPHVKYK	IRMDIDVVEK	TNKIKDRYWD	SGPRADPVED	600
	FRYIWGGFAY	LQDMVEQGIT	RSQVQAEAPV	GIYLQQMPYP	CFVDDSFMI	LNRCFPPIFMV	660
	LAWIYSVSMT	VKSIVLEKEL	RLKETLKNQG	VSNVAVICTW	FLDSFSIMSM	SIFLLTIFIM	720
	HGRILHYSDP	FILEFLFLAF	STATIMLCFL	LSTFFSKASL	AAACSGVIYF	TLYLPHILCF	780
60	AWQDRMTAEL	KKAVSLLSPV	AFGFGTEVLV	RFEEQGLGLQ	WSNIGNSPTE	GDEFSFLLSM	840
	QMMLDAACY	GLLAWYLDQV	FPGDYGTPLP	WYFLLQESY	LSGEGCSTRE	ERALEKTEPL	900
	TEETEDPEHP	EGIHDSFFER	EHPGVWPGVC	VKNLVKIFEP	CGRPAVDRLN	ITFYENQITA	960
	FLGHNGAGKT	TTLILTGLL	PPTSGTVLVG	GRDIETSLDA	VRQSLGMCPQ	HNILFHHLT	1020
	AEHMLFYAQL	KGKSQEEAQL	EMEAMLEDTG	LHHKRNEEAQ	DLSGGMQRKL	SVAIAFVGDA	1080
65	KVVILDEPTS	GVDPYSSRSI	WDLCLKYRS	RTIIMPTHM	DEADHQGDRI	AIIAQGRLYC	1140
	SGTPLFLKNC	FGTGLYTLV	RKMKNIQSQR	KGSEGTCS	SKGFSTTC	HVDDLTPQV	1200
	LDGDVNELMD	VVLHHVPEAK	LVEICIGQELI	FLLPKNKFKH	RAYASLFREL	EETLADLGLS	1260
	SFGISDTPLE	EIFLKVTEDS	DSGPLFAGGA	QOKRENVNPR	HPCLGPREKA	GQTPQDSNVC	1320
70	SPGAPAAHPE	GQPPPEPECP	GPQLNTGTQL	VLQHVQALLV	KRFQHTIRSH	KDFLAQIVLP	1380
	ATFVFLALML	SIVILPFGFY	PALTILHPWIY	GQQYTFSSMD	EPGSEQFTVL	ADVLLNKPFG	1440
	GNRCLKEGWL	PEYPCGNSTP	WKTPSVSPNI	TQLFQKQKWT	QVNPSPCSC	STREKLTMLP	1500
	ECPEGAGGLP	PPQRTQRSTE	ILQDLTDNRN	SDFLVKTYPA	LIRSSLKSKF	WVNEQRYGGI	1560
	SIGGKLFPVP	ITGEALVGFL	SDLGRIMNVS	GGPITREASK	EIPDFLKHLE	TEDNIKVWFN	1620
	NKGWHALVSF	LNVAHNAILR	ASLPKDRSPE	EYGITVISQ	LNLTKEQLSE	ITVLTTSVDA	1680
75	VVAICVIFSM	SFVPASFLVY	LIQERVNKS	HLQFISGVSP	TTYWVTNFW	DIMNYSVSAG	1740
	LUVGFIGFQ	KKAYTSPENL	PALVALLLLY	GWAVIFMMYP	ASFLEFVDPST	AYVALSCANL	1800
	FIGINSSAIT	FILELFDNDR	TLLRFNAVL	KLLIVFFHFC	LGRGLIDLAL	SQAVTDVYAR	1860
	FGEEHSANPF	HWDLIGKNFL	AMVVEGVVYF	LLTLLVQRHF	FLSQWIAEPT	KEPIVDEDD	1920
	VAEERQRIIT	GONKTDILRL	HELTKIYLG	SSPAVDRLCV	GVRPGECFGL	LGVNGAGKTT	1980
80	TFKMLTGDIT	VTSGDATVAG	KSILTNISEV	HQNMGYCPCQ	DAIDELLTGR	EHLVLYARLR	2040
	GVPAEEIEKV	ANWSTKSLGL	TVYADCLAGT	YSGGNKRRLS	TAIALIGCPP	LVLLEPTTG	2100
	MDPQARRMLW	NVIVSIIRKG	RAVVLTSHSM	EECEALCTRL	AIMVKGAFC	MGTIQHLKSK	2160
	FDGDIYVTMK	IKSPKDDLLP	DLNPVEQFFQ	GNFPGSVQRE	RHYNMLQFQV	SSSSLARIFQ	2220
	LLLSHKDSLL	IEEYSVTQIT	LDQVFNFAK	QQTESHDLPL	HPRAAGASRQ	AQD	2273

Seq ID NO: C332 Protein Sequence
Protein Accession #: NP_006662.2

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MVPHAILARG RDVCCRNGLL ILSVLSVIVG CLLGFFLRTR RLSPQEISYF QFPGELLMRM 60
LKMMLPLVV  SSLMSGLASL DAKTSSRLGV LTVAYYLWTT FMAVIVGIFM VSIHPGSAA 120
10    QKETTEQSGK PIMSSADALL DLIRNMFPAN LVEATFKQYR TKTTTPVVKSP KVAPEEAPPR 180
      RILYGVQEE  NGSHVQNFAL DLTPPEVVY KSEPGTSDGM NVLGVVFFSA TMGIMLGRMG 240
      DSGAPLVGFC QCLNESVMKI VAVAVWYFFG GIVFLIAGKI LEMDDPRAVG KKLGFYSVTV 300
      VCGLVHLGLF ILPLLYFFIT KKNPIVFIRG ILQALLIALA TSSSSATLPI TFKCLENNH 360
      IDRRIRFVL  PVGATINMDG TALYEAVAAI FIAQVNNYEL DFGQIITISI TATAASIGAA 420
      GIPQAGLVTM VIVLTSVGLP TDDITLIIAV DWALDRFRMT INVLDALAA GIMAHICRKD 480
15    FARDTGTCKL LFCETKPVSL QEIVAAQQNG CVKSVAEASE LTLGPTCPHH VPVQVERDEE 540
      LPAASLNHCT IQISELENTV

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Seq ID NO: C333 Protein Sequence
Protein Accession #: NP_005680.1

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20    1      11      21      31      41      51
      |      |      |      |      |      |
MVTVGNVCEA EGPVGPWAMQ DGLSPCFFFT LVPSTRMALG TLALVLALPC RRRERFAGAD 60
SLSWGAGPRI SPYVLQLLLA TLQALPLAG LAGRVGTARG APLPSYLLLA SVLESAGAC 120
25    GLWLLVVERS QARQRLAMGI WIKFRHSPGL LLLWTVAFAA ENLALVSWNS PQWWARADL 180
      QQVQFSLWV  LRYVVSGLF VLGLWAPGLR PQSYTLQVHE EDQDVERSQV RSAAQOSTWR 240
      DFGRLRLLS  GYLWPRGSPA LQLVVLICLG LMGLERALNV LVPIFYRNIV NLLTEKAPWN 300
      SLAWTVTSYV FLKFLQGGGT GSTGFVSNLR TFLWIRVQQF TSRRVELLIF SHLHELRLW 360
      HLGRRTGVL  RIADRGTSV TGLLSYLVFN VIPTLADIII GIIFYSMFFN AWFGLIVFLC 420
30    MSLLYLTITV VTEWRTKFRR AMNTQENATR ARAVDSLLNF ETVKYNAES YEVEYREAL 480
      IKYQGLEWKS SASLVLLNQT QNLVIGLGLL AGSLLCAYFV TEQKLQVGDY VLFGTYYIQL 540
      YMPLNWFQTY YRMIQTNFID MENMFDLLKE ETEVKDLPGA GLRFRQKRI EFENVHFSYA 600
      DGRITLQDVS FTVMPQTLA LVGPSPGAGKS TILRLFRFY DISSGCIRID QQDISQVTOA 660
35    SLRSHIGVVP QDTVLNNDTI ADNIRYGRVT AGNDEVEAAA QAAGIHDAIM AFPEGYRTQV 720
      GERGLKLSGG EKQRVAIART ILKAPGIILL DEATSALDTS NERAIQASLA KVCANRTTIV 780
      VAHRLSTVFN ADQILVIKDG CIVERGRHEA LLSRGVGYAD MWQLQQQEE TSEDTKPQTM 840
      ER

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Seq ID NO: C334 Protein Sequence
Protein Accession #: NP_000667.1

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40    1      11      21      31      41      51
      |      |      |      |      |      |
MLLETQDALY VALELVIAAL SVAGNVLVCA AVGTANTLQT PTNYFLVSLA AADVAVGLFA 60
45    IPFAITISLG FCTDFYGCFL LACFVLVLTO SSIFSLAVA VDRYLAICVP LRYKSLVTGT 120
      RARGVIAVLW VLAFIGILTP FLGWNSKDSA TNNCTEPWDG TTNESSCLVK CLFENVVPM 180
      YMVYFNFFGC VLPPLLIMLV IYIKIFLVAC RQLQRTLM D HSRTTLQREI HAAKSLAMIV 240
      GIFALCNLHV HAVNCVTLFQ PAQGNKPKW AMNMAILSH ANSVVNPIV AYRNDRFRYT 300
50    FHKIISRYLL CQADVKSNGG QAGVQPALGV GL

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Seq ID NO: C335 Protein Sequence
Protein Accession #: NP_443164

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55    1      11      21      31      41      51
      |      |      |      |      |      |
MGLGARGAWA ALLGLTLQVL ALLGAAHESA AMAETLQHVP SDHTNETSNS TVKPPTSVAS 60
DSSNTTVTMT KPTAASNTTT PGMVSTNMTS TTLKSTPKTT SVSQNTSQIS TSTMTVTNHS 120
60    SVTSAASSVT ITTTHMSEAK KGSKFDTGSF VGGIVLTLGV LSILYIGCKM YYSRRGIRYR 180
      TIDEHDAII

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Seq ID NO: C336 Protein Sequence
Protein Accession #: NP_004186.1

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65    1      11      21      31      41      51
      |      |      |      |      |      |
MAQHGMAGAF RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTARCC RVHTTRCCRD 60
YPGECCSEW  DCMCVQPEFH CGDPCTTCR HHPCPPGQGV QSQGFSGFG QCIDCASGTF 120
70    SGGHEGHCKP WTDCTQFGFL TVFPGNKTHN AVCVPGSPPA EPLGWLTVVL LAVAACVLLL 180
      TSAQLGLHIW QLRSCMWPR ETQLLLEVPP STEDARSCQF PEEERGERSA EEKRLGDLW 240
      v

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Seq ID NO: C337 Protein Sequence
Protein Accession #: BAC03767.1

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75    1      11      21      31      41      51
      |      |      |      |      |      |
MGCDGRVSGL LARNLQPTLT YWSVFFSFGI CIAFLGPTLL DLRCQTHSSL PQISWVFFSQ 60
QLCLLLGSAL GGVFKRTLQ SLWALFTSSL AISLVFAVIP FCRDVKVLAS VMALAGLAMG 120
80    CDTVANMQL  VRMYQKDSAV FLQVLHFFVG FGALLSPLIA DPFLSEANCL PANSTANTTS 180
      RGHLEHVSRL LGQHHVDKAP WSNQTFPGLT PKDGAGTRVS YAFWIMALID LPVPMVAVML 240
      LSKERILLTC PQRRLPLLSA DELALETQPP EKEDASSLPP KFQSHLGHD LFSCCQKRLN 300
      RGAPYSFFAI HITGALVLFM TDGLTGAYSA FVYSYAVEKP LSVGHKVAGY LPSLFWGFIT 360
      LGRLLSIPIS SRMKPATMVF INVVGVVVTF LVLLIFSINV VPLFVGTA SL GLFLSSTFPS 420
      MLAYTEDSLQ YKGCATTVLV TGAGVGEMVL QMLVGSIFQA QGSYSFLVCG VIFGCLAFTF 480

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YILLLFFHRM HPGLPSPVPTQ DRSIGMENSE CYQR

514

Seq ID NO: C338 Protein Sequence
Protein Accession #: NP_002194.1

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1	11	21	31	41	51	
MGP	ERT	G	A	A	P	60
L	P	L	L	L	V	120
L	L	L	L	L	V	180
L	L	L	L	L	V	240
L	L	L	L	L	V	300
L	L	L	L	L	V	360
L	L	L	L	L	V	420
L	L	L	L	L	V	480
L	L	L	L	L	V	540
L	L	L	L	L	V	600
L	L	L	L	L	V	660
L	L	L	L	L	V	720
L	L	L	L	L	V	780
L	L	L	L	L	V	840
L	L	L	L	L	V	900
L	L	L	L	L	V	960
L	L	L	L	L	V	1020
L	L	L	L	L	V	1080
L	L	L	L	L	V	1140
L	L	L	L	L	V	1181

Seq ID NO: C339 Protein Sequence
Protein Accession #: NP_113648.1

1	11	21	31	41	51	
M	R	P	R	A	A	60
E	L	L	Q	N	F	120
N	L	S	P	N	T	180
G	S	G	A	L	L	240
Y	Q	N	M	V	S	300
H	S	P	Q	G	C	332

Seq ID NO: C340 Protein Sequence
Protein Accession #: NP_004145.1

1	11	21	31	41	51	
M	E	W	D	N	G	60
T	A	V	T	L	N	120
S	F	Q	R	Y	L	180
S	P	P	A	L	A	240
A	V	V	A	A	F	300
F	Y	F	T	Q	K	328

Seq ID NO: C341 Protein Sequence
Protein Accession #: NP_009128.1

1	11	21	31	41	51	
M	Q	R	P	G	P	60
Q	R	E	A	I	Q	120
M	E	Q	F	N	K	180
P	L	K	D	G	G	240
S	S	A	F	T	V	300
Q	E	G	L	E	S	360
I	P	A	V	K	T	420
F	H	I	R	R	V	480
C	K	M	N	N	Q	540
K	K	S	R	R	K	581

Seq ID NO: C342 Protein Sequence
Protein Accession #: NP_005752.1

1	11	21	31	41	51	
M	E	V	S	R	R	60
S	G	S	C	L	D	120
G	L	L	T	G	W	180
A	T	Y	V	L	P	240
N	G	S	I	Y	F	300
E	A	L	D	V	W	360
E	R	V	Q	P	I	420
E	E	T	P	V	F	480
C	T	F	Q	D	C	540
S	S	R	E	L	C	600
C	V	E	T	G	C	660
V	F	Y	I	K	S	720

FSLPSSRKEM KDVCIQFDGG NCSSVGSLSY IALPHCSLIF PATTWISGGQ NITMMGRNFD 780
 VIDNLIISHE LKGNINVSEY CVATYCGFLA PSLKSSKVRT NVTVKLRVQD TYLDCGTLQY 840
 REDPRTGYR VESEVDTELE VKIQKENDNF NISKKDIEIT LFHGENGQLN CSFENITRNQ 900
 DLTTILCKIK GIKTASTIAN SSKKVRVKLG NLELYVEQES VPSTWYFLIV LPVLLVIVIF 960
 AAVGVTRHKS KELSRKQSQQ LELLESELRK EIRDGFELQ MDKLDVVDSP GTVPFLDYKH 1020
 FALRTFFPES GGFTHIFTED MHNRDANDKN ESLTALDALI CNKSFLVTVI HTLEKQKNFS 1080
 VKDRCLFASF LTIALQTKLV YLTSILEVLT RDLMEQCSNM QPKMLLRTE SVVEKLLTNW 1140
 MSVCLSGFLR ETVGEPFYLL VTTLNQKINK GPVDVITCKA LYTLNEDWLL WQVPEFSTVA 1200
 LNVVFEKIPE NESADVCRNI SVNVLDCDTI GQAKEKIFQA FLKNGSPYG LQLNEIGLEL 1260
 QMGTRQKELL DIDSSSVILE DGITKLNTIG HYEISNGSTI KVFCKIANFT SDVEYSDHHC 1320
 HLLLPDSEAF QDVQGRHRG KHKFKVKEMY LTKLLSTKVA IHSVLEKLFIR SIWSLPNSRA 1380
 PFAIKYFFDF LDAQAENKKI TDPDVVHIWK TNSLPLRFVW NILKNPQFVF DIKKTPHIDG 1440
 CLSVIAQAFM DAPSLTEQQQL GKEAPTNNKL YAKDIPTYKE EVKSYKPAIR DLPPLSSEM 1500
 EEFLTQESKK HENEFNEEVA LTEIYKIYVK YFDEILNKLE RERGLEEAQK QLLHVKVLF 1560
 EKKCKWM 1568

Seq ID NO: C343 Protein Sequence
 Protein Accession #: NP_002176.1

1 11 21 31 41 51
 | | | | |
 MTILGTTFGM VFSLQVVSF ESGYAQNGDL EDAELDDYSF SCYSQLEVNG SQHSLTCAFE 60
 DDPVNTTNLE FEICGALVEV KCLNFRKLQE IYFIETKKFL LIGKSNICVK VGEKSLTCKK 120
 IDLTTIVKPE APFDLSVIYR EGANDFVVTF NTSHLQKKYV KVLMDHVAYR QEKDENKWT 180
 VNLSTKLTL LQRKLQPAAM YEIKVRSIPD HYFKGFSEW SPSYFRTPE INNSSGEMDP 240
 ILLTISILSF FSVALVILA CVLWKKRIK IVWPSLPDHK KTLHLCKKP RKNLNVSFNP 300
 ESFLDCQIHR VDDIARDEV EGFLQDTFPQ QLEESEKQRL GGDVQSPNCP SEDVVVTPES 360
 FGRDSSLTCL AGNVSACDAP ILSSRSRLDC RESGKNPHV YQDLLSLGT TNSLTPPPFS 420
 LQSGILTNP VAQQPILTS LGSNQEEAYV TMSFYQNG 459

Seq ID NO: C344 Protein Sequence
 Protein Accession #: NP_002713.1

1 11 21 31 41 51
 | | | | |
 MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPEQMAQYA ADLRRYINML 60
 TRPRYGRHK EDTLAFSEWG SPAAVPREL SPLDL 95

Seq ID NO: C345 Protein Sequence
 Protein Accession #: NP_115934.1

1 11 21 31 41 51
 | | | | |
 MTWRHHVRL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSTHFE 60
 VTGSAEGWGP EEPLPYRAF GEGASARPRC CRNGGTCVLG SFCVCPAHFT GRYCEHDQRR 120
 SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL 180
 LLPALLHRL LRPDAFAHPR SLVPSVLQRE RRPGRPGLG HRL 223

Seq ID NO: C346 Protein Sequence
 Protein Accession #: NP_006524.1

1 11 21 31 41 51
 | | | | |
 MARSLVCLGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISMAYA LDYMAPDCR 60
 FLTIHRGQVV YVFSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD 120
 VKTDKWFYFC Q 131

Seq ID NO: C347 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MTQVTEKSTE HPEKTTSTTE KTRTPPEKPT LYSEKTICTK GKNTPVPEKP TENLGNTTTL 60
 TETIKAPVKS TENPEKTA AV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI 120
 TSRTKLSSIT SEATGNESH P YLNKDGSKG IHAGQMGEN D SFPAAWAIIV VLVAVILLV 180
 FLGLIFLVSY MMRTRRTLTQ NTQYNDAEDE GGPNSYPVYL MEQQNLGMGQ IPSR 235

Seq ID NO: C348 Protein Sequence
 Protein Accession #: NP_543146.1

1 11 21 31 41 51
 | | | | |
 MTQVTEKSTE HPEKTTSTTE KTRTPPEKPT LYSEKTICTK GKNTPVPEKP TENLGNTTTL 60
 TETIKAPVKS TENPEKTA AV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI 120
 TSRTKLSSIT SEATGNESH P YLNKDGSKG IHAGQMGEN D SFPAAWAIIV VLVAVILLV 180
 FLGLIFLVSY MMRTRRTLTQ NTQYNDAEDE GGPNSYPVYL MEQQNLGMGQ IPSR 235

Seq ID NO: C349 Protein Sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 | | | | |

	MWPRLAFCCW	GLALVSGWAT	FQOMSPSRNF	SFRLFPETAP	GAPGSIPAPP	APGDEAAGSR	60
	VERLGQAFRR	RVRLLRELSE	RLELVFLVDD	SSSVGEVNFR	SELMFVRKLL	SDFPVVPAT	120
	RVAIVTFSSK	NYVVRVRYDI	STRRARQHKC	ALLLQEIPIA	SYRGGGTYTK	GAFLQAAQIL	180
5	LHARENSTKV	VFLITDGYSN	GGDPRPIAAS	LRDSGVEIFT	FGIWQGNIRE	LNDMASTPKE	240
	EHCYLLHSFE	EFEALARRAL	HEDLPSGSFI	QDDMVHCSYL	CDEGKDCCDR	MGSCCKGTHT	300
	GHFECICEKG	YYGKGLQYEC	TACPSGTYKP	EGSPGGISSC	IPCPDENHTS	PPGSTSPEDC	360
	VCREGYRASG	QTCELVHCPA	LKPPENGYFI	QNTCNNHFNA	ACGVRCHPGF	DLVGSIIILC	420
	LPNGLWSGSE	SYCRVTRCPH	LRQPKHGHIS	CSTREMLYKT	TCLVACDEGY	RLEGSIDLKTC	480
10	QGNQWDGPE	PRCVERHCST	FQMPKDVIIIS	PHNCGKQPAK	FGTICYVSCR	QGFILSGVKE	540
	MLRCTTSGKW	NVGQQAAYCK	DVEAPQINCP	KDIEAKTLEQ	QDSANVTWQI	PTAKDNSGEK	600
	VSVHVHPAFT	PPYLFPIGDV	AIVYTATDLS	GNQASCFIHI	KVIDAEPPVI	DWCRSPFPVQ	660
	VSEKVHAASW	DEPQFSDNSG	AELVITRSHT	QGDLPQGET	IVQYTATDPS	GNNRTCDIHI	720
	VIKGSFCEIP	FTPVNGDFIC	TPDNTGVNCT	LTCLEGYDFT	EGSTDKYYCA	YEDGVVKPTY	780
15	TTEWPDCAKK	RFANHGFKSF	EMFYKAARCD	DTDLMKKFSE	AFETTLGKMV	PSFCSDAEDI	840
	DCRLEENLTK	KYCLEYNVDY	ENGFAIGPGG	WGAANRLDYS	YDDFLDTVQE	TATSIGNAKS	900
	SRIKRSAPLS	DYKIKLIENI	TASVPLPDER	NDTLEWENQ	RLQLTLETIT	NKLRKTLNKO	960
	PMYSFQLASE	ILIADSNMLE	TKKASPFRCR	GSVLRGRMCV	NCPLGTYYNL	EHFTCESCRI	1020
	GSYQDEEGQL	ECKLCPSGMY	TEYIHSRNIS	DCKAQCKQGT	YSYSGLETCE	SCPLGTYQPK	1080
20	FGSRSCLSGP	ENTSTVKRGA	VNISACGVPC	PEGKFSRSLG	MPCHPCPRDY	YQPNAGKAFK	1140
	LACPFYGTTP	PAGSRSITEC	STSVLNTITF	GGFGHLELLN	CPSEVFHECF	FNPCHNSGTC	1200
	QQLGRGYVCL	CPLGYTGLKC	ETDIDECSP	PCLNNGVCKD	LVGEFICECP	SGYTQQRCEE	1260
	NINECSSSPC	LNKGCVDGV	AGYRCTCVKG	FVGLHCETEV	NECQSNPCLN	NAVCEQVGG	1320
	FLCKCPGGFL	GTRCGKNVDE	CLSQPKNGA	TCKDGANFR	CLCAAGFTGS	HCELNINECQ	1380
25	SNPCRNQATC	VDELNSYSCK	CQPGFSGKRC	ETEQTSGFNL	DFEVSGIYGY	VMLDGMPLSL	1440
	HALTCTFWMK	SSDDMNYGTP	ISYAVDNGSD	NTLLLTIDYNG	WVLYVNGREK	ITNCPSVNDG	1500
	RWHHIAITWT	RANGIWKVYI	DGKLSDDGAG	LSVGLPIPGG	GALVLGQEQD	KKGEFSPAE	1560
	SFVGSISQLN	LWDYVLSQPT	VKSLATSCPE	ELSKGNVLAW	PDFLSGIVGK	VKIDSKSIFC	1620
	SDCPRLGGSV	PHLRTASEDL	KPGSKVNLFC	DGQFQLVGNP	VQYCLNQGW	TQPLPHCERI	1680
30	SCGVPPPLEN	GFHSADDFYA	GSTVTYQCN	GYLLGDSDRM	FCTDNGSWNG	VSPSCLDVIDE	1740
	CAVGSDCSEH	ASCLNVGDSY	ICSCVPPYTG	DGKNCAPPIK	CKAPGNPENG	HSSGEIYTVG	1800
	AGVTFSCQEG	YQLMGVTKKIT	CLESGEWNHL	IPYCKAVSCG	KPAIPENGCI	EELAFTFGSK	1860
	VTYRCNKGYT	LAGDKESSCL	ANSSWSHSP	VCEPVKCSSP	ENINNGKIYL	SLTYLSTAS	1920
	YSCDTGYSLQ	GPSIIETAS	GIWDRAPPAC	HLVFCGEPPA	IKDAVITGN	FTFRNTVYTY	1980
35	CKEGYTLAAG	DTIECLADGK	WSRSDQQLA	VSCDEPPIVD	HASPETAHRL	FGDIAFYICS	2040
	DGYSLADNSQ	LLCNAQGWV	PPEGQDMPRC	IAHFCEKPPS	VSYSILESVS	KAKFAAGSVV	2100
	SFKCMGEGVL	NTSAKIECMR	GGQWNPSPMS	IQCIPIVRCGE	PPSIMNGYAS	GSNYSFGAMV	2160
	AYSCNKGFIY	KGEKKSTCEA	TGQWSSPIPT	CHPVSCGEPP	KVENGFLHT	TGRIFESEVR	2220
	YQCNPGYKSV	GSFVFCQAN	RHHHSESPML	CVPLDCGKPP	PIQNGFMKGE	NFEVGSKVQF	2280
40	FCNEGVELVG	DSSWTCKQSG	KWNKSNPKC	MPAKCPEPPL	LENQLVLKEL	TTEVGVVTF	2340
	CKEGHVLQGP	SVLKLCSLQ	WNSDFPCKI	VLCTPPPLIS	FGVPIPSAL	HFGSTVKYSC	2400
	VGGFFLRNGS	TTLCQPDQGT	SSPLPECVPV	ECPOPEELPN	GIIDVQGLAY	LSTALYTCKP	2460
	GFELVGNNTT	LCGENGHWLG	GKPTCKAIEC	LKPKEILNGK	FSYTDLHYGQ	TVTYSCNRGF	2520
	RLBEGSALTC	LETGDDVDVA	PSCAIHCDS	PQPIENGFEV	GADYSYGAI	IYSCFPFGFQV	2580
45	AGHAMQTCEE	SGWSSSIPTC	MPIDCGLPPH	IDFGDCTKLK	DDQGYFEQED	DMMEVPVYTP	2640
	HPPYHLGAVA	KTWENTKESP	ATHSSNPLYG	TMVSYTCNPG	YELGPNVLI	CQEDGTWNGS	2700
	APSCISIECD	LPTAPENGFL	RFTETSMGSA	VQYSCKPGHI	LAGSDLRLCL	ENRWKSGASP	2760
	RCEAISCKKP	NPVMNGSIKG	SNYTYLSTLY	YECDPGVVLN	GTERRTQDD	KNWDEDEPIC	2820
	IPVDCSSPPV	SANGQVRGDE	YTFQKEIET	CNEGFLLEGA	RSRVCLANGS	WSGATPDCVP	2880
50	VRCATPPQLA	NGVTEGLDYG	FMKEVTFHCH	BGYILHGAPK	LTCQSDGNWD	AEIPLCKFPV	2940
	CGPPEDLAHG	FPNGFSFIHG	GHIQYQCFPG	YKLHGNSSRR	CLSNWSWSGS	SPSCLPCRCS	3000
	TPVIEYGTVN	GTFDFCGKAA	RIQCFKGFKL	LGLSEITCEA	DGQWSSGFP	CEHTSCGSLP	3060
	MIPNAFISET	SSWKNSIPTC	SCRSGYVIQ	SSDLICTEKG	VWSQPYPVCE	PLSCGSPPSV	3120
	ANAVATGEAH	TYSEVVKLRC	LEGYTMDDTD	DTFTCQKDR	WFERISCSP	KKCPLPENIT	3180
55	HILVHGDDFS	VNRQVSVSCA	EGYTFEGVNI	SVCQLDGTWE	PPFSDDESCP	VSCGKPESPE	3240
	HGFVVGSKYT	FESTIIVQCE	PGYLEGNRE	RVCQENRQWS	GGVAICKETR	CETPLEFLNG	3300
	KADIENTTGT	PNVYVSCNRG	YSLEGPSEAH	CTENGTSWHP	VPLCKPNPCP	VPFVIPENAL	3360
	LSEKEFYVDQ	NVSIKCRGEG	LLQGHGIIITC	NPDETWTQTS	AKCEKISCPG	PAHVENAIAR	3420
	GVHYQYGDMI	TYSYCSGYML	EGFLRSVCLC	NGTWTSPPIC	RAVCRFPQCN	GGICQRPNAC	3480
60	SCPEGWMLRL	CEEPICILPC	LNGGRCVAPY	QCDCPPGWTG	SRCHTAVQCS	PCLNGGKCVR	3540
	PNRCHCLSSW	TGHNCSTR					3557

Seq ID NO: C350 Protein Sequence
Protein Accession #: FGENESH predicted

65	1	11	21	31	41	51	
	MRFSVSGMRT	DYPRSVLAPA	YVSVCLLLLC	PREVIAPAGS	EPWLCQPAPR	CGDKIYNPLE	60
	QCCYNDAIVS	LSETRQCGPP	CTFWPCFELC	CLDSFGLTND	FVVKLVQGV	NSQCHSSPIS	120
70	SKCERGRIC						129

Seq ID NO: C351 Protein Sequence
Protein Accession #: AAH35671.1

75	1	11	21	31	41	51	
	MVPARGGGA	LARAAGRGLL	ALLLAVSAPL	RLQAEELGDG	CGHLVITYQDS	GTMTSKNYPG	60
	TYPNHTVCEK	TITVPKGRKL	ILRLGLDLIE	SQTCASDYLL	FTSSSDQYGP	YCGSMTVPKE	120
	LLLNTSEVTV	RFESGSHISG	RGFLLYYASS	DHPDLITCLE	RASHYLKTEY	SKFCPAGCRD	180
80	VAGDISGNMV	DGYRDTSLLC	KAAIHAGIIA	DELGGQISVL	QRKGISRYEG	ILANGVLSRD	240
	GSLSDKRFLF	TNNGCSRSLS	FEPDQGIAS	SSWQSVNESG	DQVHWSFGQA	RLQDQGPSWA	300
	SGDSSNNHKP	REWLEIDLGE	KKKITGIRTT	GSTQSNFNFY	VKSFMNFKN	NNSKWKTYKG	360
	IWNNEKVFQ	GMSNFRDPVQ	NNFIPPIVAR	YVRVVPQTWH	QRALKVELI	GQITQGNDS	420
	LWVRKTSQST	SVSTKKEDET	ITRPIPSEET	STGINITTVA	IPLVLVLVLV	FAGMGIFAAP	480
	RKKKKKGSPY	GSAAEQKTDK	WKQIKYFFAR	HQSAEFTISY	DNEKEMTQKL	DLITSDMAG	539

Seq ID NO: C352 Protein Sequence
Protein Accession #: Eos sequence

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15
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1	11	21	31	41	51	
MGFGAGQRLR	PVPAPRSSAE	EAARPGQLRL	GIRRGEAELA	KLAPSGVMVP	GARGGGALAR	60
AAGRGLLALL	LAVSAPLRLO	AEELGDGCGH	LVTYQDSGTM	TSKNYPGTYP	NHTVCEKTIT	120
VPKGRLLLR	LGDDIESQT	CASDYLLFTS	SSDQYGPYCG	SMTVPKELLL	NTSEVTVRFE	180
SGSHISGRGF	LLTYASSDHP	DLITCLERAS	HYLKTEYSKF	CPAGCRDVAG	DISGNMVDGY	240
RDTSLLCKAA	IHAGIIADEL	GGQISVLQRK	GISRYEGILA	NGVLSRDGSL	SDKRFLFTSN	300
GCSRSLSEFP	DGQIRASSSW	QSVNESGDQV	HWSPGQARLQ	DQGSPWASGD	SSNNHKPREW	360
LEIDLGEKKK	ITGIRTTGST	QSNFNFYVKS	FVMNFKNNNS	KWKTYKGIVN	NEEKVFQGNS	420
NFRDPVQNNF	IPPIVARYVR	VVPQTWHQRI	ALKVELIGCQ	ITQGNDSLWV	RKTSQSTSVS	480
TKKEDETITR	PIPSEETSTG	INITTVAIPL	VLLVVLVFAG	MGIFAAFRKK	KKKGSPYGSA	540
EAQKTDCWKQ	IKYPFARHQS	AEFTISYDNE	KEMTQKLDLI	TSDMAG		586

Seq ID NO: C353 Protein Sequence
Protein Accession #: FGENESH predicted

25
30
35
40

1	11	21	31	41	51	
MFQRQERFLD	LSSAEAVAAM	ILHQHPDIIN	KGDGCGHLVT	YQDSGTMSTK	NYPGTYPNHT	60
VCEKTITVPK	GKRLILRLGD	LDIESQTCAS	DYLLFTSSSD	QYGMQKEEET	EVLCLSVAGA	120
QRVDIPVQLL	PSFLEGWKGH	ADARGPYCGS	MTVPKELLN	TSEVTVRFES	GSHISGRGFL	180
LTASSDHPD	LITCLERASH	YLKTEYSKFC	PAGCRDVAGD	ISGNMVDGYR	DTSLCKAAI	240
HAGIIADELG	GQISVLQRKG	ISRYEGILAN	GVLSRDGSL	DKRFLFTSN	CSRSLSEFPD	300
GQIRASSSWQ	SVNESGDQVH	WSPGQARLQD	QGPSWASGDS	SSNNHKPREWL	EIDLGEKKKI	360
TGIRTTGSTQ	SNFNFYVKS	VNMNFKNNNS	WKTYKGIVN	EKVFQGNSN	FRDPVQNNFI	420
PPIVARYVRV	VPQTHQRIA	LKVELIGCQI	TQGNDSLWVR	KTSQSTSVST	KKEDETITRP	480
IPSEETSTDA	MPVQIVGDHT	QMISQRENLG	PDEGKIPFKG	TAESMVRVVF	AVVVDNLGML	540
FLAHTPEEDI	DHYCNQIKY	PFARHQSABF	TISYDNEKEM	TQKLDLITSD	MADYQQPLMI	600
GTGTVTRKGS	TFRPMDDAE	EAGVSTDAGG	HYDCPQRAGR	HEYALPLAPP	EPEYATPIVE	660
RHVLRAHTFS	AQSGYRVPGP	QPGHKHSLSS	GGFSPVAVVG	AQDGDYQRP	SAQPADRGYD	720
RPKAVSALAT	ESGHPDSQKP	PTHPGTSDSY	SAPRDCLTPL	NQTAMTALL		769

Seq ID NO: C354 Protein Sequence
Protein Accession #: NP_004607.1

45

1	11	21	31	41	51	
MAGVSACIKY	SMFTFNFLFW	LCGILILALA	IWVRVSNDSD	AIFGSEDVGS	SSYVAVDILI	60
AVGAIIMILG	FLGCCGAIKE	SRCMLLFFFI	GLLLILLLQV	ATGILGAVFK	SKSDRIVNET	120
LYENTKLLSA	TGSEKQFQE	AIIVFQBEFK	CCGLVNGAAD	WGNFNQHYPE	LCACLDKQRP	180
CQSYNGKQVY	KETCISFIKD	FLAKNLIIVI	GISFGLAVIE	ILGLVFSMVL	YCQIGNK	237

Seq ID NO: C355 Protein Sequence
Protein Accession #: NP_004608.1

50
55

1	11	21	31	41	51	
MCTGGCARCL	GGLTIPLAFF	GFLANILLFF	PGGKVIDDND	HLSQEIWFFG	GILGSGVLMI	60
FPALVFLGLK	NNDCCGCCGN	EGCGKRFAMF	TSTIFAVVGF	LGAGYSFIIS	AISINKGPCK	120
LMANSTWGYF	FHDGTYLND	ALWNKCREPL	NVVPWNLTFL	SILLVVGGIQ	MVLCAIQVVN	180
GLLGTLCGDC	QCCGCCGGDG	PV				202

Seq ID NO: C356 Protein Sequence
Protein Accession #: NP_002372.1

60
65
70

1	11	21	31	41	51	
MPRPAPARRL	PGLLLLLWPL	LLLPSAAPDP	VARPGFRRL	TRGPGGSPGR	RPSAAPDGA	60
PASGTSEPR	ARGAGVCKSR	PLDLVFIIDS	SRSVRPLEFT	KVKTFVSRII	DTLDIGPADT	120
RVAVVNYAST	VKIEFQLQAY	TDKQSLKQAV	GRITPLSTGT	MSGLAIQTAM	DEAFTVEAGA	180
REPSSNIPKV	AIIVTDGRPQ	DQVNEVAARA	QASGIELYAV	GVDRADMASL	KMMASEPLEE	240
HVFVYETYG	IEKLSRRFQE	TFCALDPCVL	GTHQCQHVCI	SDGEGKHHCE	CSQGYTLNAD	300
KKTCALDR	ALNTHGCEHI	CVNDRSGSYH	CECYEGYTLN	EDRKTCSAQD	KCALGTHGCG	360
HICVNDRGTS	HHCECYEGYT	LNADKKTCV	RDKCALGSHG	CQHICVSDGA	ASYHCDCYPG	420
YTLNEDKKTC	SATEBARRLV	STEDACGCEA	TLAFQDKVSS	YLQRLNTKLD	DILEKLKINE	480
YQIHR						486

Seq ID NO: C357 Protein Sequence
Protein Accession #: NP_057723.1

75
80

1	11	21	31	41	51	
MARGSLRRL	RLVLGLWLA	LLRSVAGEQA	PGTAPCSRGS	SWSADLDKCM	DCASCRRAPH	60
SDFCLGCAA	PPAPFRLWP	ILGGALSLTF	VLGLLSGFLV	WRRCRREKRF	TPPIETGTGE	120
GCPAVALIQ						129

Seq ID NO: C358 Protein Sequence
Protein Accession #: NP_001810.1

1 11 21 31 41 51
 | | | | |
 MQPTLLLSLL GAVGLAAVNS MPVDNRNHNE GMVTRCIIEV LSNALSKSSA PPITPECRQV 60
 5 LKTSRKDVKD KETTENENTK FEVRLLRDPA DASEAHESSS RGEAGAPGEE DIQGPTKADT 120
 EKWAEGGGHS RERADEPQWS LYPSDSQVSE EVKTRHSEKS QREDEEEEG ENYQKGERGE 180
 DSSEKHLLEE PGETQNAFLN ERKQASAIKK EELVARSETH AAGHSQEKTH SREKSSQESG 240
 EEAGSQENHP QESKQPRSQ EESEGEEDA TSEVDKRRT PRHHHGRSRP DRSSQGGSLP 300
 SEEKGHPQEE SEESNVSMAS LGEKRDHST HYRASEEEPE YGEEIKGYFG VQAPEDLEWE 360
 10 RYRGRGSEY RAPRFQSEES WDEEDKRNYP SLELDKMAHG YGEESEEEERG LEPGKGRHHR 420
 GRGGEPRAYF MSDTREEKRF LGEHHRVQE NQMDKARRHP QGAWKELDRN YLNYGEEGAP 480
 GKWQQQGLQ DTKENREAR FQDKQYSSH TAEKRRLGE LFNPHYDPLQ WKSSHFERRD 540
 NMNDNFLGE EENELTLNEK NFFPEYNYDW WEKKPFSEDV NWGYEKNLA RVPKLDLKRQ 600
 YDRVAQLDQL LHYRKSAEF PDFYDSEEPV STHQEAENEK DRADQTVLTE DEKKELENLA 660
 15 AMDLELQKIA EKFSQRG 677

Seq ID NO: C359 Protein Sequence
 Protein Accession #: XP_093082.1

1 11 21 31 41 51
 | | | | |
 MKLLCEGLKQ PNCVLQTLRW YRCLISSASC GALAAVLSTS QWLTELEFSE TKLEASALKL 60
 20 LYGGKLDPMC KLQKLNLFQS LSVTAALKPV GMVGNCSGFS GSLVQSHFGY QDSSFFKCDL 120
 CKLLWPSTRV AAADCGSPK SFLSEGLNWA GRLEAVEEVL GLGVLVQPGD PASQGGGHCE 180
 25 NYGSPRDLVD LEVKAEPSLR KGGMDLQRP LQVVLCKIF SLKFLFLIAL PNSPGQSVV 240
 QVTIPDGPNV VTVGSNVTI CIYTTTVASR EQLSIQWFF HKKEMEPISS PWEKGWPDV 300
 EAVKTLDDGQ QAEQIYFSG GQQAIAIGQF KDRITGSNDP GNASTISHM QPADSGIYIC 360
 DVNNPPDFLG QNQGILNVSV LVKPSKPLCS VQGRPETGHT ISLSCLSLG TSPVYVWHK 420
 30 LEGRDIVPVK ENFNPTTGIL VIGNLTNFEQ GYYQCTAINR LGNSSCEIDL TSSHPEVGII 480
 VGALIGSLVG AAIISVVCV ARNKAKAKAK ERNSKTIAEL EPMTKINPRG ESEAMPREDA 540
 TQLEVTLPSS IHETGPDITQ EPDYEPKPTQ EPAPEPAPGS EPMAPDLDI ELELEPETQS 600
 ELEPEPEPEP ESEPGVVVEP LSEDEKGVVK A 631

Seq ID NO: C360 Protein Sequence
 Protein Accession #: FGEMESH predicted

1 11 21 31 41 51
 | | | | |
 MVFAFWKVFL ILSCLAGQVS VVQVTIPDGF VNVTVGSNVT LICITYTTTVA SREQLSIQWS 60
 40 FFHKKEMEPI SSPWEEGKWP DVEAVKGTLD GQQAELQIYF SQGGQAVAIG QFKDRITGSN 120
 DPGNASITIS HMQPADSGIY ICDVNNPPDF LGQNQGLNV SVLVKPSKPL CSVQGRPETG 180
 HTISLSCLSA LGTPSPVYVY HKLEGRDIVP VKENFNPTTG ILVIGNLTNF EQGYVQCTAI 240
 NRLGNSSCEI DLTSSHPEVG IIVGALIGSL VGAAIIISVV CFARNKAKAK AKERNSKTIA 300
 ELEPMTKINP RGSEAMPRE DATQLEVTLP SSIHETGPDITQ EPDYEPKPTQ EPAPEPAP 360
 45 GSEPMAPVDL DIELELEPET QSELEPEPEP EPSEPGVVV EPLSEDEKGV VKA 413

Seq ID NO: C361 Protein Sequence
 Protein Accession #: NP_003011.1

1 11 21 31 41 51
 | | | | |
 MVSRMVSTML SGLLFWLASG WTPAFAYSPP TPDRVSEADI QRLHGVMEQ LGIARPRVEY 60
 50 PAQAMNLVG PQSIEGGAHE GLQHLGPFNG IPNIVAEITG DNIPKDFSED QGYDPPNPNC 120
 PVGKIDDGCL ENTPDTAEFS REFQLHQHLE DPEHDYPGLG KWNKLLYEK MKGGERRKRR 180
 55 SVNPLYQQQR LDNVVAKKSV PHFSDDEKDP E 211

Seq ID NO: C362 Protein Sequence
 Protein Accession #: NP_076926.2

1 11 21 31 41 51
 | | | | |
 MTTMQGMEQA MPGAGPGVPQ LGNMAVIHSH LWKGLQEKFL KGEPKVLGVV QILTALMSLS 60
 60 MGITMCMAS NTYGSNPISV YIGYTIWGSV MFIISGSLSI AAGIRTITKGL VRGSLGMNIT 120
 SSVLAASGIL INTFSLAFYS FHHPYCNYYG NSNNCHGTMS ILMGLDGMVL LLSVLEFCIA 180
 65 VLSAFGCKV LCCTPGGVVL ILPSHSHMAE TASPTPLNEV 220

Seq ID NO: C363 Protein Sequence
 Protein Accession #: NP_002082.1

1 11 21 31 41 51
 | | | | |
 MRGSELPLVL LALVLCAPR GRAVPLPAGG GTVLTMYPR GNHWAVGHLM GKKSTGESSS 60
 70 VSERGSLKQ LREYIRWEEA ARNLLGLIEA KENRNHQPQ PKALGNQPS WDSSESSNFK 120
 DVSGKGVGR LSAPGSQREG RNPQLNQ 148

Seq ID NO: C364 Protein Sequence
 Protein Accession #: NP_036393.1

1 11 21 31 41 51
 | | | | |
 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60
 80 EFAAKFIVP DWWASNYVDL ITEQADIALT RGAEVKGRG HSQSELQVFW VDRAYALKML 120
 FVKESHNSK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHHLS ALVTPAGKSY 180
 ECQAQQTISL ASSDPQKTVT MILSAVHIQ FDIISDFVS EEHKCPVDER EQLEETLPLI 240
 LGLILGLVIM VTLAIYVHH KMTANQVQIP RDRSQYKHM 280

Seq ID NO: C365 Protein Sequence
Protein Accession #: NP_003217.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MLGLVLALLS SSSAEYVGL SANQCAVPAK DRVDCGYPHV TPKECNRRCG CFDSRIPGVP 60
      WCFKPLTRKT ECTF 74

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Seq ID NO: C366 Protein Sequence
Protein Accession #: NP_002984.1

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15     1      11      21      31      41      51
      |      |      |      |      |      |
      MSLPSSRAAR VPGPSGSLCA LLALLLLTTP PGPLASAGPV SAVLTELRCT CLRVTLRVNP 60
      KTIGKLQVFP AGPQCSKVEV VASLKNKGQV CLDPEAPFLK KVIQKILDSG NKKN 114

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Seq ID NO: C367 Protein Sequence
Protein Accession #: NP_005233.2

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20     1      11      21      31      41      51
      |      |      |      |      |      |
      MRSPSAAWLL GAAILLAASL SCSGTIQGTN RSSKGRSLIG KVDGTSHTVG KGVTVETVFS 60
      VDEFSASVLT GKLTVFVLPV VYTIVFVVGL PSNGMALWVF LFRTKKKHPA VIYMANLALA 120
      DLLSVIWFPL KIAYHIHANN WIYGEALCNV LIGFFYGNMY CSILFMTCLS VQRYWVIVNP 180
      MGHSRKKANI AIGISLAIWL LILLVTIPLY VVKQTIPIPA LNITTCHDVL PEQLLVGDMF 240
      NYFLSLATGV FLFPAPFLAS AYVLMIRMLR SSAMDENSEK KRKRAIKLIV TVLAMYLCF 300
      TPSNLLLVVH YFLIKSQGQS HVYALYIVAL CLSTLNSCID PFVYFVSHD FRDHAKNALL 360
      CRSVRTVKQM QVSLTSKKHS RKSSSYSSSS TTVKTSY 397

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Seq ID NO: C368 Protein Sequence
Protein Accession #: NP_003460.1

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35     1      11      21      31      41      51
      |      |      |      |      |      |
      MAEAKTHWLG AALSILIPLIF LISGAEEASF QRNQLQKEP DLRLENVQKF PSEPMIRALE 60
      YIENLRQQAQ KEESPDPDYN YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ 120
      AENEPQSAPK ENKPYALNSE KNFPMDDSD YETQQWPERK LKHMQFPMPY EENSNDNPFK 180
      RTNEIVEEQY TPQSLATLES VFQELGKLTG PNNQKRERMD EEQKLYTDD EDDIYKANNIA 240
      YEDVVGGEDW NPVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSQGLGI QEEDLRKESK 300
      DQLSDDVSKV IAYLKRLLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRNLQI 360
      PPEDLIEMLK TGEKNGSVE PERELDLPVD LDDISEADLD HPDLFQNRML SKSGYPKTPG 420
      RAGTEALPDG LSVEDIILNL GMESANQKT SYFPNPNQK KVLPRLPYGA GRSRSNQLPK 480
      AAWIPHVENR QMAYENLNK DQELGEYLAR MLVKYPEIIN SNQVKRVPQG GSSEDDLQEE 540
      EQIEQAIKEH LMQGSSQETD KLAPVSKRFP VGPPKNDDTP NRQYWDDEL MKVLEYLNQE 600
      KAEKGREHIA KRAMENM 617

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Seq ID NO: C369 Protein Sequence
Protein Accession #: NP_112217.1

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50     1      11      21      31      41      51
      |      |      |      |      |      |
      MPCAQRSWLA NLSVVAQLLN FGALCYGRQP QGPEVRFPDR RQEHFIKGLP EYHVVGPRV 60
      DASGHFLSYG LHYPTITSRK KRDLDGSEDW VYRISHEEK DLFFNLTVNQ GLFSNSYIME 120
      KRYGNLSHVK MASSAPLCH LSGTVLQGGT RVGTAALSAC HGLTGFFQLP HGDDFFIEPVK 180
      KHFLVEGGYH PHIVYRRQKV PETKEPTCGL KDSVNISQKQ ELWREKWERH NLFSRSLSR 240
      SISKERWVET LUVADTKMIE YHGSENVESY ILTIMNMVTG LFHNPSIGNA IHIVVVRLL 300
      LEEEEQGLKI VHHAETLSS FCKWQKSINP KSDLNPVHHD VAVLLTRKDI CAGFNRPCT 360
      LGLSHLSGMC QPHRSCNINE DSGPLAFTI AHGLGHSFGI QHDGKENDCE PVGRHPYIMS 420
      RQLQYDPTPL TWKCSSEYI TRFLDRGWGF CLDDIPKKKG LKSKVIAPGV IYDVHHQCQL 480
      QYGPNAFCQ EVENVQCQLW CSVKGFCRSK LAAAADGTQC GEKKWCMAK CITVGGKPKES 540
      IPGGWGRWSP WSHCSRTCGA GVQSAERLCN NPEPKFGGKY CTGERKRYRL CNVHPCRSEA 600
      PTFRQMOCSE FDTVPYKNEL YHWFPIFNPA HPCELYCRPI DGQFSEKMLD AVIDGTPCFE 660
      GGNRSNVCIN GICKMVGCDY EIDSNATEDR CGVCLGDGSS CQTVRKMPKQ KEGSGYVDIG 720
      LIPKGARDIR VMEIEGAGNF LAIRSEDPEK YYLNGGFIIQ WNGNYKLAGT VFQYDRKGD 780
      EKLMTAGFTN ESUVIQLLFQ VTNPGIKY EY TIQKDGLDND VEQMYFWQYG HWTECSVTCG 840
      TGIRRTAHCH IKKGRGMVKA TFCDPETQPN GRQKKCHEKA CPPRWAGW EACSATCGPH 900
      GEKRTVLICI QTMVSDEQAL PPTDCQHLLK PKTLLSCNRD ILCPSDWTVG NWSECSVSCG 960
      GGVIRSVTC AKNHDEPCDV TRKPNRSLC GLQCCPSRR VLKPNKGTIS NGKNPPTLKP 1020
      VPPPTSRPRM LTTPTGPESM STSTPAISSP SPTTASKEGD LGGKQWQDSS TQPELSSRYL 1080
      ISTGSTSQPI LTSQSLIQP SEENVSSDT GPTSEGGLVA TTTSGSGLSS SRNPITWPVT 1140
      PFFNLTITKGP EMEIHSGSGE EREQPEDKDE SNPVIWTKIR VPGNDAPVES TEMPLAPPLT 1200
      PDLRSRQWPF PFTSVMEGLL PSQRPTTSET GTPRVEGMVT EKPAANTLLPL GGDHQPEPSG 1260
      KTANRNHLKL PNNMNQTKSS EFWLTEEDAT SLITEGFLN ASNYKQLTNG HGSAHWIVGN 1320
      WSECTTTCGL GAYNKRVECT TQMDSDCAAI QRPDPAKRCH LRPCAGWKVG NWSKCSRNC 1380
      GGFIREIQVC VDSRDHRLR PFHCQFLAGI PPPLSMSCNP EPCWAWQVEP WSCSRSCGG 1440
      GVQERGVFCP GGLCDWTKRP TSTMSCNEHL CCHWATGNWD LCSTSCGGGF QKRIVQCVPS 1500
      BGNKTEDQDQ CLCDHKPRPP BFKKCNQAC KKSADLLCTK DKLSASFQCT LKAMKCSVP 1560
      TVRAECCFSC PQTHITHQR QRRQLLQKS KEL 1593

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Seq ID NO: C370 Protein Sequence
Protein Accession #: NP_001053.1

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1      11      21      31      41      51

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	1	11	21	31	41	51	
	MRQSHQLPLV	GLLLFSFIPS	QLCEICEVSE	ENYIRLKPLL	NTMIQSNYNR	GTSAVNVVLS	60
	LKLVGIQIQT	LMQKMIQIQ	YNVKSRLSDV	SSGELALIL	ALGVCRNAEE	NLIYDYHLTD	120
	KLENKFQAEI	ENMEAHNGTP	LTNYQLSLD	VLALCLFNGN	YSTAEVNVHF	TPENKNYYFG	180
5	SQFSVDTGAM	AVLALTCVKK	SLINGQIKAD	EGSLKNISYI	TKSLVEKILS	EKKENGLIGN	240
	TFSTGEAMQA	LFVSSDYNE	NDWNCQQTIN	TVLTEISQGA	FSNPNAAAQV	LPALMGKTFL	300
	DINKDSSCVS	ASGNFNISAD	EPITVTPDS	QSYISVNYSV	RINETYFTNV	TVLNGSVFLS	360
	VMEKAQKMND	TIFGFTMEER	SWGPYITCIQ	GLCANNNDRT	YWELLSGGEP	LSQGAGSYVV	420
10	RNGENLEVRW	SKY					433
	Seq ID NO: C371 Protein Sequence						
	Protein Accession #: NP_004582.1						
	1	11	21	31	41	51	
	MCCTKSLLLA	ALMSVLLHL	CGESEASNF	DCCLGYTDRI	LHPKFIVGFT	RQLANEGCDI	60
15	NAIIFHTKKK	LSVCANPKQT	WVKYIVRLLS	KKVKNM			96
	Seq ID NO: C372 Protein Sequence						
	Protein Accession #: NP_037403.1						
	1	11	21	31	41	51	
	MAGSPLLWGP	RAGGVGLLVL	LLLGLFRPPP	ALCARPVKEP	RGLSAASPPL	AETGAPRRFR	60
25	RSVPRGEAAG	AVQELARALA	HLEAERQER	ARAEAEAEED	QCARVLAQLL	RVWGAPRNSD	120
	PALGLDDDDP	APAAQLARAL	LRARLDPAAL	AAQLVPAPVP	AAALRP RPVP	YDDGPAGPDA	180
	EEAGDETPDV	DELLRLYLLG	RILAGSADSE	GVAAPRRLRR	AADHDVGSEL	PPEGVLGALL	240
	RVKRLETPAP	QVPARLLLP					260
30	Seq ID NO: C373 Protein Sequence						
	Protein Accession #: NP_002236.1						
	1	11	21	31	41	51	
35	MLQSLAGSSC	VRIVERHRSA	WCFGFLVLGY	LLYLVPFVAV	FSSVELPYED	LLRQELRKLK	60
	RRFLEEHECL	SEQQLEQFLG	RVLEASNYGV	SVLSNASGNW	NWDFTSALFF	ASTVLSTTGY	120
	GHTVPLSDGG	KAFCIISVSI	GIPFTLLFLT	AVVQRITVHV	TRRPVLYFHI	RWGFSGQVVA	180
	IVHAVLLGFV	TVSCFFFIAP	AVFSVLEDDW	NFLESFYFCF	ISLSTIGLGD	YVPGEGYNQK	240
40	FRELYKIGIT	CYLLGLLIAM	LVVLETFCEL	HELKKFRKMF	YVKKDKDEDQ	VHIEHDQLS	300
	FSSITDQAAG	MKEDQKQNEP	FVATQSSACV	DGPANH			336
	Seq ID NO: C374 Protein Sequence						
	Protein Accession #: NP_005463.1						
45	1	11	21	31	41	51	
	METTINGTETW	YESLHAVLKA	LNATLHSNLL	CRPGPGLGPD	NQTEERRASL	PGRDDNSYMY	60
	ILFVMFLFAV	TVGSLILGYT	RSRKVDKRSD	PYHVYIKNRV	SMI		103
50	Seq ID NO: C375 Protein Sequence						
	Protein Accession #: NP_005236.1						
	1	11	21	31	41	51	
55	MGRHLALLLL	LLLLFQHFQD	SDGSQRLEQT	PLQFTHLEYN	VTVQENSAAK	TYVGHVPKMG	60
	VYITHPAWEV	RYKIVSGDSE	NLFKAEEYIL	GDFCFLRIRT	KGGNTAILNR	EVKDYHTLIV	120
	KALEKNTNVE	ARTKVRVQVL	DTNDRPLFS	PTSYSVSLPE	NTAIRTSIAR	VSATDADIGT	180
	NGEFYYSFKD	RTDMFAIHPT	SGVIVLTGRL	DYLETKLYEM	EILAADRGMK	LYGSSGISSM	240
	AQLTVHIEQA	NECAPVITAV	TLSPSELDRD	PAYAIVTVDD	CDQGGANGDIA	SLSIVAGDLL	300
60	QQFRTRVSFP	GSKEYKVKAI	GDIDWDSHPF	GYNLTQAKD	KGTTPQFSSV	KVIHVTSPQF	360
	KAGPVKFEKD	VYRAEISEFA	PENTPVVMVK	AIPAYSHLRY	VFKRTPGKAK	FSLNNTGLI	420
	SILEPVKRQQ	AAHFELEVTT	SDRKASTKVL	VKVLGANSNP	PEFTQTAYKA	AEDENVPIGT	480
	TIMSLSAVDP	DEGENGYVTY	SIANLNHVPF	AIDHFTGAVS	TSENLDYELM	PRVYTLRIRA	540
	SDWGLPYRRE	VEVLATITLN	NLNDNTPLFE	KINCEGTIPR	DLGVGEQITT	VSAIDADELQ	600
65	LVQYQIEAGN	ELDLFSLNPN	SGVLSLKRSL	MDGLGAKVSF	HSLRITATDG	ENFATPLYIN	660
	ITVAASHKLV	NLQCEETGVA	KMLAEKLLQA	NKLHNQGEVE	DIFFDSSHVN	AHIPQFRSTL	720
	PTGIQVKENQ	PVGSSVIFMN	STDLDITGFNG	KLIVYAVSGGN	EDSCFMIDME	TGMLKILSPL	780
	DRETTDKYTL	NITVYDLGIP	QKAAWRLLHV	VVDANDNPP	EFLQESYFVE	VSEDKEVHSE	840
	IIQVEATDKD	LGPNGHVTYS	ILTDITDTFSI	DSVTGVVNIA	RPLDRELQHE	HSLKIEARDQ	900
70	AREEPQLFST	VVVKVSLSDV	NDNPTTFIPP	NYRVKVRDL	PEGTVIMWLE	AHDPLDQSGS	960
	QVRYSLLDHG	EGNFVDVKLS	GAVRIVQQLD	FEKKQVYNLT	VRAKDKGKPV	SLSSTCYEV	1020
	EVVDVNEHLH	PPVFSFVEK	GTVKEDAPVG	SLVMTVSAHD	EDAGRDGEIR	YSIRDGSGVG	1080
	VFKIGEETGV	IETSDRLDRE	STSHYWLTVF	ATDQGVVPLS	SFIEIYIEVE	DVNDNAPQTS	1140
	EPVYYPEIME	NSPKDVSUVQ	IEAFDPDSSS	NDKLMYKITS	GNPQGFSSIH	PKTGLITTS	1200
75	RKLDREQQDE	HILEVTVDN	GSPPKSTIAR	VIVKILDEND	NKPQFLQKFY	KIRLPEREKP	1260
	DRERNARREP	LYRVIAATDK	EGPNAEISYS	IEDGNEHGKF	FIEPKTGVVS	SKRFSAAAGEY	1320
	DILSLKAVDN	GRPQKSSTTR	LHIEWISKPK	QSLPISFEE	SFFTFTVMES	DPVAHMIGVI	1380
	SVEPPGIPLV	FDITGKNYDS	HFDVDKGTGT	IIVAKPLDAE	QKSNYNLTVE	ATDGTTLTIL	1440
80	QVFIKVIDTN	DHRPQFSTSK	YEVVIPEDTA	PETEILQISA	VQDEKKNLI	YTLQSSRDPL	1500
	SLKKFRLLDP	TGSLYTSEKL	DHEAVSPAHL	TVMVRDQDVP	VKRNFARIVV	NVSDTNDHAP	1560
	WFTASSYKGR	VYESAAGVSV	VLQVTALDKD	KGKNAEVLVS	IESGNIGNIG	NSFMIDPVLG	1620
	SKTKAKELDR	SNQAEYDLMV	KATDKGSPPM	SEITSVRIFV	TIADNASPKF	TSKEYSVELS	1680
	ETVSIGSFGV	MVTAHSQSSV	VYEIKDGNTE	DAFDINPHSG	TIITQKALDF	ETLPIYTLII	1740
	QGTNMAGLST	NTTVLVHLQD	ENDNAPVFMQ	AEYTGILISES	ASINSVVLTD	RNVPLVIRAA	1800

	DADKDSNALL	VYHIVEPSVH	TYFAIDSSTG	AIHTVLSLDY	EETSIFHFTV	QVHDMGTPRL	1860
	FAEYAAENVTV	HVIDINDCPP	VFAKPLYEAS	LLLPTYKGVK	VITVNATDAD	SSAFSGLIYS	1920
	ITEGNIGKFK	SMDYKTGALT	VQNTTQLRSR	YELTVRASDG	RFAGLTSVKI	NVKESKESHL	1980
5	KFTQDVYSAV	VKENSTEAE	LAVITAIGSP	INEPLFYHIL	NPDRRFKISR	TSGLVSTGT	2040
	PFDRBQAEAF	DVVVEVIEEH	KPSAVAHVVV	KVIVEDQNDN	APVFNLPYY	AVVKVDTEVG	2100
	HVIRYVTAVD	RDSGRNGEVH	YYLKEHHEHF	QIGPLGEISL	KKQFELDTLN	KEYLVTVVAK	2160
	DGGNPAFSAE	VIVPITVNNK	AMPVEKEPFY	SAEIAESIQV	HSPVVHVQAN	SPEGLKVFYS	2220
	ITDGDPPFSQF	TINFNTGVIN	VIAPLDFEAF	PAYKLSIRAT	DSLTGAHAEV	FVDIIVDDIN	2280
10	DNPPVFAQQS	YAVTLSEASV	IGTSVVQVRA	TDSDSEPNRG	ISYQMFNGHS	KSHDHFHVDS	2340
	STGLISLLRT	LDYEQSRQHT	IFVRAVDGGM	PTLSSDVIPT	VDVTDLNGNP	PLFEQQLIYEA	2400
	RISEHAPHGH	FVTCVKAYDA	DSSDIDKLQY	SILSGNDHKK	FVIDSATGII	TLSNLHRHAL	2460
	KPFYSLNLSV	SDGVFRSSTQ	VHVTVIGGNL	HSPAFLQNEY	EVELAENAPL	HTLVMEVKT	2520
	DGDSGIYGHV	TYHIVNDFAK	DRFYINERGO	IFTLEKLDRE	TPAEKVISVR	LMAKDAGGKV	2580
15	AFCTVNVILT	DDNDNAPQFR	ATKYEVNIGS	SAAKGTSVVK	SASDADEGSN	ADITYAIEAD	2640
	SESUKENLEI	NDLSGVITTK	ESLIGLENEF	FTFFVRAVDN	GSPSKESVVL	VYVKILPPEM	2700
	QLPKFSEPFY	TFTVSEDVPV	GTEIDLIRAE	HSGTVLYSLV	KGNTPESNRD	ESFVIDRQSG	2760
	RLKLEKSLDH	ETTKWYQFSI	LARCTQDDHE	MVASVDVSIQ	VKDANDNSPV	FESSPYEAFI	2820
	VENLPGGSRV	QIRASDADS	GTNGQVMYSL	DQSQSVEVIE	SFAINMETGW	ITTLKELDHE	2880
20	KRDNYQIKV	ASDHGEKIQ	SSTAIVDVT	TDVNDSPPRF	TAEIYKGTVS	EDDPQGGVIA	2940
	ILSTTDADSE	EINRQVTYFI	TGGDPLGQFA	VETIQNEWKV	YVKKPLDREK	RDNYLLTTA	3000
	TGDTFSSKAI	VEVKVLDAND	NSPVCEKTLV	SDTIPEDVLP	GKLIMQISAT	DADIRSNAEI	3060
	TYTLGLSGAE	KFKLNPDTGE	LKTSTPLDRE	EQAVYHLLVR	ATDGGGRFCQ	ASIVVTLDEV	3120
	NDNAPEFSAD	PYAITVVFENT	EPGTLTLRVQ	ATDADAGLNR	KILYSLIDSA	DGQFSINELS	3180
25	GIIQLEKPLD	RELQAVYTIS	LKAVDQGLPR	RLTATGTIVV	SVLDINDNPP	VFEYREYGAT	3240
	VSEDILVGT	VLQVYAASRD	IEANAEITYS	IISGNEHGKF	SIDSKTGAVF	IIENLDYESS	3300
	HEYYLTVEAT	DGGTSPSLSDV	ATVNVNVTDI	NDNTPVFSQD	TYTTVISED	VLEQSVITVM	3360
	ADDADGPSNS	HIHYSIIDGN	QSSSFTIDPV	RGEVKVTKLL	DRETISGYTL	TVQASDNGSP	3420
	PRVNTTTVNI	DVSDVNDNAP	VFSRGNYSVI	IQENKPVGFS	VLQLVVTDED	SSHNGPPFFF	3480
30	TIVTGNDEKA	FEVNPQGVLL	TSSAIKRKEK	DHYLLQVKVA	DNGKPOLSSL	TYIDIRVIEE	3540
	SIYPPAILPL	EIFITSSGEE	YSGGVIGKIH	ATDQDVYDTL	TYSLDPQMDN	LFSVSSTGGK	3600
	LIAHKLDIG	QYLLNVSVTD	GKFTTVADIT	VHIRQVTQEM	LNHTIAIRFA	NLTPEEFVGD	3660
	YWRNFQALR	NILGVRNRDI	QIVSLQSSEP	HPHLDVLLFV	EKPGSAQIST	KQLLHKINS	3720
	VTDIEELIGV	RILNVFQKLC	AGLDPCWKFC	DEKVSVDSEV	MSTHSTARLS	FVTPRHHRAA	3780
35	VCLCKEGRCP	PVHGGCEDDP	CPEGSECVSD	PWEEKHTCVC	PSGRFGQCPG	SSSMTLTGNS	3840
	YVKYRLTENE	NKLEMKLTMR	LRTYSTHAVV	MYARGTDYSI	LEIHHGRLQY	KFDCGSGPGI	3900
	VSVQSIQVND	GQWHAVALV	NGMYARLVLD	QVHTASGTAP	GLTKTLNLDN	YVFFGGHIRQ	3960
	QGTRHGRSPQ	VGNNGFRGCM	SIYINGQELP	LNSKPRSYAH	IEESVDVSPG	CFLTATEDCA	4020
	SNPCQNGGVC	NPSAPAGGYC	KCSALYIGTH	CEISVNPCCS	NPCLYGGTCV	VNNGGFVCQC	4080
40	RGLYTGQRQC	LSPYCKDEPC	KNGGTCFDSL	DGAVCQCDSD	FRGERCQSDI	DECSGNPCLH	4140
	GALCENTHGS	YHCNCSEHYR	GRHCEDAAPN	QYVSTPWNI	LAGIGIGIVF	VAGIFLLVVV	4200
	FVLCRKMISR	KKKHQAEPKD	KHLGPATAFL	QRPYFDSKLN	KNIYSDIPPQ	VVPVRISYTP	4260
	SIPSDSRNNL	DRNSFEGSAI	PEHPEFSTFN	PESVHGHRKA	VAVCSVAPNL	PPPPPSNSPS	4320
	DSDSIQKPSW	DFDYDTKVVD	LDPCLSKKPL	EEKPSQPYSA	RESLSEVQSL	SSPQSESCDD	4380
45	NGVHWDTSW	MPGVLPEDIQ	EFNPNYVIDE	QTPLYSADPN	AIDTDYVPEG	YDIESDFPPP	4440
	PEDFPAADEL	PPLPPEFSNQ	FESIHPPRDM	PAAGSLGSSS	RNRQRFLNLQ	YLPNFYPLDM	4500
	SEPMQTKTGE	NSTCREPHAP	YPPGYQRHFE	APAVESMFMS	VYASTASCSD	VSACCEVESE	4560
	VMMSDYESGD	DGHFEVITIP	PLDSQQHTEV				4590

Seq ID NO: C376 Protein Sequence
Protein Accession #: NP_055035.1

	1	11	21	31	41	51	
55	MCYKGCARCI	GHSVLGLALL	CIAANILLYF	PNGETKYASE	NHLSRFVWFV	SGIVGGGLLM	60
	LLPAFVFIGL	EQDDCCGCCG	HENCGKRCAM	LSSVLAAALIG	IAGSGYCVIV	AALGLAEGPL	120
	CLDSLQWQNY	TFASTEGQYL	LDTSTWSECT	EPKHIVEWNV	SLFSILLALG	GIEFILCLIQ	180
	VINGVLGGIC	GFCCSHQQYQ	DC				202

Seq ID NO: C377 Protein Sequence
Protein Accession #: NP_003750.1

	1	11	21	31	41	51	
65	MSTENVEGKP	SNLGERGRAR	SSTFLRVVQP	MFNHSIFTS	VSPAARIRIF	ILGEEDDSPA	60
	PPQLFTELDE	LLAVDQEME	WKETARWIKF	EEKVEQGGER	WSKPHVATLS	LHSLFELRTC	120
	MEKGSIMLDR	EASSLPQLVE	MIVDHIQETG	LLKPELKDQV	TYTLRKRHRH	QTKKSNLRS	180
	ADIGKTVSSA	SRMFTNPNG	SPAMTHRNLT	SSSLNDISDK	PEKQQLKNKF	MKKLPRDAEA	240
	SNVLVGEVDF	LDTPFIAFVR	LQQAIVMLGAL	TEVPVPTRFL	FILLGPKGKA	KSYHEIGRAI	300
70	ATLMSDEVFH	DIAYAKAKRH	DLIAGIDEFL	DEVIVLPPGE	WDPAIRIEPP	KSLPSSDKRK	360
	NMYSGGENVQ	MNGDTPHDGG	HGGGGHGDCE	ELQRTGRFCG	GLIKDIKRKA	PPFASDFYDA	420
	LNQIALSAIL	FYILATVTNA	ITFGGLLGD	TDMMQGVLES	FLGTAVSGAI	FCLFAGQPLT	480
	ILSSSTGPVLV	FERLLENFSK	DNNFDYLEFR	LWIGLWSAFL	CLILVATDAS	FLVQYVTRFT	540
	EEGFSSLSIF	IFIYDAFKKM	IKLADYYPIN	SNFKVGYNTL	FSCTCVPPDP	ANISISNDIT	600
75	LAPYLPTMS	STDMYHNTTF	DWAFLSKKEC	SKYGGNLVGN	NCNFVPDITL	MSFILFLGT	660
	TSSMALKKFK	TSYPFTTAR	KLISDFAILL	SILIFCVIDA	LVGVDPKPLI	VPSEFKPTSP	720
	NRGWFPVPPG	ENPWWVCLAA	AIPALLVTIL	IFMDQQTAV	IVNRKHEKLL	KGAGVHLDLF	780
	WVAILMVICS	LMALPWVYAA	TVISIAHIDS	LKMETETSAP	GEQPKFLGVR	EQRVGTGLVF	840
	ILTGLSVFMA	PILKFIMPV	LYGVFLYMGV	ASLNGVQFMD	RLKLLMLPLK	HQPDFIYLRLH	900
80	VPLRRVHLFT	FIQVLCALAL	WILKSTVAAI	IFPVMILALV	AVRKGMDYLF	SQHDLSFLDD	960
	VIPEKDKKKK	EDEKDKKKKK	GSLDSNDNDS	DCPYSEKVP	IKIPMDIMEQ	QPFLSDSKPS	1020
	DRERSPTFLE	RHTSC					1035

Seq ID NO: C378 Protein Sequence
Protein Accession #: NP_000949.1

1 11 21 31 41 51
 5 MSTPGVNSSA SLSPDRLNSP VTIPAVMFIF GVVGNLVAIV VLCKSRKEQK ETTFYTLVCG 60
 LAVTDLGLTL LVSPVTIATY MKGQWPGGQP LCEYSTFILL FFSLSGLSII CAMSVERYLA 120
 INHAYFYSHY VDKRLAGLTL FAVYASNVLFCALPNMGLGS SRLQYPTDWC FIDWTTNVTA 180
 HAAYSIMYAG FSSFLILATV LCNVLVCGAL LRMHRQFMRR TSLGTEQHAH AAAASVASRG 240
 HPAASPALPR LSDFRRRRSF RRIAGAEIQM VILLIATSLV VLICSIPLVV RVFVNQLYQP 300
 10 SLEREVSQNP DLQAIRIASV NPILDPIYI LLRKTVLSKA IEKIKCLPCR IGGSRRRRSRG 360
 QHCSDSQRTS SAMSGHSRSF ISRELKEISS TSQTLPLDLS LPDLSENGLG GRNLLPGVFG 420
 MGLAQEDTTS LRTLRISETS DSSQGDSES VLLVDEAGGS GRAGPAPKGS SLQVTFPSET 480
 LNLSEKCI 488

Seq ID NO: C379 Protein Sequence
 Protein Accession #: NP_002650.1

1 11 21 31 41 51
 20 MGHPLPLPLL LLLHTCVPAS WGLRCMQCKT NGDCRVEECA LGQDLCRTTI VRLWEEGEEL 60
 ELVEKSCTHS EKTNRNLSYR TGLKITSLTE VVCGLDLCNQ GNSGRAVTYS RSRYLECISC 120
 GSSDMSCERG RHQSLQCRSP EEQCLDVVTH WIEGEEGRP KDDRHLRGCG YLPGCPGSGNG 180
 FHNNDTFHFL KCCNTTKCNE GPILELENLP QNGRCQYSCK GNSTHGCSSE ETFLIDCRGP 240
 MNQCLVATGT HEPKNQSYMV RGCATASMCQ HAHLGDAFSM NHIDVSCCTK SGCNHPDLV 300
 25 QYRSGAAPQP GPAHLSLTIT LLMTARLWGG TLLWT 335

Seq ID NO: C380 Protein Sequence
 Protein Accession #: BAB55406.1

1 11 21 31 41 51
 30 MDFESGQVDP LASVILPPNL LENLSPEDSV LVRRQAQTFE NKTGLFQDVG PQRKTLVSYV 60
 MACSIGNITI QNLKDPVQIK IKHTRTQEVH HPICAFWDLN KKSFGGWNW SGCAVHRDSD 120
 ASETVCLCNH FTHFGVIMDL PRSASQLDAR NTKVLTFISY ICGGISAIFS AATLLTYVAF 180
 35 EKLRRDYPSPK ILMNLSLALL FLNLLFLLDG WITSFNVDGL CIAVAVLLHF FLATFTWMG 240
 LEATHMYIAL VKVFNTYIRR YILKFCIIGW GLPALVSVV LASRNNNEVY GKESYGKEKG 300
 DEFCWIQDPV IFYVTCAGYF GVMFFLNIAM FIVVMVQICG RNGKRSNRTL REEVLNRLRS 360
 VVSLTFLGGM TWGFAFFAWG PLNIPFMYLF SIFNSLQGLF IFIFHCAMKE NVQKQWRRLH 420
 CCGRFRILADN SDWSKTATNI IKKSSDNLGK SLSSSSISGN STYLTSSKSKS SSTTYFKRNS 480
 40 HTDNVSYEHS FNKSGSLRQC FHGQVLVKTG PC 512

Seq ID NO: C381 Protein Sequence
 Protein Accession #: NP_000565.1

1 11 21 31 41 51
 45 MTVARPSVPA ALPLLGLPRL LLLLVLCLLP AVWGDCGLPP DVPNAQPALE GRTSFPEDTV 60
 ITYKCEESFV KIPGEKDSVI CLKGSQWSDI EEFENRSCFV PTRLNSASLK QPYITQNYFP 120
 VGTVVEYECR PGYRREPSLS PKLTCLQNLK WSTAVEFCKK KSCPNPGEIR NGQIDVPGGI 180
 LFGATISFSC NTGYKLGST SSFCLISGSS VQWSDPLPEC REIYCPAPPQ IDNGIIQGER 240
 50 DHYGYRQSVT YACNKGFTMI GEHSIYCTVN NDEGEWSGPP PECRGKSLTS KVPPTVQKPT 300
 TVNVPTTEVS PTSQKTTTKT TTPNAQATRS TPVSRRTTKHF HETTPNKGSG TTSQTTRLLS 360
 GHTCFTLTGL LGTLVTMGLL T 381

Seq ID NO: C382 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 60 MDTSLRGLVL SLPVLLQLAT GGSSPRSGVL LRGCPHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSVFTSY LDLSMNNISQ LLNPLPLSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120
 LQNNQLRHVP TEALQNLRSQ QSLRLDANHI SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD 240
 LNNYNNLDEFP TAIRTLNLSK ELHFYDNPIQ FVGRSAFQHL PELRTLTLNG ASQITEFPDL 300
 65 TGTANLESIT LTGAQISSLP QTVCNQLPNL QVLDLSYNLL EDLPSEFVCQ KLQKIDLRHN 360
 EIYEIKVDTF QQLLSLRSIN LAWNKIAIHH PNAFSTLPSL IKLDLSSNLL SSFPITGLHG 420
 LTHLKLGTGNH ALQSLISSEN FPELVIEIMP YAYQCCAFGV CENAYKISNQ WNKGDNSMMD 480
 DLHKKDAGMF QAQDERDLED FLDDFEEDLK ALHSVQCSPS PGPFKPEHL LDGWLIRIGV 540
 WTIAYLALTC NALVTSTVFR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDAFTFGSF 600
 70 ARHGAWWENG VGCHVIGFLS IFASESSVFL LTLAALERGF SVKYSKPFET KAPFSSLKVI 660
 ILLCALLALT MAAPVLLGGS KYGASPLCLP LPFGEPSTMG YMALILLNS LCFLMMTIAY 720
 TKLYCNLDKG DLENINWDCM VKHIALLLFT NCILNCPVAF LSFSSLINLT FISPEVIKFI 780
 LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS 840
 TQALVTFTSS SITYDLPPSS VSPAYPVTE SCHLSSVAFV PCL 883

Seq ID NO: C383 Protein Sequence
 Protein Accession #: NP_003658.1

1 11 21 31 41 51
 80 MDTSLRGLVL SLPVLLQLAT GGSSPRSGVL LRGCPHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSVFTSY LDLSMNNISQ LLNPLPLSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120
 LQNNQLRHVP TEALQNLRSQ QSLRLDANHI SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD 240
 LNNYNNLDEFP TAIRTLNLSK ELGFHSSNNIR SIPEKAFVGN PSITIHFDY NPIQFVGRSA 300

FQHLPELRTL TLNGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS 360
 YNLLEDLPSPF SVCQKLKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIHPNAPST 420
 LPSLTKLDLS SNLLSSEFPIT GLHGLTHLKL TGNHALQSLI SSENFPPELKV IEMPYAYQCC 480
 AFGVCENAYK ISNQWNKGDN SSMDDLHKKD AGMFQAQDER DLEDFLDDE EDLKALHSVQ 540
 CSPSPGPFKP CEHLLDGWL I RIGVWTIAVL ALTICNALVTS TVFRSPLYIS PIKLLIGVIA 600
 AVNMLTGVSS AVLAGVDAFT FGSFARHGAW WENGVCCHVI GFLSIFASES SVFLLTLAAL 660
 ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLFPGEF 720
 STMGYMVALI LLNSLCFLMM TIAYTKLYCN LDKGDLNENI DCSMVKHIAL LFTNCILNC 780
 VVAFLSFSSL INLTIFISPEV IKFILLVVVP LPACLNPLLY ILFNPHFKED LVSLRKQTYV 840
 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900
 VAFVPC 907

Seq ID NO: C384 Protein Sequence
 Protein Accession #: NP_003497.1

1 11 21 31 41 51
 MEMFTFL LTC IFLLPLRGHS LFTCEPITVP RCMKMAYNMT FFPNLMGHYD QSIAAVEMEH 60
 FLPLANLECS PNIEFTLCKA FVPTCIEQIH VVPPCRKLCE KVS DCKKLI DTFGIRWPPEE 120
 LECDR LQYCD ETVPVTFDPH TEFLGPQKKT EQVQRDIGFW CPRHLKTS GG QGYKFLGIDQ 180
 CAPP CPNMYF KSDELEFAKS FIGTVSIFCL CATLFTFLTF LIDVRRFRYP ERPIIYYSVC 240
 YSIVSLMYFI GFLLGDS TAC NKADEKLELG DTVVLG SQNK ACTVLFMLLY FFTMAGTVVW 300
 VILTITWFLA AGRKWSCEAI EQKAVWFHAV AWGTPGFLTV MLLALNKVEG DNISGVCVFG 360
 LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHGRNQEKL KKFMRIGVF 420
 SGLYLVLPIV LLGCYVYEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALFMIKY 480
 LMTLIVGISA VFWVGSKKT TEWAGFFKRN RKRDPISER RVLQESCEFF LKHNSKVKKH 540
 KKHVKPSSH KLVISKSMGT STGATANHGT SAVAITS HDY LGQETLTIEI TSPETSMREV 600
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660
 TGLAQSNLQ VPSSSEPSL KGSTSLLVHP VSGVRKEQGG GCHSDT 706

Seq ID NO: C385 Protein Sequence
 Protein Accession #: NP_000573

1 11 21 31 41 51
 MRIAVICFCL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLAPQTL 60
 PSKSNESH DH MDDMDEDDD DHVDSQDSID SNDSDDVDDT DDSHQSDSH HSDESDELVT 120
 DFPTDL PATE VFTPVVPTVD TYDGRGDSV YGLRSKSKKF RRPDIQYPA TDEDITSHME 180
 SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
 NEHSDVIDSQ ELSKVSREFH SHEFHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN 300

Seq ID NO: C386 Protein Sequence
 Protein Accession #: NP_002812

1 11 21 31 41 51
 MGAARGSPAR PRRLPLLSVL LLPLLGGTQT AIVFIKQPSS QDALQRRAL LRCEVEAPGP 60
 VHVVYLLDGA PVQDTERRFA QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANASFN 120
 IKWIEAGPVV LKHPASEABI PQQTQVTLRC HIDGHPRTY QWFRDGTPLS DGQSNHTVSS 180
 KERNLTLRPA GPEHSGLYSC CAHSAPGQAC SSQNF TSLIA DESFARVVLA PQDVVVARYE 240
 EAMFHCQFSA QPPPSLQWLF EDETPTITNRS RPPHLRRATV FANGSLLLTQ VPRNAGIYR 300
 CTGQQRGPP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPPKGLP EPSVWWEHAG 360
 VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKKPQD 420
 SQLEEGKPGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEVDGTWYR 480
 CMSSTPAGSI EAQARVQVLE KLKFTPPPQP QCCMEFDKEA TVPCSATGRE KPTIKWERAD 540
 GSSLPEWVTD NAGTLHFARV TRDDAGNYTC IASNGPQQQI RAHVQLTVAV FITFKVEPER 600
 TTVYQGH TAL LQCEAQGDPK PLIQWKGKDR ILDP TKGPR MHIFQNGSLV IHDVAPEDSG 660
 RYTCIAGNSC NIKHTEAPLY VVDKPVPEES EGPSPPPYK MIQTIGLSVG AAVAYIIAVL 720
 GLMFYCKKRC KAKRLQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780
 KRHSTD KMH FPRSSLQPI T LGKSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ 840
 LDPRELEMF KGLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSQ 900
 PLSTKQKVAL CTQVALGMEH LSNNRVFKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960
 YHFRQAWPV RWMSPEALE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEV LADLQ 1020
 AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDSPK 1070

Seq ID NO: C387 Protein Sequence
 Protein Accession #: NP_002300.1

1 11 21 31 41 51
 MKVLAAGVVP LLLVLHWKHG AGSPLPITPV NATCAIRHPC HNNLMNQIRS QLAQLNGSAN 60
 ALFILIYTAQ GEPEPNLNDK LCGPNVTDFP PFHANGTEKA KLVELYRIV YLGTSLGNIT 120
 RDQKILNP SA LSLHSLKMAT ADILRGLLSN VLCRLCSKYH VGHVDVTYGP DTSGKDVFOK 180
 KKLGCQLLGK YKQIIAVLA AF 202

Seq ID NO: C388 Protein Sequence
 Protein Accession #: XP_097508

1 11 21 31 41 51
 MGRPRLTLVC HVSIISARD LSMNNLTQL PGLFHHRLFL EELRLSGNHL SHIPQAFSG 60
 LYSLKILMLQ NNQLGGIPAE ALWELPSLQS LRLDANLISL VPERSFEGLS SLRHLWLDN 120
 ALTEIPVRAL NNKALQAMT LALNRISHIP DYAFQNL TSL VVLHLHNNRI QHLGTHSFEG 180
 LHNLETLDLN YNKLEFPVA IRTLGRQLQL GFHNNNIKAI PEKAFMGNPL LQTIHFDYDN 240

IQFVGRSAFQ YLPKLHTLSL NGAMDIQEFF DLKGTTSLEI LTLTRAGIRL LPSGMCQQLP 300
 RLRVLELSHN QIEELPSLHR CQKLEETGLQ HNRIWEIGAD TFSQLSSLQA LDLSWNAIRS 360
 IHPEAFSTLH SLVKLDLTDN QLTTLPLAGL GGLMHLKLG NLALSQAFSK DSFFKLRILE 420
 5 VPYAYQCCFY GMCASFVKAS QWEAEDLHL DDEESSKRPL GLLARQENH YDQDLDELQL 480
 EMEDSKPHPS VQCSPTPGPF KPCEYLFESW GIRLAVWAIV LLSVLCNGLV LLTVFAGGPV 540
 PLPPVKFVVG AIAGANTITG ISCGLLASVD ALTFGQFSEY GARWETGLGC RATGFLAVLG 600
 SEASVLLTL AAVQCSVSVS CVRAYGKSPS LGSVRAGVLG CLALAGLAAA LPLASVGEYG 660
 10 ASPLCLPYAP PEGQPAALGF TVALVMMNSF CFLVVGAYI KLYCDLPRGD FEAVWDCAMV 720
 RHVAWLIFAD GLLYCPVAFI SFASMLGLFP VTPEAVKSVL LVVLPPLACL NPLLYLLFNP 780
 HFRDDLRLR PRAGDSGPLA YAAAGELEKS SCDSTQALVA FSDVDLILEA SEAGRPPGLE 840
 TYGFPSVTLI SCQPGAPRL EGSCHVEPEG NHFGNPQPSM DGELLLRAEG STPAGGGLSG 900
 GGGFQPSGLA FASHV 915

Seq ID NO: C389 Protein Sequence
 Protein Accession #: NP_570901

1 11 21 31 41 51
 MASLVSELEL LLLAVLVVTA TASPPAGLLS LLTSGQGALD QEALGGLLNT LADRVHCTNG 60
 20 PCGKCLSVED ALGLGEPEG GLPPGPVLEA RYVARLSAAA VLYLSNPEGT CEDTRAGLWA 120
 SHADHLLALL ESPKALTPLG SWLLQRMQAR AAGQTPKTAC VDIPQLLEEA VGAGAPGSAG 180
 GVLAALLDHW RSGSCFHAP SPQYFVDFV QHSSEVPMT LAELSALMQR LGVGREAHSD 240
 HSHRHGASS RDPVPLISS NSSSVWDTVC LSARDVMAAY GLSEQAGVTP EAWAQLSPAL 300
 25 LQQQLSGACT SQSRPPVQDQ LSQSERYLYG SLATLLICLC AVFGLLLTTC TGCRCVAHYI 360
 LQTFLSLAVG ALTGDVAVLH TPKVGLGLHTH SEEGLSPOPT WRLLAMLAGL YAFFLFENLF 420
 NLLLPDPDED LEDGPGCHSS HSHGGHSHGV SLQLAPSELR QPKPPHEGSR ADLVAEESPE 480
 LLNPEPRRLS PELRLPLPMI TLGDVAVHFA DGLAVGAAFA SSWKTGLATS LAVFCHELPH 540
 ELGDFAALLH AGLSVRQALL LNLASALTAF AGLYVALAVG VSESESEWIL AVATGLFLYV 600
 30 ALCDMLPAML KVRDPRPWLL FLLHNVGLLG GWTVLLLSL YEDDITF 648

Seq ID NO: C390 Protein Sequence
 Protein Accession #: NP_061844

1 11 21 31 41 51
 35 MANASEPGGS GGGEAAALGL KLATLSLLLC VSLAGNVLFA LLIVRERSLH RAPIYLLLDL 60
 CLADGLRALA CLPAVMLAAR RAAAAAGAPP GALGCKLLAF LAALFCFHAA FLLLVGVVTR 120
 YLAIAHHRFY AERLAGWPCA AMLVCAAWAL ALAAAFPPVL DGGGDEDEDAP CALEQRPDGA 180
 40 PGALGFLLLL AVVVGATHLV YLRLLFFIHD RRMKRPARLV PAVSHDWTFF GPGATQAAA 240
 NWTAGFGRGP TPAALVGIRP AGPGRGARRL LVLEEFKTEK RLCKMFYAVT LLFLLWGPY 300
 VVASYLRVLV RGPALVQAYL TASVWLTFQA AGINPVVCFI FNRELRLDCFR AQFPCCQSPR 360
 TTQATHPCDL KGIGL 375

Seq ID NO: C391 Protein Sequence
 Protein Accession #: NP_005622

1 11 21 31 41 51
 50 MAAARPARGP ELPLLGLLLL LLLGDPGRGA ASSGNATGPG PRSAGGSARR SAAVTGPPPP 60
 LSHCGRAAPC EPLRYNVLG SVLPYGATST LLAGDSDSQE EAHGKLVLS GLRNAPRCWA 120
 VIQPLLCAVY MPKCENDRVE LPSRTLQCAT RGPCAIVERE RGWPDFLRCT PDRFPEGCTN 180
 EVQNIKFNSS GQCEVPLVRT DNPKSWYEDV ECGGIQCONP LFTEAEHQDM HSYIAAFGAV 240
 TGLCTLFETLA TFVADWRNSN RYPAVILFYV NACFFVGSIG WLAQFMDGAR REIVCRADGT 300
 55 MRLGEPTSNE TLSCVIFVI VYYALMAGVV WFWVLTIAWH TSFKALGTTY QPLSGKTSYF 360
 HLLTWSLPFV LTVAILAVAQ VDGDSVSGIC FVGYKNYRIR AGFVLAPIGL VLVGGYFLI 420
 RGVMTLFSIK SNHFGLLSEK AASKINETML RLGIFFGLAF GFVLITFSCH FYDFFNQAEW 480
 ERSFRDYVLK QANVTIGLPT KQPIPDCEIK NRPSLLVEKI NLFAMFGTGI AMSTWVTKA 540
 60 TLLIWRRTWC RLTGQSDDEP KRIKSKMIA KAFSKRHELL QNPQQLSFS MHTVSHDGPV 600
 AGLAFDLNRP SADVSSAWAQ HVTMVARRG AILPQDISVT PVATPVPPPEE QANLWLVEAE 660
 ISPQLQKRLG RKKKRRKRKK EVCPLAPPE LHPPAPAPST IPRLPQLPRQ KCLVAAGAWG 720
 AGDSCRQGAW TLVSNPFCPE PSPPDQDFLP SAPAPVAWAH GRRQGLGPIH SRTNLMDEL 780
 MDADSDF 788

Seq ID NO: C392 Protein Sequence
 Protein Accession #: BAC04382

1 11 21 31 41 51
 70 MGARSGARGA LLLALLLWCD PRLSQAGRKR SGEVLPSDFP SAPAEPLPYF LQEPQDAYIV 60
 KNKPVELRCR AFPATQIYFK CNGEWVSQND HVTQEGLEDEA TLGARGGLRV REVQIEVSRQ 120
 QVEELFGLSD YWCQCVAWSS AGTTKSRRAY VRIAYLRKNF DQEPGLKEVP LDHEVLLQCR 180
 PPEGVPVAEV EWLKNEDVID PTQDTNFLT IDHNLIIIRA RLSDTANYTC VAKNIVAKRR 240
 75 STTATVIVYV NGGWSSWAEW SPCSNRCCRG WQKTRTRCTN PAPLNGGAF CEGQAFQKTAC 300
 TTICPVDGAW TEWSKWSACS TECAHWSRE CMAPPQNGG RDCSGTLLDS KNCTDGLCMQ 360
 NKKTLSDPNS HLLASGDAA LYAGLVVAIF VVVAILMAVG VVVYRNRCD FDTIDTSSA 420
 ALTGGFHEVN FKTRARSPNQ LLHPSVPPDL TASAGIYRGV VYALQDSTDK IPMTNSPLD 480
 PLPSLKVEVY SSSTTGSGBP LADGADLLGV LPPGTYPDF ARDTFHLHL SASLGSQQLL 540
 GLPRDPGSSV SGTFCGLGGR LSIPGTGVS LVPNGAIPQG KFYEMYLLIN KAESTLPLSE 600
 80 GTQTVLSPSV TCGPTGGLLC RPVILTMPHC AEVSARDWIF QLKTAHQGH WEEVVTLDDE 660
 TLNTPCYQL EPRACHILLD QLGTIVFTGE SYSRSVAVKRL QLAVFAPALC TSLEYSRLVY 720
 CLEDTPVALK EVLELERTLG GYLVEEPKPL MFKDSYHNLR LSLHDLPHAH WRSKLLAKYQ 780
 EIPFYHIWSG SQKALHCTET LERHSLASTE LTCKICVRQV EGEGQIFQLH TTLAETPAGS 840
 LDTLCSAPGS TVTTQLGPYA FKIPLSIRQK ICNSLDAPNS RGNDWRMLAQ KLSMDRYLNY 900
 FATKASPTGV ILDLWEALQQ DDGDLNSLAS ALEEMGKSEM LVAVATDGDC 950

Seq ID NO: C393 Protein Sequence
Protein Accession #: NP_004616

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MNRKARRCLG HLFLSLGMVY LRIGGFSSVV ALGASII CNK IPGLAPRQRA ICQSRPDAIL 60
VIGEGSQMGL DECQFQFRNG RWNCSALGER TVFGKELKVG SREAAFTYAI IAAGVAHAIT 120
10    AACTQGNLSD CGCDKEKQGG YHRDEGWKWG GCSADIRYGI GFAKVFVDAR EIKQNARTLM 180
      NLHNEAGRK ILEENMKLEC KCHGVSGSCT TKTCWTTLPQ FRELGVVLKD KYNEAVHVEP 240
      VRASRNKRPT FLKIKKPLSY RKPMDTDLVY IEKSPNYCEE DPVTGSVGTQ GRACNKTA PQ 300
      ASGCDLMCCG RGYNTHQYAR VWQCNCCKFWH CCYVKCNTCS ERTEMYTCK 349

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Seq ID NO: C394 Protein Sequence
Protein Accession #: NP_003777

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15      1      11      21      31      41      51
      |      |      |      |      |      |
MDALCGSGEL GSKFWDNSNL VHTENPDLTP CFQNSLLAWV PCIYLWVALP CYLLYLRRHHC 60
20    RGYIILSHLS KLKMLVGLV WCVSWADLFY SFHGLVHGRA PAPVFFVTPL VVGVTMLLAT 120
      LLIQYERLQG VQSSGVLIIF WFLCVVCAIV PFRSKILLAK AEGEISDPFR FTTFYIHFAL 180
      VLSALILACF REKPPFFSAK NVDPNPYPET SAGFLSRLFF WWFTKMAIYG YRHPLEEKDL 240
      WSLKEEDRSQ MVVQQLLEAW RKQEKQTARH KASAAPGKNA SGEDEVLLGA RPRPRKPSFL 300
25    KALLATFGSS FLISACFKLI QDLLSFINPQ LLSILIRFIS NPMAPSWWGF LVAGLMFLCS 360
      MMQSLILQHY YHYIFVTGVK FRTGIMGVIV RKALVITNSV KRASTVGEIV NLMVSVDQRF 420
      MDLAPFLNLL WSAPLQIILA IYFLWQNLGP SVLAGVAFMV LLIPLNGAVA VKMRAFQVKQ 480
      MKLKDSRIKL MSELNLNGIKV LKLYAWEPSF LKQVEGIRQG ELQLLRTAAY LHTTTTTFTWM 540
      CSPFLVLTIT LWVYVYVDPN NVLDAEKAFF SVSLFNILRL PLNMLPQLIS NLTAQASVSLK 600
30    RIQQFLSQEE LDPQSVERKT ISPGYAITIH SGTFTWAQDL PPTLHSLDIQ VPKGALVAVV 660
      GPVCGGKSSL VSALLGEMEK LEGKVHMKGS VAYVPQQAWI QNCTLQENVL FGKALNPKRY 720
      QOTLEACALL ADLEMLPGGD QTEIGEKGIN LSGGQQRQVS LARAVYSADAD IFLLDDPLSA 780
      VDSHVAKHIF DHVIGPEGV L AGKTRVLVTH GISFLPQTD F IIVLADGQVS EMGPYPALLQ 840
      RNGSFANFLC NYAPDEDQGH LEDSWTALEG AEDKEALLIE DTLSNHTDLT DNDPVTYVVQ 900
35    KQFMRQLSAL SSDGEGQGRP VPRRHLGPSE KVQVTEAKAD GALTQEEKAA IGTVELSVFW 960
      DYAKAVGLCT TLAICLLYVG QSAAAIKANV WLSAWTNDAM ADSRQNNNTSL RLGYYAALGI 1020
      LQGFLVMLAA MAMAAGGIQA ARVLHQALLH NKIRSPQSFF DTTPSGRILN CFSKDIYVVD 1080
      EVLAPVILML LNSFFNAIST LVVIMASTPL FTVVILPLAV LYTILVQRFYA ATSRQLKRLE 1140
      SVSRSPYISH FSETVTGASV IRAYNRSRDF EIIISDTKVID NQRSCYPYII SNRWLSIGVE 1200
40    FVGNCCVLF AALFAVIGRSS LNPGLVGLSV SYSLOQTFAL NWMIRMMSDL ESNIVAVERV 1260
      KEYSKTETEA PMWVEGSRFP EGWPPRGEVE FRNYSVRYRP GLDLVLRLDL LHVHGGEKVG 1320
      IVGRTGAGKS SMTLCLFRIL EAAKGEIRID GLNVADIGLH DLRSQLTII P QDPILFSGTL 1380
      RMNLDPFGSY SEEDIWWALE LSHLHTFVSS QPAGLDFQCS EGGENLSVGG RQLVCLARAL 1440
      LRKSRILVLD EATAAIDLET DNLIQATIRT QFDTCTVLT I AHRINTIMDY TRVLVLDKGV 1500
45    VAEPDSPANL IAARGIFYGM ARDAGLA 1527

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Seq ID NO: C395 Protein Sequence
Protein Accession #: NP_004617

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50      1      11      21      31      41      51
      |      |      |      |      |      |
MRARPQVCEA LLFALALQTG VCYGIKWLAL SKTPSALALN QTQHCQKLEG LVSAQVQLCR 60
      SNLELMHTVV HAAREVMKAC RRAFADMWRN CSSIELAPNY LLDLERGTRE SAFVYALSAA 120
      AISHAIARAC TSGDLPGCSC GPVPGEPGPG GNRWGGCADN LSYGLLMGAK FSDAPMKVKK 180
55    TGSQANKLMR LHNSEVGRQA LRASLEMKCK CHGVSGS CSI RTCWKGQLQEL QDVAADLKTR 240
      YLSATKVVRH PMGTRKHLVP KDLDIRPVKD SELVYLQSSP DFCMKNEKVG SHGTQDRQCN 300
      KTSNGSDSCD LMCCGRGYNP YTRDVVERCH CKYHWCYVIT CRRCERTVER YVCK 354

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Seq ID NO: C396 Protein Sequence
Protein Accession #: NP_114072

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60      1      11      21      31      41      51
      |      |      |      |      |      |
MEWGYLLEVT SLLAALALLQ RSSGAAAASA KELACQEITV PLCKGIGYNY TYMPNQFNHD 60
65    TQDEAGLEVH QFWPLVEIQ SPDLKFFLCS MYTPICLEDY KKPLPPCRSV CERAKAGCAP 120
      LMRQYGFAPW DRMRCDRLPE QGNPDTLCD YNRDTLTAA PSPRRRLPPP PGGEQPPSGS 180
      GHGRPPGAR PRRGGGRGGG GGDAAAPPAR GGGGGGKARP PGGAAPCEP GCQCRAPMVS 240
      VSSERHPLYN RVKTGQIANC ALPCHNPFPS QDERAFTVFW IGLWSVLCFV STFATVSTFL 300
      IDMERFKYPE RPIIFLSACY LFVSVGYLVR LVAGHEKVAC SGGAPGAGGA GGAGGAAAGA 360
70    GAAGAGAGGP GGRGEYBELG AVEQHVRVET TGPALCTVVF LLVYFFGMAS SIWVILSLT 420
      WFLAAGMKWG NEAIAAGSYQ FHLLAAWLVP VKSIAVLALS SVDGDPVAGI CYVGNQSLDN 480
      LRGFVLAPLV IYLFITMFL LAGFVSLFRI RSVIKQDQGP TKTHKLEKLM IRLGLFTVLY 540
      TVPAAVVAC LFYEQHNRP WEATHNCPCL RDLQPDQARR PDYAVFMLKY FMCLVVGITS 600
      GVVWVSGKTL BSWRSLCTRC CWASKGAAVG GGAGATAAGG GGGPGGGGGG GPGGGGGGPGG 660
75    GGGSLYS DVS TGLTWRSGTA SSVSYPKQMP LSQV 694

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Seq ID NO: C397 Protein Sequence
Protein Accession #: XP_050625

```

80      1      11      21      31      41      51
      |      |      |      |      |      |
MLQGPGLSL LFLASHCCLG SARGFLFLGQ PDFSYKRSNC KPIPANLQLC HGIEYQNMRL 60
      PNLLGHETMK EVLEQAGAWI PIVMKQCHPD TKKFLCSLFA PVCLDDLDL ET IQPCHSLCVQ 120
      VKDRCAPVMS AFGFPWPDML ECDRFPQDND LCIPLASSDH LLPATEEAPK VCEACKNKND 180
      DDNDIMETLC KNDFALKIKV KEITYINRDT KIILETKSKT TYKLVNGVSR DLKKSVLWLK 240

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DSLQCTCEEM NDINAPYLVM GQKQGGLVI TSVKRWQKGQ REFKRISRSI RKLQC 295

Seq ID NO: C398 Protein Sequence
Protein Accession #: NP_001297.1

1 11 21 31 41 51
| | | | | |
MSMGLEITGT ALAVLGWLGTVCCALPMWR VSAFIGSNII TSQNIWEGWL MNCVVQSTGQ 60
MQCKVYDSSL ALPQDLQAAR ALIVVAILLA AFGLLVALLV AQCTNCVQDD TAKAKITIVA 120
10 GVLFLAALL TLVPVSWAN TIIRDFYNPV VPEAQKREMG AGLYVGWAAA ALQLLGGALL 180
CCSCPPREKK YTATKVYVSA PRSTGPGASL GTGYDRKDYV 220

Seq ID NO: C399 Protein Sequence
Protein Accession #: NP_036581.1

1 11 21 31 41 51
| | | | | |
MESRKDITNQ EELWKMMPRR NLEEDDYLHK DTGETSMLKR PVLLHLHQTA HADEFDCPSE 60
LQHTQELFPQ WHLPKIAAI TASLTFLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLPM 120
20 VSITLLALVY LPGVIAIIVQ LHNGTKYKKF PHWLDKMWLT RKQFGLLSFF FAVLHAIYSL 180
SYPMRRSYRY KLLNWAYQOV QONKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240
VSDSLTWREF HYIQSKLGIV SLLGTIHAL IFAWNKWIDI KQFVWYTPPT FMIAVFLPIV 300
VLIFKSILFL PCLRKILKI RHGWEDVTIKI NKTEICSQL 339

Seq ID NO: C400 Protein Sequence
Protein Accession #: NP_001766.1

1 11 21 31 41 51
| | | | | |
MANCEFPVS GDKPCRLSR RAQLCLGVSI LVLILVVVLA VVVPRWRQTW SGPGTTKRFP 60
ETVLARCVKY TEIHPEMRHV DCQSVWDAFK GAFISKHPCN ITEEDYQPLM KLGTQIVPCN 120
KILLWSRIKD LAHQFTQVQR DMFTLEDTL GYLADDLTWC GEFNTSKINY QSCPDRKDC 180
30 SNPNVSVFWK TVSRFAEAA CDVVHVMLNG SRSKIFDKNS TFGSVEVHNL QPEKVQTLA 240
WVIHGGREDS RDLCDPTIK ELESISKRN IQFSCNKIYR PDKFLQCVKN PEDSSCTSEI 300

Seq ID NO: C401 Protein Sequence
Protein Accession #: XP_120513.2

1 11 21 31 41 51
| | | | | |
MVSTFSGPL RETNENVKKF YALRAFMRM SSEAAMLGES RTFKPRKHRA TTRAKIFKRF 60
FSEGESNSR LVEELAVIHT YSDDPAPPTS PSSVQPREFG VMQAPRARF GSRTTPAAAE 120
ASSPHLGIGE AACQSGARAA APRAGARRCQ PQQAASAAAA TAQTHLPLHA RTRADPAGR 180
45 RRHPRSPAPG GEGTCEGPA PRRMEEMQ PAEEGSPVVK IYKQSPYSV LKTFPSKRPA 240
LAKRYERPTL VELPHGLRT PAQPPASPA ASSSSFAAV VRLGAPPRPP RRGFRAGTI 300
PPLLAPGVA GTLLPPTSS SPSPRPRPW HAAAPRGTS HTHMWSQST LPSGDTMVS 360
FGLMAQRRWQ HRSCLKFEWG ILGSGTWPC QDWLEKEGQ VAVLLPRSEG NTAPKKSRMI 420
LDFAQQCSR VLSLLNCGGK LLDNSHSQSM ISCVKQEGSS YNERQEHCHI GKGVHSQTS 480
50 NVDIEMQYMQ RKQTSAPFLR VFTDSLQNYL LSGSFPTPNP SSASEYGHLL DVDPLSTSPV 540
HTLENISLDS TASLCKSRHL SREPPVKSDF FNPLQALAG GASRPFSGAQ QSIAYRVNSE 600
LEDGIRSPVP LSCEALEMDL TSLGSKQLLN NYPVYITSKQ WDEAVNSSKK DGRRLRLRYLI 660
RFVFTTDELK YSCGLGKRKR SVQSGETGPE RRPLDPVKVT CLRGTASFRS VSPSVISFHR 720
IGCGSPRTSV QPSVF 735

Seq ID NO: C402 Protein Sequence
Protein Accession #: BAA92562.1

1 11 21 31 41 51
| | | | | |
METTVLSGIN FEYKGMTWE VAGDHIYTA GASDNDFMIL TLVVPGRFP QVMADTENK 60
EVARITFVFE TLCVSNCELY FMVGVNSRTN TPVETWKGSK GKQSYTYIIE ENTTSFTWA 120
FORTTFHEAS RKYTNDVAKI YSINVTVNMN GVASYCRPCA LEASDVGSSC TSCPAGYID 180
RDSGTCHSCP PNTILKAHQ YGVQACVPCG PGTKNNKIHS LCYNDCTFSR NTPTRTFN 240
65 FSALANTVTL AGGPSFTSKG LKYFHHFTLS LCGNQGRKMS VCTDNVTDLR IPEGESGFSK 300
SITAYVCQAV IIPPEVTGYK AGVSSQPVSL ADRLIGVTTD MTLDGITSPA ELFHLESGLI 360
PDVIFYRSN DVTQSCSSGR STTIRVRCSP QKTVPGSLLL PGTCSDGTCD GCNFHFLWES 420
AAACPLCSVA DYHAIVSSCV AGIQKTTYVW REPKLCSGGI SLPEQRTVIC KTIDFWLVK 480
ISAGTCTAIL LTVLTCYFWK KNQKLEYKYS KLVMNATLKD CDLPAADSCA IMEGEDVEDD 540
70 LIFTSKSLF GKIKSFTSKQ PAPVTISLSE DS 572

Seq ID NO: C403 Protein Sequence
Protein Accession #: NP_055139.1

1 11 21 31 41 51
| | | | | |
MALQGISVVE LSGLAPGRXC AMVLADFGAR VVRVDRPGSR YDVSRLGRGK RSLVLDLKQP 60
REPRAAASVQ AVGCAAGALP PRCHGETPAG PRDSAAGKSK AYLCAEWIIV PVQESFCRLA 120
GHDNLYLALS GVLSTKIGSG ENPYAPLNLV ADFAGGGLMC ALGIIMALFD RTRTDKGQVI 180
80 DANMVEGTAY LSSFLWKTQK SSLWEAPRGQ NMLDGGAPFY TTYRTADGEF MAVGAIEPQF 240
YELLIKGLGL KSEDELPMQMS TDDWPEMKK FADVFAKTK AEWCQIFDGT DACVTPVLT 300
EEVHHHDHKN ERGSFITSEE QDVSPRLAPL LLNTFAIPSS KGDPFIEGHT EEILEEFGFS 360
REEIYQLNSD KIIESNKVKA SL 382

Seq ID NO: C404 Protein Sequence

Protein Accession #: XP_091332.1

	1	11	21	31	41	51	
5	MQRWTLWAAA	FLTLHSAQAF	PQTDISISPA	LPELPLPSLC	PLFWMEFKGH	CYRFFPLNKT	60
	WAEADLYCSE	FSVGRKSAKL	ASIHSEENV	FVYDLVNSCV	PGIPADVWTG	LHDHRQEGQF	120
	EWTGSSSYDY	SYWDGSPDD	GVHADPEED	CVQIWRPTS	EQLQAPPEQL	PLSISEATDV	180
	YLPEDFPAEP	KLMDQSWVSR	KSLKPSKSHL	MEPPTPAKH	QKAKTRHRL	RGVWWPSGKA	240
	GSWKERMNAD	YGRRKRSAPR	QEGRLRCRER	RLRAASGQGR	PEGQRKQRR	ERQERGWEL	300
10	GGVSPMRGAQ	AWQHGLGAGS	QRGAAPCEGE	NHQAPELGST	WRGQRLQPT	AALCHFALRK	360
	LPGNAHGLAA	AFVQPALQVQ	EKKNNRTRFS	GAYFTMSDPT	CDQDSKEQSL	RRHGREAED	420
	GPYRLVKKKR	GPVACPSSFE	LQSGGEVCLD	FPVELRAGTW	IAREPP		466

Seq ID NO: C405 Protein Sequence
Protein Accession #: XP_054869.2

	1	11	21	31	41	51	
20	MHTCCPPVTI	EQDLHRKMHS	WMLQTLFAV	TSLVLSCAET	IDYYGEICDN	ACPCEEKDGI	60
	LTVSCENRGI	ISLSEISPPR	FPIYHLLLSG	NLLNRLYPNE	FVNYTGASIL	HLGSNVIQDI	120
	ETGAFFGLRG	LRRLHLNNNK	LELLRDDTFL	GLENLEYLQV	DYNYISVIEP	NAFGKLHLQ	180
	VLILNDNLLS	SLPNNLFRFV	PLTHLDLRGN	RLKLLPYVGL	LQHMDKVVEL	QLEENPWNC	240
	CELISLKDWL	DSISYSALVG	DVVCETPFRL	HGRDLDEVSK	QELCPRLIS	DYEMRPQTPL	300
	STTGYLHTTP	ASVNSVATSS	SAVYKPPLKP	PKGTRQPNKP	RVRPTSRQPS	KDLGYSNYGP	360
25	STAYQTKSPV	PLECPTACSC	NLQISDLGLN	VNCQERKIES	IAELQPKPVN	PKMYLTENY	420
	IAVVRRTDFL	EATGLDLLHL	GNNRISMIQD	RAFGLDNLRL	RLYLNGNRIE	RLSPELFYGL	480
	QSLQYLFLOQ	NLIRESQSTG	FDPVPNLQLL	FLNNNLLQAM	PSGVFSGTLT	LRLNLRSNHF	540
	TSLEPVSGLD	QLKSLQIDIL	HNNPMDCTCD	IVGMKLWVEQ	LKGVGLVDEV	ICKAPKKFAE	600
	TDNRSLKSEL	LCEDYSDVVV	STPTPSSIQV	PARTSAVTPA	VRNLSTGAPA	SLGAGGGSSA	660
30	VPLSVLILSL	LLVFIMSVFV	AAGLFVLVMK	RRKKNSDHT	STNNSDVSSF	NMQYSVYGGG	720
	GGTGGHFAH	VHHRGPALPK	VKTPAGHVYE	YIPHLGHMC	KNPIYRSREG	NSVEDYKDLH	780
	ELKVITYSSNH	HLQQQQQPPP	PPQQPQQQPP	PQLQLQPGEE	ERRESHLRS	PAYSVSTIEP	840
	REDLLSPVQD	ADRFYRGILE	PDKHCSTTPA	GNSLPEYKPF	PCSPAAYTFS	PNYDLRRPHQ	900
35	YLHPGAGDSR	LREPVLYSPP	SAVFVEPNRN	EYLELKAKLN	VEPDYLEVLE	KQTTFSQF	958

Seq ID NO: C406 Protein Sequence
Protein Accession #: NP_000784.2

	1	11	21	31	41	51	
40	MGILSVDLLI	TLQILPVFFS	NCLFLALYDS	VILLKHVVLL	LSRSKSTRGE	WRRMLTSEGL	60
	RCVWKSFLLD	AYKQVKLGED	APNSSVVHVS	STEGGDNSGN	GTQEKIABGA	TCHLLDFASP	120
	ERPLVNVFGS	ATUPPPTSQI	PAFRKLVEEF	SSVADFLLVY	IDEAHPSDGW	AIPGDSLSLF	180
45	EVKKHQNQED	RCAAAQQLLE	RFSLPPQCRV	VADRMNNAN	IAYGVAFERV	CIVQRQKIAY	240
	LGGKGPFPSY	LQEVHRWLEK	NFSKRUKKTR	LAG			273

Seq ID NO: C407 Protein Sequence
Protein Accession #: NP_006540.2

	1	11	21	31	41	51	
50	MSSCVSSQPS	SNRAAPQDEL	GGRGSSSSSES	QKPCBALRGL	SSLSIHLGME	SFIVVTECEP	60
	GCAVDLGLAR	DPLEADGQEE	VPLDSSGSQA	RPHLSGRKLS	LQERSQGGGLA	AGGSIDMNGR	120
	CICPSLPYSP	VSSPQSSPRL	PRRPTVESHH	VSITGMQDCV	QLNQYTLKDE	IGKGSYGVVK	180
55	LAYNENDNTY	YAMKVLSSKK	LIRQAGFPRR	PPPRGTRPAP	GGCIQPRGPI	EQVYQEIAIL	240
	KKLDPHPNVV	LVEVLDDFNE	DHLYMVFEVL	NQGFVMEVPT	LKPLSEDAAR	FYFQDLIKGI	300
	EYLYYQKIIH	RDIKPSNLLV	GEDGHIKIAD	FGVSNFPGKS	DALLSNTVGT	PAFMAPELSL	360
	ETRKIFSGKA	LDVWAMGVTL	YCFVFGQCPF	MDERIMCLHS	KIKSQALEFF	DQPDIAEDLK	420
60	DLITRMLDKN	PESRIVVPEI	KLHPWVTRHG	AEPLPSEDEN	CTLVEVTEEE	VENSVKHIPS	480
	LATVILVKTM	IRKRSFGNPF	EGSRREERSL	SAPGNLLTKK	PTRECELSLE	LKEARQRRQP	540
	PGHRPAPRG	GGGSLVRGSP	CVESCWAPAP	GSPARMHLPL	PEEAMEPE		588

Seq ID NO: C408 Protein Sequence
Protein Accession #: NP_061116.2

	1	11	21	31	41	51	
65	MGLSLPKEKG	LILCLWSKFC	RWFQRRESWA	QSRDEQNLLQ	QKRIWESPLL	LAAKDNDVQA	60
	LNKLLKYEDC	KVHQRGAMGE	TALHIAALYD	NLEAAMVLME	AAPELVFEPM	TSELYEGQTA	120
70	LHIAVVNQNM	NLVRALLARR	ASVSARATGT	AFRRSPCNLI	YFGEHPLSFA	ACVNSEEIVR	180
	LLIEHGADIR	AQDSLGNVTI	HILILQPNKT	FACQMYNLLL	SYDRHGDHLQ	PLDLVPNHQG	240
	LTPPKLAGVE	GNTVMFQHLM	QKRKHTQWTY	GPLTSTLYDL	TEIDSSGDEQ	SLLELIITTK	300
	KREARQILDQ	TPVKELVSLK	WKRYGRPYFC	MLGAIYLLYI	ICFTMCCIYR	PLKPTNNRNT	360
75	SPRDNLTLLQ	KLLQRAYMTP	KDDIRLVGEL	VTVIGAIIL	LVEVPDIFRM	GVTRFFGQTI	420
	LGGPFHVLI	TYAFMVLVTM	VMRLISASGE	VVPMFSFALV	GWCNVMYFAR	GFQMLGPFTI	480
	MIQKMIFGDL	MRFCWLMVAV	ILGFASAFYI	IFQTEDEPEL	GHFYDYPMAL	FSTFELFTI	540
	IDGPANYNDV	LFFMYSITYA	AFALIIATLLM	LNLLIAMMGD	THWRVAHERD	ELWRAQIVAT	600
	TVMLERKLPR	CLWPRSGICG	REYGLGDRWF	LRVEDRQDLN	RQRIQRYAQA	FHTRGSEDL	660
80	KDSVEKLELG	CPFSPHLSLP	MPSVSRSTSR	SSANWERLRQ	GTLRRDLRGI	INRGLEDGES	720
	WEYQI						725

Seq ID NO: C409 Protein Sequence
Protein Accession #: NP_068710.1

1 11 21 31 41 51
 | | | | |
 MQKVTLGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSEW 60
 RSSGEQAQRG WGSPLTTQL SPTGAKCKCK FGQKSGHHPG ETPPLITPGS AQS 113

Seq ID NO: C410 Protein Sequence
 Protein Accession #: NP_005962.1

1 11 21 31 41 51
 | | | | |
 MQKVTLGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSAK 60
 CKCKFGQKSG HHPGETPPLI TPGSAQS 87

Seq ID NO: C411 Protein Sequence
 Protein Accession #: NP_004952.1

1 11 21 31 41 51
 | | | | |
 MLSKVLPLVL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60
 TGSRVGKLPE ASRIINTILS NYDHLKLRPGI GEKPTVVTV E IAVNSLGPLS ILDMEYTTIDI 120
 IFSQTYWDER LCNNDTFESL VLNNGNVVSQL WIPDTFFRNS KRTHEHEITM PNQMVRIYKD 180
 GKVLTYTIRM IDAGCSLHML RFPMDSHSCP LSFSSFSYPE NEMIYKWNF KLEINEKNSW 240
 KLFQDFDTGV SNKTEIITP VGDFMVTIF FNVSRFGYV AFQNYVPSSV TTMLSWVSEW 300
 IKTESAPART SLGITSVLTM TILGTFSRKN FPRVSYITAL DFYIACFVF CFCALLEFAV 360
 LNFLIYNQTK AHASPKLRHP RINSRAHART RARSACARQ HQEAFVCQIV TEGSDGGER 420
 PSCSAQQPPS PGSPGPRSL CSKLACCEWC KRFKKYFCMV PDCEGSTWQQ GRLCIHVYRL 480
 DNYSRVVFPV TFFFNVLVW LVCLNL 506

Seq ID NO: C412 Protein Sequence
 Protein Accession #: NP_068819.1

1 11 21 31 41 51
 | | | | |
 MEYTIIDIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ 60
 MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120
 INEKNWKLFE QLDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTM 180
 LSWVSWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240
 ALLEFAVLNF LIYNQTKAHA SPKLHRPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE 300
 GSDGEERPSC SAQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPCD EGSTWQQARL 360
 CIHVYRLDNY SRVFPVPTFF FPNVLYWLVC LNL 393

Seq ID NO: C413 Protein Sequence
 Protein Accession #: NP_068822.1

1 11 21 31 41 51
 | | | | |
 MEYTIIDIFS QTWNSKRTHE HEITMPNQMV RIYKDGKVLV TIRMTIDAGC SLHMLRFPMD 60
 SHSCPLSFSS FSYPENEM IYKWNFKLEIN EKNWKLQFQ DFTGVSNKTE IITTPVGDFM 120
 VMITIFFNVSR RFGYVAFQNY VPSSVTMLS WVSFWIKTES APARTSLGIT SVLMTTLTGT 180
 FSRKNFPRVS YITALDFYIA ICFVFCFCAL LEFAVLNFLI YNQTAKAHASP KLRHPRINSR 240
 AHARTRARSR ACARQHQAFA VCQIVTTEGS DGEERPSCSA QPPSPGSPE GPRSLCSKLA 300
 CCEWCKRFFK YFCMVPCDEG STWQQGRLCI HVYRLDNYSR VVFPVTFVFF NVLYWLVCNL 360
 L 361

Seq ID NO: C414 Protein Sequence
 Protein Accession #: NP_068830.1

1 11 21 31 41 51
 | | | | |
 MEYTIIDIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ 60
 MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120
 INEKNWKLFE QLDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTM 180
 LSWVSWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240
 ALLEFAVLNF LIYNQTKAHA SPKLHRPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE 300
 GSDGEERPSC SAQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPCD EGSTWQQARL 360
 CIHVYRLDNY SRVFPVPTFF FPNVLYWLVC LNL 393

Seq ID NO: C415 Protein Sequence
 Protein Accession #: NP_068591.1

1 11 21 31 41 51
 | | | | |
 MPAVSGPGPL FCLLLLLLDL HSPETGCPPL RFEYKLSFK GPRLALPGAG IPFWSHHGDA 60
 ILGLEEVRLT PSMRNRSGAV WSRAVVFSA WEVEVQMRVT GLGRRGAHGM AVWYTRGRGH 120
 VGSVLGGLAS WDIGIGFIDS PAEDTQDSPA IRVLASDGH I PSEQPGDGAS QGLGSHWDF 180
 RNRPHFPFR ITYVQRLRM SLNSGLTPSD PGEFCVDVGP LLLVPGGFFG VSAATGTLD 240
 DHDVLSFLT SLSEPSPEVP PQPFLEMQLL RLARQLEGLW ARLGLGTRED VTPKSDSEAQ 300
 GEGERLFDLE ETLGRHRRIL QALRGLSKQL AQAERQWKQ LGPPGQAREP GGWALDASCQ 360
 IPSTPGRGGH LSMSLNKDSA KVGALLHGQW TLLQALQEMR DAAVRMAAEA QVSVPVGGIE 420
 HHFLELDHIL GLLQBELRGP AKAAAKAPRP PGQPPRASSC LQPGIFLFYL LIQTGVGFFGY 480
 VHFRLQELNKS LQECLESTGSL PLGPAHTPR ALGILRRQPL PASMPA 526

Seq ID NO: C416 Protein Sequence
 Protein Accession #: XP_117036.1

1 11 21 31 41 51
 5 MERRTRGALG SRRPPPLPA LRHLCTGLQA AGMAWPGLTW RHTCQGRAXA AEGPWGLFRP 60
 HRCPREAGQA PVGSPSPETQG VAHVCSRARV SVDEREPGGG AYAMHVTPRW KGCHRHSGRT 120
 VRGSVSWKRP EQAAPETGRG PAVARGSGDG NECGWG 156

Seq ID NO: C417 Protein Sequence
 Protein Accession #: XP_167803.2

10 1 11 21 31 41 51
 15 MPGKGQRKTA TNKPGGLPGA PGVGIGGHCL YVLECKCFIK NKTKTHHHKK KNFAAKRNEE 60
 KKKKKKQEK KNHTKFFHHT YPLSQQDFLF AKSYFCGNPG CFLWQGLF 108

Seq ID NO: C418 Protein Sequence
 Protein Accession #: NP_079056.1

20 1 11 21 31 41 51
 MFRLVERYEM PRHEVYVLLI RNIFLKISII GILCYWLNT VALSGEECWE TLIGQDIYRL 60
 LLMDVFVSLV NSFLEFLRR IIGMQLITSL GLQEFDIARN VLELIYAQTL VWIGIFFCPL 120
 LPFIQMIMLF IMFYSKNISL MMNFQPPSKA WRASQMMTFF IFLFFPSFT GVLCTLAITI 180
 25 WRLKPSADCG PFRGLPLFIH SIYSWIDTSL TRPGYLWVWV IYRNLIGSVH FFFILTLIVL 240
 IITLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP SSLVLERREV 300
 EQQGFLHLGE HDGSLDLRSR RSVQEGNPRA 330

Seq ID NO: C419 Protein Sequence
 Protein Accession #: Eos sequence

30 1 11 21 31 41 51
 35 MLSDDHVNEI IIQVENVSSG VQSHPSNQI FQEKVLLDSS INMVLISIDI DVIDSQTIVSK 60
 RNDQKGNQVL RFSTSLNESM SQTLSLECM GIDTPGSSHE TVQGQKLIAS LIPMTSRDRI 120
 KAIRNQPRTM EEKRNLRKIV DKEKSKQTHR ILQLNCCIQC LNSISRAYRR SKNSLSEILN 180
 SISLWQKTLK IIGGKFGTSV LSYPNFLRWL LKFNIFSFIL NFSFIIIPQF TVAKNTLQF 240
 TGLEFFTGVG YFRDVTVMYIG FYTNSTIQHG NSGASYNMQL AYIFTIGACL TTCFFSLLFS 300
 MAKYFRNNFI NPHIYSGGIT KLIFCWDFTV THEKAVKLKQ KNLSTEIREN LSELROENSK 360
 40 LTFNQLLTRF SAYMVAVVVS TGVAIACCAA VYLAEYNLE FLKTHSNPGA VLLLPFVVSC 420
 INLAVPCIYS MFRLVERYEM PRHEVYVLLI RNIFLKISII GILCYWLNT VALSGEECWE 480
 TLIGQDIYRL LLMDVFVSLV NSFLEFLRR IIGMQLITSL GLQEFDIARN VLELIYAQTL 540
 VWIGIFFCPL LPFIQMIMLF IMFYSKNISL MMNFQPPSKA WRASQMMTFF IFLFFPSFT 600
 GVLCTLAITI WRLKPSADCG PFRGLPLFIH SIYSWIDTSL TRPGYLWVWV IYRNLIGSVH 660
 45 FFFILTILVL IITLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP 720
 SSLVLERREV EQQGFLHLGE HDGSLDLRSR RSVQEGNPRA 760

Seq ID NO: C420 Protein Sequence
 Protein Accession #: NP_002241.1

50 1 11 21 31 41 51
 MGGDLVLGLG ALRRRKRLLE QEKSLAGWAL VLAGTGIGLM VLHAEMLWFG GCSWALYLF 60
 VKCTISISTF LLLCLIVAFH AKEVQLFMTD NGLRDWRVAL TGRQAAQIVL ELVVCGLHPA 120
 55 PVRGPCVQDQ YSSKGLIQRS KDKPYLLYFN IFSCILSSNI ISVAENGLQC PTPQVCVSSC 180
 SIGALNQVRF RHWFAKLYM NTHPGRLLLG LTLGLNLTTA WVLSVAERQA VNATGHLSDT 240
 LWLIPITFLT IGYGDVVPQT MWGKIVCLCT GVMGVCTTAL LVAVVARKLE FNKAEKHVHN 300
 FMMDIQYTK EKFIFLNRN EAWMFYKHTR RKESHAARRH QRKLLAANA FRQVRLKHRK 360
 60 LREQVNSMVD ISKMHMILYD LQQLNLSSSH ALEKQIDTLA GKLDALTELL STALGPRQLP 420
 EPSQSK 427

Seq ID NO: C421 Protein Sequence
 Protein Accession #: NP_079533.1

65 1 11 21 31 41 51
 MGGKQRDEDD EAYGKPVKYD PSFRGPIKNR SCTDVICCVL FLLFILGYIV VGIVAWLYGD 60
 PRQVLYPRNS TGAYCGMGEN KDKPYLLYFN IFSCILSSNI ISVAENGLQC PTPQVCVSSC 120
 PEDPWTVGKN EFSQTVEVF YTKNRNFCPL GVPWNMTVIT SLQQELCPSE LLPSAPALGR 180
 70 CFPWTNITPP ALPGITNDIT IQQGISGLID SLNARDISVK IFEDFAQSWY WILVALGVAL 240
 VLSLLFILLL RLVAGPLVLV LILGVLGVLA YGIYCWEEY RVLDRKGASI SQLGFTTNLS 300
 AYQSVQETWL AALIVLAVLE AILLLVLIFL RQRIRIAIAL LKEASKAVGQ MMSTMFYPLV 360
 TFVLLLICIA YWAMTALYPL PTQPATLGIV LWASNISSPG CEKVPINTSC NPTAHLVNSS 420
 CPGLMCVFQG YSSKGLIQRS VFNLIYGVV GLFWTLNWL ALGCQCVLAGA FASFYWAFHK 480
 75 PQDIPTFPLI SAFIRTLRYH TGSALFAGALI LTLVQIARVI LEYIDHKLGR VQNPVARCIM 540
 CCFKCCCLWCL EKFIKFLNRN AYIMIAIYK NFCVSAKNAF MLLMRNIVRV VVLDKVTDDL 600
 LFFGKLLVVG GVGVLSEFFF SGRIPGLGKD FKSPHLNYYW LPIMTSILGA YVIASGFFSV 660
 FGMCVDTLFL CFLEDLERNN GSLDRPYMS KSLKILGKK NEAPPDNKKR KK 712

80 Seq ID NO: C422 Protein Sequence
 Protein Accession #: NP_057264.1

1 11 21 31 41 51
 MGSNSGQAGR HIYKSLADDG PFDSVEPPKR PTSRLIMHSM AMFGREFCYA VEAAYVTPVL 60

LSVGLPSSLY SIVWFLSPIL GFLLPVVGVS ASDHCRSRWG RRRPYILTLG VMMLVGMALY 120
 LNGATVVAAL IANPRRLKLV AISVTMIGVV LFDFAADFID GPIKAYLFDV CSHQDKEKGL 180
 HYHALFTGFG GALGYLLGAI DWAHLELGR LGEFQVMVF FSALVLTLCF TVHLCISEA 240
 5 PLTEVAKGIP PQQTPQDPPL SSDGMYEYGS IEKVNGYVN PELAMQGAKN KNHAEQTRRA 300
 MTKSLRLRAL VMMPPHYRYL CISHLIGWTA FLNMLFFTD FMQIVYRGD PYSAHNSTEF 360
 LIYERGVEVG CWGFCINSVF SLSYSYFQKV LVSYIGLKGL YFTGYLLFGL GTGFIGLFPN 420
 VYSTLVLCSL FGVMSSTLYT VPFNLITEYH REEEKERQQA PGDDPDNSVR GKGMDCATLT 480
 CMVQLAQILV GGGGLFLVNT AGTVVVVVIT ASAVALIGCC FVALFVRYVD 530

Seq ID NO: C423 Protein Sequence
 Protein Accession #: NP_003264.1

1 11 21 31 41 51
 15 MEGFGGVGGR GTRGFAAKGV WRGRAEEGPV LGAAERGFMV STGSRRRVFE GPGGGGLRWT 60
 PGKGTGRQRG AWGPRADGIV RRRTLGMPRG SRRDVRAPCG PAGSWGARGG RRRDGPSSRR 120
 RGSATAARH HVPAPAGGPF GPRAPAGSTR VPARAGGAVE PTGAAAVARL ARPAGGALPT 180
 AGAQQAGPAR GRSGEGSEWA RRGKGRPGPY QSPLGPAVAE GQELKDKSRL RYPINGFQAL 240
 20 VLTALLVLGL MSAGLPLGAL PEMLLPLAFV ATLTAFIFSL FLYMKAQVAP VSALAPGGSN 300
 GNPIYDFLGL RELNPRICFF DFKYFCELRP GLIGWVLINL ALLMKEAELR GSPSLAMWLV 360
 NGFQLLYVGD ALWHEEAVLT TMDITHDGFG FMLAFGDMAN VPFTYSLQAQ FLLHHPQPLG 420
 LPMASVICLI NATGYIYFRK ANSQKNTFRK NPSDPRVAGL ETISTATGRK LLVSGWWMGV 480
 RHPNYLGLDI MALAWSLPCG VSHLLPYFYL LYFTALLVHR EARDERSACR STAWPGRSTA 540
 25 GVCLTASCPT STEAAPPQV GHVPTHPPAH PGPGASTHLG LKGLHPTQP 589

Seq ID NO: C424 Protein Sequence
 Protein Accession #: NP_056535.1

1 11 21 31 41 51
 30 MGRLLRAARL PPLLSPLLL LVGGAFLGAC VAGSDEPGPE GLTSTSLDDL LLPTGLEPLD 60
 SEEPSETMGL GAGLGAPGSG FPSEENEESR LIQPPQYFWE EEEEEENDSSL DLGPTADYVF 120
 PDLTEKAGSI EDTSAQELP NLPSLPKMN LVEPPWHMPP REEEEEEEEE EEREKEEVEK 180
 35 QEEEEEEELL PVNGSQEAK PQVRDFSLTS SSQTPGATKS RHEDSGDQAS SGVEVESSMG 240
 PSLLLPSVTP TTVTPGDQDS TSQEAETVL PAAGLGVEFE APQEAEEAT AGAAGLSGQH 300
 EEVPALPSFP OTTAPSGAEH PDDEPLGSRT SASSPLAPGD MELTPSSATL GQEDLNQQLL 360
 EGQAAEAQSR IPWDSQVIC KDWSNLAGKN YIILNMTENI DCEVFRQHRG PQLLALVEEV 420
 LPRHSGSHHG AWHISLSKPS EKEQHLLMTL VGEQGVVPTQ DVLSMLGDIR RSLEEIGIQN 480
 40 YSTTSSCQAR ASQVRSDYGT LFVVLVVIGA ICIIIIALGL LYNQCWRRLP KLKHVSHGEE 540
 LRFVENGCHD NPTLDVASDS QSEMKEKHPN LGGGALNGP GSWGALMGK RDPEDSDVFE 600
 EDTHL 605

Seq ID NO: C425 Protein Sequence
 Protein Accession #: NP_001188.1

1 11 21 31 41 51
 45 MSEVRPLSRD ILMETILLYEQ LLEPPTMEVL GMTDSEEDLD PMEDFDSLEC MEGSDALALR 60
 LACIGDEMVD SLRAPRLAQ SEVAMHSLGL AFYDQTEDI RDVLRFSFMDG FTTLKENIMR 120
 50 FWRSPNPGSW VSCEQVLLAL LLLLALLLPL LSGGLHLLK 160

Seq ID NO: C426 Protein Sequence
 Protein Accession #: AAF76225.1

1 11 21 31 41 51
 55 MATPLPPSP RHLRLRLRL SGLVLGAALR GAAAGHPDVA ACPGSLDCAL KRRARCPFGA 60
 HACGFCLOPF QEDQQLCVP RMRRPPGGGR PQPRLEDEID FLAQELARKE SGQSTPPLPK 120
 60 DRQRLPEPAT LGFSARGQGL ELGLPSTPGT PTPTPHTSLG SPVSSDPVHM SPLEPRGGQG 180
 DGLALVLILA FCVAGAAALS VASLCWCRLQ REIRLTQKAD YATAKAPGSP AAPRISPGDQ 240
 RLQAQSAEMH YQHQRQMLC LERHKEPPE LDTASSDEEN EDGDFTVYEC PGLAPTGE 300
 VRNPLFDHAA LSAPLPAPSS PPALP 325

Seq ID NO: C427 Protein Sequence
 Protein Accession #: NP_004436.1

1 11 21 31 41 51
 70 MVCSLWVLL VSSVLALIEV LDDTTGETSE IGWLTYPFGG WDEVSVLDDQ RRLTRTFEAC 60
 HVAGAPPPTG QDNWLQTHFV ERRGAQRAHI RLHFSVRACS SLGVSGGTCR ETFTLYYRQA 120
 EEPDPSDVS SWHLKRWTKV DTIAADESFP SSSSSSSSS SAAWAVGPHG AGQRAGLQLN 180
 VKERSFGPLT QRGFYVAFQD TGACIALVAV RLFSYTCFAV LRSFASFPE QASGAGGASL 240
 75 VAAVGTCAVA AEPEEDGVGG QAGGSPPLRH CNGEGKMWVA VGGCRCQPGY QPARGDKACQ 300
 ACPRGLYKSS AGNAPCSCP ARSHAIPNAA PVPCLLEGFY RASSDPPEAP CTGPPSAPQE 360
 LWFEVQGSAL MLHWRLPREL GGRGDLLENV VCKECEGRQE PASGGGGTCH RCRDEVHFD 420
 RQGLTESRV LVGGLRAHVP YILEVQAVNG VSELSPDPFP AAAINVSTSH EVPSAVPVVH 480
 QVSRASNSIT VSWPQPDQTN GNILDYQLRY YDQAEDESHS FTLTSETNTA TVTQLSPGHI 540
 YGFQVRARTA AGHFGYGGKV YFQTLQGEL SSQLEPRLSL VIGSILGALA FLLLAITVL 600
 80 AVVFQRKRRG TGYTEQLQY SSPGLGVKYY IDPSTYEDPC QAIRELAREV DPAYIKIEV 660
 IGTGSFGEVR QGRLOPRGR EQTVAIQALW AGGAEQLQMT FLGRAAVLQ FQHPNIRLE 720
 GVVTKSRPLM VLTEFMEGFP LDSFLRQREG QFSSLQLVAM QRGVAAAMQY LSSFAFVHRS 780
 LSAHSVLVNS HLVCKVARLG HSPQGFSCLL RWAAPVIAH GKHTTSSDVW SFGILMWEVM 840
 SYGERPYWDM SEQEVINATE QEFRLPPPG CFFGLHLLML DTWQKDRARR PHFDQLVAAF 900
 DKMIRKPDTL QAGGDFGERP SQALLTPVAL DFPCLDSPQA WLSAIGLECY QDNFSKFGLC 960

TFSDVAQLSL EDLPALGITL AGHQKKLLHH IQLLQQHLRQ QGSVEV 1006

Seq ID NO: C428 Protein Sequence
Protein Accession #: XP_043340.2

```

1      11      21      31      41      51
|      |      |      |      |      |
MPFDFRRFDI YRKVPKDLTQ PTYTGAIIIS CCCLFILFLF LSELTGFITT EVVNELYVDD 60
PDKDSGGKID VSLNISLPLN HCELVGLDIQ DEMGRHEVGH IDNSMKIPLN NGAGCRFEGQ 120
FSINKVPGNF HVSTHSATAQ FQNPDMTHVI HKLSFGDTLQ VQNIHGAFNA LGGADRLTSN 180
PLASHDYILK IVPTRYVEDKS GKQRYSYQYT VANKEYVAYS HTGRIIPAIW FRYDLSPITV 240
KYTERRQPLY RFTITICAII GGTFTVAGIL DSCIFTASEA WKKIQLGKMH 290

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Seq ID NO: C429 Protein Sequence
Protein Accession #: NP_002142.1

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1      11      21      31      41      51
|      |      |      |      |      |
MAQKEGGRTV PCCSRPKVAA LTAGTLLLLT AIGAASWAIV AVLLRSDQEP LYPVQVSSAD 60
ARLMVFDKTE GTWRLLCSSR SNARVAGLSC EEMGFLRALT HSELDVRTAG ANGTSGFFCV 120
DEGRLPHTQR LLEVISVCDG PRGRFLAAIC QDCGRRKLEPV DRIVGGDRDTS LGRWFWQVSL 180
RYDGAHLCCG SLLSGDWLVT AAHCFFPERNR VLSRWRVFAG AVAQASPHGL QLGVQAVVYH 240
GGYLPFRDPN SEENSNDIAL VHLSSPLPLT EYIQPVCLPA AGQALVDGKI CTVTGWGNTQ 300
YYGQAGVLQ EARVPIISND VCNAGDFYGN QIKPKMFCAG YPEGGIDACQ GDSGGPFVCE 360
DSISRTPRWR LCGIVSWGTV CALAQKPGVY TKVSDPREWI FQAIKTHSEA SGMVTQL 417

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Seq ID NO: C430 Protein Sequence
Protein Accession #: BAA92562.1

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1      11      21      31      41      51
|      |      |      |      |      |
METTVLSGIN FEYKGMTGWE VAGDHIYTAA GASDNDFMIL TLVVPGRFRPP QSVMA DTENK 60
EVARITFVEE T LCSVNCELY FMVGVNSRTN TPVETWKGSK GKQSYTYIIE ENTTTSFTWA 120
FQRTTFHEAS RKYTNDVAKI YSINVTVNMN GVASYCRPCA LEASDVGSSC TSCPAGYIID 180
RDSGTCHSCP PNTILKAHQF YGVQACVPCG PGTKNNKIHS LCYNDCFTSR NTPTRTFNKN 240
FSALANTVTL AGGPSTFSKG LKYFHHFTLS LCGNQGRKMS VCTDNVTDLR IPEGESGFSK 300
SITAVVCAV IIPPEVTGYK AGVSSQPVSL ADRLIGVTTD MTLDGITSPA ELFHLESGLI 360
PDVIFFYRSN DVTQSCSSGR STTIRVRCSP QKTVPGLSL L PGTCSDGTCD GCFHFLWES 420
AAACPLCSVA DYHAI VSSCV AGIQKTTYVW REPKLCSGSI SLPEQRVTIC KTIIDFWLVKG 480
ISAGTCTAIL LTVLTCYFWK KNQKLEYKYS KLVMNATLKD CDLPADSCA IMEGEDVEDD 540
LIFTSKKSLF GKIKSFTSQ PAPVTISLSE DS 572

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Seq ID NO: C431 Protein Sequence
Protein Accession #: NP_004855.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MPGQELRTVN GSQMLLVLLV LSWLPHGGAL SLAEASRAS FPGPSELHSED SRFRELKRY 60
EDLLTLRLAN QSWEDNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLPASRL 120
HRLFLRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPFSQSDQLL AESSSARPQL 180
ELHLRPQAA RRRRARARNG DDCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC 240
IGACPSQFRA ANMHAQIKTS LHRLKPDTEP APCCVPASYN PMVLIQKTD T GVS LQTYDDL 300
LAKDCHCI

```

Seq ID NO: C433 Protein Sequence
Protein Accession #: NP_443090.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MEDPSGAREP RARPRERDPG RRPHPDQGR T HDRPRDRPGD PRKRSSDGN RRRDGD RDPK 60
RDQERDGNRD RNRDRERERE RERDPRDGR RDTHRDAGPR AGEHGVWEKP RQSRTRD GAR 120
GLTWDAAPP GPAPWEAPEP PQPQKGDGP RRRPESEPPS ERYLPSTPRP GREVEYYQS 180
EAEGLLECHK CKYLC TGRAC CQMLEVLLNL LILACSSVSY SSTGGYTGIT SLGGIYYQF 240
GGAYSGFDGA DGEKAQQLDV QFYQLKLP MV TVAMACSGAL TALCCLFVAM GVL RVPWHCP 300
LLLVT EGLLD MLIAGGYIPA LYFYFHYLSA AYGPSVCKER QALYQSKGYS GFGCSFHGAD 360
IGAGIFAALG I VV FALGAVL AIKGYRKVRK LKEKPAEMFE F 401

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Seq ID NO: C435 Protein Sequence
Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
MGAAGRQDFL FKAMLTISWL TLTCTPGATS TVAAGCPDQS PELQPWNPGH DQDHHVHIGQ 60
GKTLTLTSSA TVYSIHISEG GKLVIKDHDE PIVLRTRHIL IDNGGELHAG SALCPFGGNF 120
TIILYGRADE GIQDPFYYGL KYIGVGKGA LELHGQKKLS WTLFNKTLHP GGMAEGGYFF 180
ERSWGHGRV VHVLDPKSGT VIHSDRFDY RSKKESERLV QYLNVPDGR ILSVAVNDEG 240
SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLT VKGNPSS SVEDHIEYHG HRGSAARVF 300
KLFTHEGEY FNVLSSEWV QDVEWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID 360
IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYRVR FLCGKPV RPK LTVTIDTNVN 420
STILNLEDNV QSWKPGDTLV IASTDYSMYQ ABEFQVLP CR SCAPNQVKA GKPMY LHIGE 480
EIDGVMRAE VGLLSRN IIV MGEMEDKCYP YRNHICNFFD FDTFGGHKIF ALGFKAHLE 540
GTE LKHMGOQ LVGQYPIHFE LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI 600
KDVVGYN SLG HCFPTEDGPE ERNTFDHC LG LLVKS GTLLP SDRDSKMCKM ITEDSYPGYI 660
PKPRQDCNAV STFWMANPNN NLINCAAAGS EETGFWFIFH HVPTGPSVGM YSPGYSEHIP 720

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LGKFYNNRAH	SNYRAGMIID	NGVKTTEASA	KDKRPFLSII	SARYSPHQDA	DPLKPREPAI	780
IRHFIAYKNQ	DHGAWLRGGD	VWLDSCHFRG	EAQEGFLTG	MKAGGILLGG	DEAASGMAQG	840
FSPPCRCLLK	LVTGSEFFAH	VSLAHS				866

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein
5 incorporated by reference as if each individual publication, accession number, or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1 1. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80%
3 identical to a sequence as described in Tables 2A-80 in a biological sample from said patient,
4 thereby determining the presence or absence of said pathological cell.

1 2. The method of Claim 1, wherein:

- 2 a) said pathology is described in Table 1, including a cancer; and/or
- 3 b) said biological sample comprises isolated nucleic acids.

1 3. The method of Claim 1, wherein said biological sample is tissue from an organ
2 which is affected by said pathology of Table 1, including a cancer.

1 4. The method of Claim 2, wherein said nucleic acids are mRNA

1 5. The method of Claim 2:

- 2 a) further comprising a step of amplifying nucleic acids before said step of detecting
- 3 said nucleic acid; or
- 4 b) where said detecting is of a protein encoded by said nucleic acid.

1 6. The method of Claim 1, wherein said nucleic acid comprises a sequence as
2 described in Tables 2A-80.

1 7. The method of Claim 2, wherein:

- 2 a) said detecting step is carried out by:
 - 3 i) using a labeled nucleic acid probe;
 - 4 ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence
 - 5 as described in Tables 2A-80; or
 - 6 iii) detecting a polypeptide encoded by said nucleic acid; or
- 7 b) said patient is:
 - 8 i) undergoing a therapeutic regimen to treat said pathology of Table 1; or
 - 9 ii) is suspected of having said pathology or cancer.

1 8. An isolated nucleic acid molecule comprising a sequence as described in
2 Tables 2A-80.

- 1 9. The nucleic acid molecule of Claim 8, which is labeled.
- 1 10. An expression vector comprising the nucleic acid of Claim 8.
- 1 11. A host cell comprising the expression vector of Claim 10.
- 1 12. An isolated polypeptide which is encoded by a nucleic acid molecule
2 comprising a sequence as described in Tables 2A-80.
- 1 13. An antibody that specifically binds a polypeptide of Claim 12.
- 1 14. The antibody of Claim 13:
2 a) conjugated to an effector component;
3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a
4 cytotoxic chemical;
5 c) which is an antibody fragment; or
6 d) which is a humanized antibody.
- 1 15. A method for specifically targeting a compound to a pathological cell in a
2 patient, said method comprising administering to said patient an antibody of Claim 13,
3 thereby providing said targetting.
- 1 16. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising contacting a biological sample with an antibody of Claim 13.
- 1 17. The method of Claim 16, wherein:
2 a) said antibody is conjugated to:
3 i) an effector component; or
4 ii) a fluorescent label; or
5 b) said biological sample is a blood, serum, urine, or stool sample.
- 1 18. A method for identifying a compound that modulates a pathology-associated
2 polypeptide, said method comprising the steps of:

- 3 a) contacting said compound with a pathology-associated polypeptide, said
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence
5 at least 80% identical to a sequence as described in Tables 2A-80; and
6 b) determining the functional effect of said compound upon said polypeptide.

1 19. A drug screening assay comprising the steps of:

- 2 a) administering a test compound to a mammal having a pathology of Table 1 or a
3 cell isolated therefrom; and
4 b) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as described in
6 Tables 2A-80 in a treated cell or mammal with the level of gene expression of said
7 polynucleotide in a control cell or mammal, wherein a test compound that
8 modulates said level of expression of the polynucleotide is a candidate for the
9 treatment of said pathology.
10

(19) World Intellectual Property
Organization
International Bureau



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C07H 21/02, 21/04

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60/350,666	13 November 2001 (13.11.2001)	US
60/332,464	21 November 2001 (21.11.2001)	US
60/334,393	29 November 2001 (29.11.2001)	US
60/335,394	3 December 2001 (03.12.2001)	US
60/340,376	14 December 2001 (14.12.2001)	US
60/347,211	8 January 2002 (08.01.2002)	US
60/347,349	10 January 2002 (10.01.2002)	US
60/355,250	8 February 2002 (08.02.2002)	US
60/356,714	13 February 2002 (13.02.2002)	US
60/359,077	20 February 2002 (20.02.2002)	US
60/368,809	29 March 2002 (29.03.2002)	US
60/370,110	4 April 2002 (04.04.2002)	US
60/372,246	12 April 2002 (12.04.2002)	US
60/386,614	5 June 2002 (05.06.2002)	US
60/396,839	16 July 2002 (16.07.2002)	US
60/397,775	22 July 2002 (22.07.2002)	US
60/397,845	22 July 2002 (22.07.2002)	US
60/409,450	9 September 2002 (09.09.2002)	US

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Richard [US/US]; 22643 Woodridge Court, Cupertino, CA 95014 (US). **WATSON, Susan, R.** [GB/US]; 805 Balra Drive, El Cerrito, CA 94530 (US). **WILSON, Keith, E.** [US/US]; 219 Jeter Street, Redwood City, CA 94062 (US). **ZLOTNIK, Albert** [US/US]; 507 Alger Drive, Palo Alto, CA 94306 (US).

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:

— of inventorship (Rule 4.17(iv)) for US only

Published:

— with international search report
— before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

(88) Date of publication of the international search report:
28 October 2004

(15) Information about Correction:

Previous Correction:

see PCT Gazette No. 42/2003 of 16 October 2003, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



WO 2003/042661 A3

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; C07H 21/02, 21/04

US CL : 435/6; 536/23.1, 24.3

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6; 536/23.1, 24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
WEST, PubMed

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SATO, H. et al., Cloning and Expression of a Plasma Membrane Cystine/Glutamate Exchange Transporter Composed of Two Distinct Proteins, J. Biol. Chem. 23 April 1999, Vol. 247, No. 17, pp. 11455-11458.	1-7
A	KIM, J. Y. et al., Human cystine/glutamate transporter: cDNA cloning and upregulation by oxidative stress in glioma cells, B.B. Acta. June 2001, Vol. 1512, pp. 335-344.	1-7

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T"

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&"

document member of the same patent family

Date of the actual completion of the international search

04 August 2004(04.08.2004)

Date of mailing of the international search report

13 SEP 2004

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US
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P.O. Box 1450
Alexandria, Virginia 22313-1450

Facsimile No. (703) 872-9306

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Teresa Strzelecka

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T. Roberts for

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7, SEQ ID NO: 19

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

PCT/US02/36810

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-7, drawn to a special technical feature of a method for determining presence or absence of a pathological cell in a patient, said method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from said patient, thereby determining the presence or absence of said pathological cell.

Group II, claim(s) 8-11, drawn to a special technical feature of an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, expression vector comprising the nucleic acid and a host cell comprising the expression vector.

Group III, claim(s) 12, drawn to a special technical feature of an isolated polypeptide which is encoded by an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80.

Group IV, claim(s) 13, 14, drawn to a special technical feature of an antibody which specifically binds to polypeptide of claim 12.

Group V, claim(s) 15, drawn to a special technical feature of a method for specifically targeting a compound to a pathological cell in a patient, comprising administering to a patient an antibody of claim 13.

Group VI, claim(s) 16, 17, drawn to a special technical feature of a method for determining the presence or absence of a pathological cell in a patient, comprising contacting a biological sample with an antibody of claim 13.

Group VII, claim(s) 18, drawn to a special technical feature of a method for identifying a compound that modulates a pathology-associated polypeptide by contacting the compound with a pathology-associated polypeptide encoded by a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 and determining the functional effect of the compound on the polypeptide.

Group VIII, claim(s) 19, drawn to a special technical feature of a drug screening assay comprising the steps of: administering a test compound to a mammal having pathology of Table 1 or a cell isolated therefrom; comparing the level of gene expression of a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal.

The inventions listed as Groups I-VIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: claim 8 is anticipated by a sequence with accession No. BE440042 (Table 2A, first entry) (July 25, 2000), therefore there is no contribution of claim 8 over prior art.

CORRECTED VERSION

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International Bureau



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60/335,394	3 December 2001 (03.12.2001)	US
60/340,376	14 December 2001 (14.12.2001)	US
60/347,211	8 January 2002 (08.01.2002)	US
60/347,349	10 January 2002 (10.01.2002)	US
60/355,250	8 February 2002 (08.02.2002)	US
60/356,714	13 February 2002 (13.02.2002)	US
60/359,077	20 February 2002 (20.02.2002)	US
60/368,809	29 March 2002 (29.03.2002)	US
60/370,110	4 April 2002 (04.04.2002)	US
60/372,246	12 April 2002 (12.04.2002)	US
60/386,614	5 June 2002 (05.06.2002)	US
60/396,839	16 July 2002 (16.07.2002)	US
60/397,775	22 July 2002 (22.07.2002)	US
60/397,845	22 July 2002 (22.07.2002)	US
60/409,450	9 September 2002 (09.09.2002)	US

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(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



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